

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2005, 13:20:55 ; Search time 12298 Seconds

(without alignments)
11690.244 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967
Sequence: 1 atgcgtgaagcttccttca.....ctcgtgcttattattacg 2967

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2077.2	70.0	2913	6	AX814112 Sequence
2	2077.2	70.0	2913	6	AX816331 Sequence
3	1973.8	66.5	79178	8	AY303170 Solanum b
4	1860.8	63.4	3971	6	AX814116 Sequence
5	1880.8	63.4	3971	6	AX816335 Sequence
6	1880.8	63.4	3971	6	AX426261 Solanum b
7	1876.2	63.2	163635	8	AY303171 Solanum b
8	1832.2	61.8	3689	8	AY426264 Solanum c
9	1805.8	60.9	3592	6	AX814113 Sequence
10	1805.8	60.9	3592	6	AX816332 Sequence
11	1805.8	60.9	5191	6	AX816333 Sequence
12	1805.8	60.9	6824	6	AY336128 Solanum b
13	1805.8	60.9	7349	6	AX814114 Sequence
14	1805.8	60.9	7349	6	AY426259 Solanum b
15	1797.2	60.6	3641	8	AY426266 Solanum c
16	1786.2	60.2	3344	6	AY426265 Solanum c
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18	1771.6	59.7	3260	6	AX816334 Sequence
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20	1736.2	58.5	3899	6	AX814117 Sequence
21	1736.2	58.5	3899	6	AX816336 Sequence
22	1736.2	58.5	3899	8	AY426262 Solanum b
23	1736.2	58.5	79178	8	AY303170 Solanum b
24	1734.6	58.5	163635	8	AY303171 Solanum b
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28	592.6	20.0	120197	2	AC124216 Medicago
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ALIGNMENTS

RESULT 1	AX814112	2913 bp	DNA	linear	PAT 05-DEC-2003
LOCUS	AX814112	Sequence 35 from Patent EP1334979.			
DEFINITION	AX814112				
ACCESSION	AX814112				
VERSION	AX814112.1	GI:39103414			
KEYWORDS					
SOURCE					
ORGANISM	Solanum bulbocastanum				
	Solanum bulbocastanum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	asterids; lamiales; Solanales; Solanaceae; Solanum.				
REFERENCE					
1	van der Vossen, B.A. and Allefs, J.J.				
AUTHORS					
TITLE	Gene conferring resistance to phytophthora infestans (late-blight)				
JOURNAL	In solanaceae				
	Patent: EP 1334979-A 35 13-AUG-2003;				
	Kweek-en Researchbedrijf Agrico B.V. (NL)				
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7	CTTGATTTGATTTCTTGGTTTAAAGATGCTGAAAGCTTCAAGCAAGTTACTACA	420			
8	CTTGATTTGATTTCTTGGTTTAAAGATGCTGAAAGCTTCAAGCAAGTTACTACA	480			
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Db 1018 GGAAGAGAGATTTGAAAAAATATGATGCTGCTAGCAGGCTAAACCTTGAAGGT 1077
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AX816331			
LOCUS	AX816331	2913 bp	Linear
DEFINITION	Sequence 48 from Patent WO03066675.		PAT 09-DEC-2003
ACCESSION	AX816331		
VERSION	AX816331.1	GI:39646822	
KEYWORDS			
SOURCE			
ORGANISM	Solanum bulbocastanum		
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	Burkholderia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;		
	asterids; lamids; Solanales; Solanaceae; Solanum.		
REFERENCE			
AUTHORS	Allefs,J.V. and van der Vossen,E.A.		
TITLE	Gene conferring resistance to phytophthora infestans (late-blight)		
JOURNAL	in Solanaceae		
	Patent: WO 03066675-A 48 14-AUG-2003;		
FEATURES	Kweek- en Researchbedrijf Agrico B.V. (NL)		
source	Location/Qualifiers		
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ORIGIN			
Query Match	70.0%;	Score 2077.2;	DB 6; Length 2913;
Best Local Similarity	83.5%;	Pred. No. 0;	

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QY	361	GCAGCGGACGAATTAAGTTCAATTGAGTGAAGAAGCACTATGAGACCAAGTTCTACA	420							
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Db	418	CGGAAACAGGTTCTGATTTAACCGAACCGCAGGTTATGGAAGAGCAAGAAAGAAAT	477							
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Db	718	GACTTGGCTCCACTTCAAAAGAAAGCTTCAGAGTGTGCTGAATGAAAAAGATACTGGCT	777							
QY	778	GCTTGAATGATGTTTGGAAATGAAGATCAAGATTAAGTGGGCTAAGTGAACAATCTCTG	837							
Db	778	GCTTGAATGATGTTTGGAAATGAAGATCAAGAGTGGGCTAATTTAAGAGCAGTCTTG	837							
QY	838	AAGGTGAGCAAGTGGGACTTCTGTTCTTAAACACTACTCGTCTTGAAAAAGTTGATATCA	897							
Db	838	AAGGTGAGCAATGTTGGTCTTCTGTTCTTAAACACTACTCGTCTTGAAAAAGTTGATATCA	897							
QY	898	ATTATGGGAACATTGCAACCATATGAATCTGATCTCAATCTGATCAAGAAATGTTGGTGG	957							
Db	898	ATTATGGGAACATTGCAACCATATGAATCTGATCTCAATCTGATCAAGAAATGTTGGTGG	957							
QY	958	TTGTTTCATGCAAGTGCATTTGGGACACCAAGAAATAAATCTTAATCTTTGTCATC	1017							
Db	958	TTGTTTCATGCAAGTGCATTTGGGACACCAAGAAATAAATCTTAATCTTTGTCATC	1017							
QY	1018	GGAAGAGGATTTGGAATAAATGATGATGCTCTAGACGCTAAACCTTGGAGGT	1077							
Db	1018	GGAAGAGGATTTGGAATAAATGATGATGCTCTAGACGCTAAACCTTGGAGGT	1077							

QY	1078	ATTTCGCGCTTTAAGAGAGAAAGAACAGTGGGAAACATGTGAGAGATGTGAAGTTTGG	1137
Db	1078	ATTTCGCGCTTTAAGAGAGAAAGAAAGAGATGGGAAACATGTGAGAGACAGTCCGATTTTGG	1137
QY	1138	AAATTGCGCTCAAGAAAGAAAGTTCTATTCTGCGCTGGCCGTGAGCTTAGTTACATCAACCTT	1197
Db	1138	AAATTGCGCTCAAGATGAAAGTTCTATTCTGCGCTGGCCGTGAGGCTTAGTTACATCAACCTT	1197
QY	1198	CCACTTGATTTGAGACATGCTTTTACATATTGTGCGATATTCCAAAGATACCGAAATG	1257
Db	1198	CCACTTGATTTTAAACAAATGCTTTGCGAATTGTGGGAGTTCCCAAAGATGCCAAATG	1257
QY	1258	GAAGAAAGGAAATCTATCTCTCGTGGATGGGACATGGTTTTATTATCGAAGGAAC	1317
Db	1258	GAAGAAAGAAAGCTATCTCTCTCGATGGGCGATGGTTTTCTTTATCAAAGGAAC	1317
QY	1318	TTGAGACTAGAGAAATGTAGTAAATGATGAATGATGATTAATTACTTGAGGCTCTTCTTC	1377
Db	1318	ATGGAGCTAGAGAGATGGGGCGATGAAATGTAAGAAAGATTAATCTTGAGGCTCTTTTTC	1377
QY	1378	CAAGGATTTGAAGTTAAATCTGTGTCAACCTTATTTCAAGATGCATGTCTCATTCATGAT	1437
Db	1378	CAAGGATTTGAAGTTAAAGATGATTAACCTTATTTCAGAGCATGATCTCATCCATGAT	1437
QY	1438	CTGGCAACATCTCTATTTCGGCAAGCACATCAAGCAGCATATCCGAGAAATTAATGTA	1497
Db	1438	TTGGCAACATCTCTGTTTTTCAGCAAAACACATCAAGCAGCATATCCGTGAATTAATTA	1497
QY	1498	GAAATTTACATACATATATATGTCCTCATTTGGTTTCACTAAAGTGATCTTCTACTCTT	1557
Db	1498	CACAGATTAACAACATATATGTCCTCATTTGGTTTCCCAAGTGATGTTTTTTTATCACTCTT	1557
QY	1558	TCCCACTTGCAAGAGTTTGTCTCGTGGAGGGTGCTTATCTAAGTGAATPAACCTTAAG	1617
Db	1558	CCCCCTTGAAAAAGTTTATCTCGTTAAGAGTCTTATCTAGGTAAATTGCACTTTAAT	1617
QY	1618	CAGTTACCGTCTTCCATTGAGATCTAGATCTAGACATTTAAGATACCTAACTTGTCTGGCAAT	1677
Db	1618	AAGTTACCATCTTCCATTGAGATCTAGTACATTTAAGATACCTTGAACGTATAGGC---	1674
QY	1678	ACTAGTATCGTAGCTTCCAAACCAAGTTATGCAAGCTTCAAAAATCTGCGACCTCTGAT	1737
Db	1675	AGTGCGATGCTATGCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTGCAACCTCTTGAT	1734
QY	1738	CTACATGCGTGTCACTCACTTGTGTTTGGCCAAAGAAACAAAGCAAACTTGTAAGCTT	1797
Db	1735	CTACAAATTTGCAACCAAGCTTGTGTTTGGCCAAAGAAACAAAGTAACTTGTAAGCTT	1794
QY	1798	GGAATCTTTTACTTGATGTGATGCAATGTGACTTTGTATGTGCACCAAGATAGATCA	1854
Db	1858	TTGACATGCGCTTAAAGCTTAAGTAAAGTTTGTGTGGGAAATTCAGAAAGAAAGTTTGCA	1917
QY	1855	TTGACATGCGCTTAAAGCTTAAGTAAAGTTTGTGTGGGAAATTCAGAAAGAAAGTTTCA	1911
Db	1918	CTTGAGTAAATTAAGAACTGAACTCTATAGTCTCAATTGAATCAAGCATCTTGAGAGA	1977
QY	1912	CTTGAGTAAATTAAGAACTGAAATCTCTATAGTCTCAATTGAATCTCGCATCTTGAGAGA	1971
QY	1978	GTAAGAAATGATGATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAAGAAATCTGACTTC	2037
Db	1972	GTAAGAAATGATGATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAAGAAATCTGCAATTC	2031
QY	2038	TTAAGCATGAAATGGGATGACGATGAACGTCAACGTATATATGATCAGAAAAAGTTGGA	2097
Db	2032	TTAAGCATGATGATGAAATTAACCTTTGGAC---CATATATATATGAAATCAAGAAAGTTTAA	2088
QY	2098	GTCGTTGAAGCTCTCAAAACACACTCCAAATCTGATCTTTGTTAACAATCAAGGCGCTTGAGA	2157
Db	2089	GTCGTTGAAGCGCTCTCAAAACACACTCCAAATCTGATCTTTGTTAATAATCTATGCGCTTGAGA	2148

QY	2156	GGAAATCCGCTCCCGAGCTGGATGAATACACAGTTTGGAAAATGTTGCTCTAATTGAA	2217
Db	2149	GGAAATCCATCTCCAGAGTGGATGAATACACAGATTGGAAAAAATTTGCTTAATCTA	2208
QY	2218	ATCATCAGTTGCAAAAACCTGCTCAATGCTTACCAACCTTTGGTGAAGTCCCTTGTCTAAA	2277
Db	2209	ATTAGCACTTCAGAAACTGCTCAATGCTTACCAACCTTTGGTGAATGCTTGTCTAGAA	2268
QY	2278	AGCTTAGAGTTGTGAGAGGGGGGTCTGCGGAAGTGGATATGTTG-----	2320
Db	2269	AGCTTAGAGTTTACACTGGGGGTCTGCGGAGTGTGAGATATGTTGAAAGATGGATATTGAT	2328
QY	2321	----ATTCTGATTCCTTACAAAGAAAGAGTTTCCATCTCTGAGAAAACTTAATATACG	2376
Db	2329	GTTCACTTCTGATTCCTCCACAAAGAAATAGTTTCCATCTCTGAGAAACTTGATATATGG	2388
QY	2377	GAATTTGGTAACTCGAAAGATTTGCTGAAAAAGAGAGAGAGCAATGCCCTGTGCTT	2436
Db	2389	GACTTTGGTAGTCTGAAAGGATTTGCTGAAAAAGAGAGAGAGCAATGCCCTGTGCTT	2448
QY	2437	GAAGAGATAGAGATTTAATATGTTGCCCTAATGTTGTTATTTCCAAACCTTTCTTCTGCAAG	2496
Db	2449	GAAAGAGATAGATTAATTCACAGATGCC-----TTTCTGACCCCTTCT-----	2490
QY	2497	AAATTGGATAGTAGGGGACAAGTACAGATGCAATAGGTTTCAAGTCCATATCTAATCTTC	2556
Db	2491	-----TCTAATCTT	2499
QY	2557	ATGAGCTCTTACTTCCTCCCTCCAAATTCGCTATPACAAAGAAAGATCTTCACTCCAGAGAG	2616
Db	2500	AGGAGCTCTTACTTCCTCCCTCCAAATTTGCTATPATAAGATAGCTACTTCATCTCCAGAGAG	2559
QY	2617	ATGTTCAAAAGCCCTGAGAAATCTCAAAATCTTGAATATCTCTTTTACTTCAATCTTAAA	2676
Db	2560	ATGTTCAAAACCCTGAGAAATCTCAAAATCTTGAATATCTCTGAGCAATATCTTCAAA	2619
QY	2677	GAGCTGCTTACAGAGCTGGCTAGTCTCAATGCTTTAAGATCTGAAATTCATAGTTGT	2736
Db	2620	GAGCTGCTTACAGAGCTTGGCTAGTCTGAATGCTTTGAAAAAGTCTAAAAATTCATTTGTGT	2679
QY	2737	TATGCACTAAGAGTCTCCCGGAGAAAGTGTGAAGAGTTTAATTTCACTCACACAGTTA	2796
Db	2680	TGGGCACTAAGAGTCTCCCTGAGAAAGGCTGGAAGGTTTATCTTCACTCACAGAGTTA	2739
QY	2797	TCCATTAACATACAGTGAATATGCTACATGTTTACCGGAGAGGATTTGAGACCTTACAGGC	2856
Db	2740	TTTGTGTAACACTGTAAATGCTTAAATGTTTACAGAGGAGATTTGAGACCTTACAAAC	2799
QY	2857	CTCACAAAATTTATCAGTTGAGTTTGTCTCAACACTGACCAGCGGTGTGAGAGGGAGATA	2916
Db	2800	CTCACAAGTTTAAAAATTTGGGGAGTGTCCACAACTGATCAACCGGTGTGAGAGGGAGATA	2859
QY	2917	GGAGAAAGCTGGTACAAAATTTGCTCAATTTCTCGTGTGTTAATTTAT	2964
Db	2860	GGAGAAAGCTGGCAAAAATTTCTCAATTTCTCAATTTGTAATTTAT	2907

RESULT 3	AY303170/c	LOCUS	79178 bp	DNA	linear	PLN 15-AUG-2003
DEFINITION		<i>Solanum bulbocastanum</i>	chromosome 8	clone CB3A14,	complete sequence.	
ACCESSION	AY303170					
VERSION	AY303170.1	GI:32470628				
KEYWORDS	HTG.					
SOURCE	<i>Solanum bulbocastanum</i>					
ORGANISM	<i>Solanum bulbocastanum</i>					
REFERENCE						
AUTHORS	Song, J., Bradeen, J.M., Neese, S.K., Raasch, J.A., Wielgus, S.M., Haberland, G.T., Liu, J., Kuang, H., Austin-Phillips, S., Buell, C.R., Helgeson, J.P. and Jiang, J.					

TITLE Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)

PUBMED 12872003

REFERENCE 2 (bases 1 to 79178)

AUTHORS Song, J., Braeden, J.M., Naess, K.S., Raasch, J.A., Wielgus, S.M., Haberlach, G.T., Kuang, H., Austin-Phillips, S., Helgeson, J.P., Liu, J., Tallon, L.J., Zaborcky, J., Buell, C.R. and Jiang, J.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-2003) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

COMMENT Address all correspondence to: rbuelli@tigr.org. Clone CB3A14 is from Solanum bulbocastanum chromosome 8. The orientation of the sequence is from SP6 to T7 end of the clone. Genes were identified by a combination of several methods: Gene prediction programs including GenScan+ (Chris Burge, <http://CCK-081.mtc.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and GenesPllicer (Mhaela Perlea and Steven Salzberg, [contact mperlea@tigr.org](http://www.tigr.org/cdb/tgi.shtml)), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/cdb/tgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Location/Qualifiers

FEATURES

SOURCE

1. 79178

/organism="Solanum bulbocastanum"

/mol_type="genomic DNA"

/db_xref="taxon:147425"

/chromosome="8"

/clone="CB3A14"

gene

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/note="similar to growth regulating factor 1 GB:AAE17567 GI:6573149 (Oryza sativa); EST BE922572 from this gene"

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/product="putative growth-regulating factor"

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/codon_start=1

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repeat_region

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repeat_region

5478..5502

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repeat_region

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repeat_region

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gene

/locus_tag="CB3A14.12"

/note="highly similar to Mob1 like protein GB:CAC41010 GI:19309913 (Medicago sativa subsp. falcata); contains Pfam profile PF03637 (Mob1 phocein family); EST B6589654,

mRNA

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/db_xref="GI:32470635"

/translation="MSLFGLRNQRTERPKKSAFGSKAGQARHIDATLGSGNLR EA VRLPEGRDINEMLVNTVDENQYNLLYGLTECTECNCTMTAGPYEYRMDGVQ IKKPIEVSAPYKVEYLMNDIETOLDDESLFPGAGAPSPNFKDVVKTIFRLRPVYA HIYSHRQKIVSLSEAHNLTCFHFILFTEPGLIDIKKELAPQGEIIESILIVY"

16833..16854

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/note="contains Pfam profile PF04819 (plant viral response family)"

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22668..22692

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22954..23034

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23085..23140

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23319..23371

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23685..23705

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23772..23821

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24167..24292

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24312..24369

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/note="similar to transposase related protein GB:CB51950 GI:5690095 (Zea mays)"

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/locus_tag="CB3A14.3"

/product="putative transposase-related protein"

complement(join(24447..24871,24982..25195,25412..25663,25874..26005,26221..26418,26711..26791))

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OY	1086	CTTTAAGAGAAAGAAAGCACTGGGAAACATGTGAGATATGTGATTTGGAAATTTGCC	1145
Db	2114	CTTCAAGAGAGAAAGAAAGGAAATGGGAAACATGTGAGACAGTCCGATTTTGGAAATTTGCC	2173
OY	1146	TCAGAAGAAAGTCTTATTTCTGCTCCCTGAGACTTATGTTACATCACTTCCACTTGA	1205
Db	2174	TCAGATGAAAGTCTTATTTCTGCTCCCTGAGGCTTATGTTACATCACTTCCACTTGA	2233
OY	1206	TTTGAGACAAATCCTTACATATTTGGCAGTATTTCCCAAGGATACCGAAATGGAAAAAGG	1265
Db	2234	TTTGAGACAAATCCTTGTGTATTTGGCGGTATTTCCCAAGGACACCAAAAATGGCAAAAGA	2293
OY	1266	AAATCTAATCTCTCTGTGATGGCAGATGGTTTATTTTATCGAAAGAAACTTGAAGCT	1325
Db	2294	AAATCTAATCTGTTTTTGGATGGCAGATGGTTTTCTTTTATCGAAGAAATTTGGAGCT	2353
OY	1326	AGAGAAATGAGTAAATGAAAGTATGGAAATTAATTAATTAGTAGTCTTTCTTCCAAAGAT	1385
Db	2354	AGAGATGTAGGTAAATGAAAGTATGAAATTAATTAATTAAGTGGTCTTTCTTCCAAAGAT	2413
OY	1386	TGAATTAATCTGGTCAAACTTATTTCAAGTGCATGTCATTCATGATCTGGAAC	1445
Db	2414	TGAATTAATCTGTTAAATCTTATTTCAAGTGCATGTCATTCATGATTTGGCTAC	2473
OY	1446	ATCTCTATTTTTCGAGACACATCAAGCAGCAATATCCGAGAAATTAATGTAGAAATTA	1505
Db	2474	ATCTCTGTTTTTCAGCAAAACATCAAGCAGCAATATTCGAAATTAATGTCTAATTAATGA	2533
OY	1506	CATACATATGATATGTCATTTGGTTTCACTAAAGTGTATCTTCAATCTTTCCCACTT	1565
Db	2534	TGATATATATGATATGATTTGGTTTGCAGAGTGTATCTTCAATCTTTCCCACTT	2593
OY	1566	GCAGAAGTTTGTCTCGTTGAGGATGCTTAATCTAATGTCACATAAATCTTAAGCAGTTACC	1625
Db	2594	GCAAAAGTTTGTCTCATTAAGGATGCTTAATCTAAGAAATCTGAACCTAATCAATTAACC	2653
OY	1626	GTCCTTCATTTGGAATCTTAATGCAATTTAAGTACTTAACTTGTCTGTGGCAATACTAGAT	1685
Db	2654	ATCTTCAATTTGGAATCTTAATGCAATTTAAGTACTTAACTTGTCTGTGGCAATTTAGAAT	2713
OY	1686	TCGTATGCTTCCAAACAGTTATCAAGCTTCAAAATCTGACAGCTCTGTATCTACATGG	1745
Db	2714	TCGTATCTTCCAAAGAGTATTAATGACAGCTTCAAAATCTGACAGCTCTGTATCTACATTA	2773
OY	1746	CTGTCAATTCATTTGTTGTTTTCGCAAAAGAAACAGCAAACTTGTAGTCTTGGAAATCT	1805
Db	2774	TTGGACATCTTCTTCTTGTGTTTTCGCAAAACAAACAGTAAACTTGTAGTCTTGGAAATCT	2833
OY	1806	TTTACTTGATGGTTGCTATGGAATGACTGTATAGCCACCAAGATATGAGATCTTTGACATG	1865
Db	2834	TTTACTTGATG--GCTGTTCAATTTAGCTCAACCCACCAAGATATGAGATTTGACATG	2890
OY	1866	CCTTAAAGCTCTTAAGTATTTGTGTGGGAATTCAGAAAGAAAGTTGTCAACTTGGTGA	1925
Db	2891	CCTTAAAGCTCTTAAGTATTTGTGTATTTGGCA--AAGAAAGGTTATCAACTTGGTGA	2947
OY	1926	ATTACGAAACCTGAATCTCTATAGCTCAATTTGAATTAAGCATCTTGAAGGTGAAGAA	1985
Db	2948	ACTTAAAAAATCTTAATCTTAATGCTCAATTTCAATCAAAAATCTTGAAGGTGAAGAA	3007
OY	1986	TGATATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCATCTTTAAGCAT	2045
Db	3008	AGATATGAGATGCAAAAGAAAGCTAATTTATCTGCTAAAGCAAACTTGCACTTTATAGCT	3067
OY	2046	GAAATGGGATGACATGACGTCCAGTATATATGATACGAAAAAGTTGAAGTGGCTTGA	2105
Db	3068	GAGTTGGGACCTTGATGAA--ACATATATATGATTA-----GAAGTCTTGA	3115
OY	2106	AGCTCTCAAAACACATCTCAATCTGACTTGTATTAACATCAAGGGCTTGAGAGAAATCCG	2165
Db	3116	AGCTCTCAAAACACATCTCAATCTGAATATTTAGAAATCAATAGGCTTGAGAGAAATCCG	3175

QY	2166	TCTCCGAGACTGAGATGATCACTCAGTTTGAAAAATGTTGCTCTAATTGGAATCATCAG	2222
Db	3176	TCTCCGAGATTGGATGAAATCAATCAGTTTGAAAAATGTTGCTCTAATTGGAATTTAGAG	3233
QY	2226	TTGCAAAAACCTGCTCATGCTTACCAACCCCTTTGGTAGCTGCCTTGTCTAAAAAGCTAGA	2285
Db	3236	TTGTGAATAACCTGCATGCTTACCAACCCCTTTGGTAGCTGCCTTGTCTAGAAAAGCTAGA	3295
QY	2286	GTTGTGGAGGGGGGTCTGGGAAAGTGAGATGTTGATTCTGGATTTCCCTACAAGAAAG	2345
Db	3286	GTTACACACCGGGGTACGAGATGGAGATGTTGAAGATATATGTTATCTCTG---GAAG	3352
QY	2346	GTTTCATCTCTGAGAAAACTTAATATACGGCAATTTGTTAATCTGAAGGATTTGCTGAA	2405
Db	3353	GTTTCATCTCTGAGAAAACTTGTATATAGGCACTTTAGTATCTAATAAGGATTTGCTGAA	3412
QY	2406	AAAGAAAGAGAGAGACATATGCTCTGTGCTTGAAGAATAGATTAATATGTTCCCTAT	2465
Db	3413	AAAGAAAGAGAGAAAGCAATTCCTGTGCTTGAAGAATAGACATTTATCTGTGCTCCAT	3472
QY	2466	GTTTGTATTTCAAACCTTCTCTGTGCAAGAAATGATGTATGATGAGGAGCAAGTCAGA	2525
Db	3473	GTTTGTATTTCGACCCCTTCTCTGTGCAAGCAATTAAGTTATTTG----CGACAGA	3526
QY	2526	TGCATATAGTTTCACTTCATATCTAATCTCATGCTCTTACTTCCCTCCAAATTCGCTA	2585
Db	3527	TGCAACAGTTTGAAGTCCATATCTAATCTTAGGGCTCTTACTTCCCTGACATTACCA	3586
QY	2586	TAAACAAGAAAGATGCTTCACTCCCAAGAAAGATGTTCAAAAAGCTTGCAAAATCCAAATA	2645
Db	3587	TAAAGTGAAGACTACTCACCTCCAGAAGAGATGTTCAAAAAGCTTGCAAAATCCAAATA	3646
QY	2646	CTTGAATATCTCTTTTACTCTCAATCTTAAAGATGCTCCACAGCTGCTGATGTCAA	2705
Db	3647	CTTGAATATCTCTTTCTTTAGGATCTCAAGATGTGCTTACCAAGCTGCTGATGTCCAA	3706
QY	2706	TGCTTTGAAGCATCTGAAATTCATATGTTGTTATGCACTAGAGAGTCTCCCGAGAAAG	2765
Db	3707	TGCTTTGAAGAGTCTCAATTTGAATTTGTAAAGCACTAGAGAGTCTCCAGAGAAAG	3766
QY	2766	TGTGAAGAAGTTTAATTTCACTCAACAGTTATCATATACACTCTGGAATGCTACATG	2825
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QY	2826	TTTACCGAGAGGATTTGAGACACTTAACAGCCCTCACAAATTTATCATGTTAGTTTGTC	2885
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QY	2886	AACACTGGCCAAAGCGGTGTGAGAAAGGAATAGAGAGAACTGTGTACAAATTTGCTCAT	2945
Db	3887	AATAGTATTTCAACGGGTGTGAGAGAAATAGAGAAAGACTGTGCACAAATTTGCTCAT	3946
QY	2946	TCTCTGATGTTTATTTATTTAG 2967	
Db	3947	TCCATATTTGACTCTATATGAG 3968	

RESULT 5				
AX816335				
LOCUS	AX816335	3971 bp	DNA	linear
DEFINITION	Sequence 52 from Patent WO03066675.			
ACCESSION	AX816335			
VERSION	AX816335.1	GI:39646826		
KEYWORDS	.			
SOURCE	Solanum bulbocastanum			
ORGANISM	Solanum bulbocastanum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.			
REFERENCE	1			
AUTHORS	Allefs, J. J. and van der Vossen, E. A.			
TITLE	Gene conferring resistance to phytophthora infestans (late-blight) in solanaceae			

JOURNAL Patent: WO 0306675-A 52 14-AUG-2003;

Kweek- en Researchbedrijf Agrico B.V. (NL)

Location/Qualifiers

FEATURES 1. :3971

SOURCE /organism="Solanum bulbocastanum"

/mol_type="unassigned DNA"

/db_xref="taxon:147425"

misc_feature

1. :3971

/note="#RGC3-Dlb#"

ORIGIN

Query Match 63.4%; Score 1880.8; DB 6; Length 3971;

Best Local Similarity 85.5%; Pred. No. 0;

Matches 2173; Conservative 0; Mismatches 342; Indels 27; Gaps 6;

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Db	3947	TCCATATTTGACTATATATGAG 3968	
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LOCUS		Solanum bulbocastanum blight resistance protein RGA3 gene, complete	
DEFINITION			
ACCESSION	AY426261		
VERSION	AY426261.1	GI:39636739	
KEYWORDS			
SOURCE			
ORGANISM			
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		Solanum bulbocastanum	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
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REFERENCE		1 (bases 1 to 3971)	
AUTHORS		Van Der Vossen,E., Sikkema,A., Hekkert Bt.B.L., Gros,J.,	
		Stevens,P., Muskens,M., Wouters,D., Pereira,A., Stiekema,W. and	
		Allefs,S.	
TITLE		An ancient R gene from the wild potato species Solanum	
		bulbocastanum confers broad-spectrum resistance to Phytophthora	
		infestans in cultivated potato and tomato	
JOURNAL		Plant J. 36 (6), 867-882 (2003)	
PUBMED		14675451	
REFERENCE		2 (bases 1 to 3971)	
AUTHORS		van der Vossen,E. and Allefs,S.	
JOURNAL		Direct Submission	
TITLE		Submitted (03-OCT-2003) Bioscience, Plant Research International,	
		Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands	
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 163635)
Song,J., Bradeen,J.M., Naese,S.K., Raasch,J.A., Wielgus,S.M.,
Haberlach,G.T., Liu,J., Kuang,H., Austin-Phillips,S., Buell,C.R.,
Helgeson,J.P. and Jiang,J.
Gene RB cloned from Solanum bulbocastanum confers broad spectrum
resistance to potato late blight
Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)
2 (bases 1 to 163635)
Song,J., Bradeen,J.M., Naese,S.K., Raasch,J.A., Wielgus,S.M.,
Haberlach,G.T., Kuang,H., Austin-Phillips,S., Helgeson,J.P.,
Liu,J., Tallon,L.J., Zaborcky,J., Buell,C.R. and Jiang,J.
Direct Submission
Submitted (22-MAY-2003) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Address all correspondence to: rbuell@tigr.org
Clone 177013 is
from Solanum bulbocastanum chromosome 8. The orientation of the
sequence is from SP6 to T7 end of the clone. Genes were identified
by a combination of several methods: Gene prediction programs
including Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHM (Mark Borodovsky,
http://genemark.biology.gatech.edu/GeneMark/), and Gensplice
(Mahaeta Perlea and Steven Salzberg, contact mperlea@tigr.org),
searches of the complete sequence against a peptide database and
the plant EST database at TIGR (http://www.tigr.org/tdb/cgi.shcml).
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are
named after the database hits. Genes without significant peptide
similarity but with EST similarity are named as unknown proteins.
Genes without protein or EST similarity, that are predicted by more
than two gene prediction programs over most of their length are
annotated as hypothetical proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
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http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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QY 2946 TCCGCGTGGTTATTATTA 2966
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RESULT 8	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	REFERENCE AUTHORS	TITLE	JOURNAL.	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL.	FEATURES
AY426264	Solanum tuberosum blight resistance protein SH10 gene, partial cds		AY426264	GI:39636784	Solanum tuberosum (potato)	Van Der Vossen,E., Sikkema,A., Hekkert Bt,B.L., Gros,J., Stevens,P., Muskens,M., Wouters,D., Pereira,A., Stiekema,W. and Allefs,S. An ancient R gene from the wild potato species Solanum bulbocastanum confers broad-spectrum resistance to Phytophthora infestans in cultivated potato and tomato Plant J. 36 (6), 867-882 (2003) 14675451 2 (bases 1 to 3689) van der Vossen,E. and Sikkema,S. Direct Submission Submitted (03-OCT-2003) Bioscience, Plant Research International, Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands	Journal of Plant Pathology	14675451	van der Vossen,E. and Sikkema,S. Direct Submission Submitted (03-OCT-2003) Bioscience, Plant Research International, Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands	Location/Qualifiers 1..3689 /organism="Solanum tuberosum" /mol_type="genomic DNA" /db_xref="taxon:4113" /chromosome="VIII" /map="CT88-CT64" /note="SH83-92-488" join<L1.427,1271..>(3689) /product="Blight resistance protein SH10" join(1..427,1271..>(3689) /note="confers broad-spectrum resistance to Phytophthora infestans in potato and tomato" /codon_start=1 /product="Blight resistance protein SH10" /protein_id="BAR29074.1" /db_xref="GI:39636785" /translation="MAEAFIVLDINDVTSFLKELVLLRGFONEFORLSISTQIAV HKGADRKOLNDKPLENWLQKNATYEVDVIDEYTKATRFSQASGRVHPVIPFR LEAGDQDMKKINAIEBRKNFHLEKIIEQAARERGSVLTEPVGVRKPEDE IVKLINNVSADQLHSVLPILGWGSGKTLLQMVFENDRITETHFSKIWI CVSEPD EKLLKAIESIEGRPLGMDLAPOKLOELNGKRFEVLVDVWNEDOOKMANLR AVAKVASAPVATAATRLKEKVS IMGTLOPYELSNISORDCWLIFLOCAFGHEETNP NVALKERIKYKSGVPLAALKTIGTLRRKEREMEHARDSTINMLPOBERSITAL RSLYNHLPLDRCPAVCAVFPEDOTMEKELSLMWAGFFLLBEGLKPEDVGENVS KETCLSPFOELIENKAGKGYFKMHDLDLATSLSFASRTSSNIIRINVKGPYKXWS IGTEVASSYSPSLSQKFVSLRYNLNSHFELSISIDLVMRCLIDSSENSGISL PKOLCIOMIQTLDLNENCYSLSCPKEPKLSIRNFLPHGCDELNSMPRIISLTPL KITLKLCGIGKGGYOLGKLDVNYLGSIEITHLEKNVMMAKEANLSAKGNLSLI NMMSRRGHPIYESEEVRAVELALKPHPNLITISGRGPRPPMNASHLKVAVSTEI SOCKNCSCLPPEGELPCULKLELOKSAAVEYVDSGFPTRRRPESIRKLFIGEPMK GLUKGGEKPFVLERMTIFYCHMFVTYLLSSFRALTSLNHSHNEASTLSPEERTKS FANLKXTLSLTFVNTELPSLSLACLNALTYLETHSCSALESIPBGVKGLTSLTELEV YCCEMKLFPBEGIOHTALTSLDKLRCPOLIRKC"				

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RESULT 9
AX814113
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DEFINITION Sequence 36 from Patent EP1334979.
ACCESSION AX814113
VERSION AX814113.1 GI:39103415
KEYWORDS
SOURCE
ORGANISM Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS 1
TITLE van der Vossen, R.A. and Allefs, J.J.
JOURNAL Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
Patent: EP 1334979-A 36 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
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ORIGIN

Query Match 60.9%; Score 1805.8; DB 6; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;

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Db 1162 AGTAAAAATCTGATTAACCATGTTAGTATGCCCAACACTTCAGTCTCCCAATCT 1221
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ACCESSION AX816332
VERSION AX816332.1 GI:39646823
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Solanium bulbocastanum
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asterids; lamids; Solanales; Solanaceae; Solanium.
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Allefs, J. J. and van der Vossen, E. A.
Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
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ACCESSION AX816333
VERSION AX816333.1 GI:39646824
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
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AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
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RESULT 12
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 LOCUS Solanum bulbocastanum putative disease resistant protein RGA2 gene,
 DEFINITION complete cds.
 ACCESSION AY336128
 VERSION AY336128.1 GI:32693280
 KEYWORDS
 SOURCE
 ORGANISM
 Solanum bulbocastanum
 Solanum bulbocastanum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 (bases 1 to 6824)
 Song, J., Bradeen, J.M., Naess, K.S., Raasch, J.A., Wielgus, S.M.,
 Haberlach, G.T., Huang, H., Austin-Phillips, S., Helgeson, J.P.,
 Liu, J., Tallon, L.J., Zaborosky, J. and Buell, C.R.,
 Solanum bulbocastanum disease resistance gene RGA-2
 Proc. Natl. Acad. Sci. U.S.A. (2003) In press
 2 (bases 1 to 6824)
 Song, J., Bradeen, J.M., Naess, K.S., Raasch, J.A., Wielgus, S.M.,
 Haberlach, G.T., Huang, H., Austin-Phillips, S., Helgeson, J.P.,
 Liu, J., Tallon, L.J., Zaborosky, J. and Buell, C.R.

TITLE Direct Submission
 JOURNAL Submitted (02-JUL-2003) Department of Horticulture, University of
 Wisconsin-Madison, Madison, WI 53706, USA
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LOCUS AX814114 7349 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 37 from Patent EP134979.
ACCESSION AX814114
VERSION AX814114.1 GI:39103416
KEYWORDS
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1
AUTHORS van der Voessen, E.A. and Allefs, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
JOURNAL Patent: EP 1334979-A 37 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
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RESULT 14

AY426259 7349 bp DNA linear PLN 16-DEC-2003
 LOCUS Solanum bulbocastanum blight resistance protein RPI gene, complete
 DEFINITION cds.

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ACCESSION AY426259
VERSION AY426259.1 GI:39636704
KEYWORDS
SOURCE
ORGANISM Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanales; Solanum.
REFERENCE
AUTHORS Van Der Vossen, F., Sikkema, A., Hekkert, B., L., Gros, J.,
Stevens, P., Muskens, M., Mouters, D., Peirl, A., Sikkema, W. and
Allefs, S.
TITLE An ancient R gene from the wild potato species Solanum
bulbocastanum confers broad-spectrum resistance to Phytophthora
infestans in cultivated potato and tomato
Plant J. 36 (6), 867-882 (2003)
JOURNAL 14675451
PUBMED 2 (bases 1 to 7349)
AUTHORS van der Vossen, F. and Allefs, S.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
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ACCESSION AY426266
VERSION AY426266.1 GI:39636815
KEYWORDS

SOURCE Solanum tarijense
ORGANISM Solanum tarijense

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AUTHORS 1 (bases 1 to 3641)
Van Der Vossen, E., Sikkema, A., Hekkert B., L., Gros, J.,
Stevens, P., Mueken, M., Mouters, D., Pereira, A., Sikkema, W. and
Allefs, S.

TITLE An ancient R gene from the wild potato species Solanum
bulbosasanum confers broad-spectrum resistance to Phytophthora
infestans in cultivated potato and tomato
Plaut J. 36 (6), 867-882 (2003)

JOURNAL 2 (bases 1 to 3641)
PUBMED 14675451
AUTHORS van der Vossen, E. and Allefs, S.
TITLE Direct Submission

JOURNAL Submitted (03-OCT-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
FEATURES

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Query Match 60.6%; Score 1797.2; DB 8; Length 3641;
Best Local Similarity 84.6%; Pred. No. 0;
Matches 2116; Conservative 0; Mismatches 293; Indels 93; Gaps 5;

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Qy	2685	TACCAAGCTGGCTAGTCTCATGCTGTTGAAGCATCTGAAATATATATGTTATGCACT		2744
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Qy	2745	AGAGAGTCTCCCGAGGAAGGTGTGAAGGTTTAATTCACTCACACAGTTATTCATTAAC		2804
Db	3480	AGAGAGTATCCCGAGGAAGAGTGAAGGTTTAATCTCACTCACAGAGTTAATTGCCAA		3539
Qy	2805	ATACTGTGAATGCTACAAATGTTTACCAGAGGATTCAGCACTTAACAGCCTCACAA		2864
Db	3540	GTTCTCGAAGATGCTAAATAGTTTACCGAGGAGATGACACACTTAACAGCCTCACAA		3599
Qy	2865	TTTATCAGTTGAGTTTGCCAAACACTGGGCAAGCGGTGGA		2906
Db	3600	AGTTAAATTTGGGAGATGTCCAACTGATCAACGGGTGGA		3641

Search completed: April 16, 2005, 18:12:16
Job time : 12320 secs

XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a plant disease resistance polypeptide. The preferred plant is a
CC solanaceous plant that is potato. The resistance is to late blight
CC disease, caused by the fungus *Phytophthora infestans*. The invention is
CC useful for conferring pathogen resistance in plants using a *Solanum*
CC bulbocastanum late blight resistance gene. The present sequence is the S
XX bulbocastanum cDNA sequence of the invention.

Sequence 3193 BP; 1031 A; 543 C; 671 G; 948 T; 0 U; 0 Other;

Query Match 100.0%; Score 2967; DB 12; Length 3193;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCGTGAAGCTTCTTCAAGTCTGTTAGCAATCTGACTGTTTCAATCCAGGAGAA 60
DB 52 ATGGCTGAAGCTTCTTCAAGTCTGTTAGCAATCTGACTGTTTCAATCCAGGAGAA 111
QY 61 CTYGGATTGATCTTGTTTAAAGTAGTGTGAAAAGCTTCAAGGACGTTTACTTACA 120
DB 112 CTYGGATTGATCTTGTTTAAAGTAGTGTGAAAAGCTTCAAGGACGTTTACTTACA 171
QY 121 ATCCAACTGTGCTTGAAGATGCTCAGAAAGCAATTGAAAGACAAAGCAATGAAAT 180
DB 172 ATCCAACTGTGCTTGAAGATGCTCAGAAAGCAATTGAAAGACAAAGCAATGAAAT 231
QY 181 TGGTTCGAGAAACCTAATGCTGCTGCATATGAGGCTGATGACATCTTGAGAGATGAAA 240
DB 232 TGGTTCGAGAAACCTAATGCTGCTGCATATGAGGCTGATGACATCTTGAGAGATGAAA 291
QY 241 ACTGAGGACCAATTTAGACAGAGAGAAACAAATATGAGTGTATCATCCAAACGTTATC 300
DB 292 ACTGAGGACCAATTTAGACAGAGAGAAACAAATATGAGTGTATCATCCAAACGTTATC 351
QY 301 ACTTTTCTCAAGATTTGGAAAAAGATGAAAAAATTATGAGAAACCTAGATGTAAAT 360
DB 352 ACTTTTCTCAAGATTTGGAAAAAGATGAAAAAATTATGAGAAACCTAGATGTAAAT 411
QY 361 GCAGGGAACGAATTAAGTTTCAATTTGATGAAAGGACTATAGAGAGCAAGTTGTACA 420
DB 412 GCAGGGAACGAATTAAGTTTCAATTTGATGAAAGGACTATAGAGAGCAAGTTGTACA 471
QY 421 CGCCAAACAGGTTTGTTTTGAATGAACCAAGTTTATGAAAGACAAAGAAAGGAC 480
DB 472 CGCCAAACAGGTTTGTTTTGAATGAACCAAGTTTATGAAAGACAAAGAAAGGAC 531
QY 481 GAGATAGTGAATAATCTGATTAACCAATGTTAGCAATGCCCAACACTTCCAGTCTCCA 540
DB 532 GAGATAGTGAATAATCTGATTAACCAATGTTAGCAATGCCCAACACTTCCAGTCTCCA 591
QY 541 ATACTGGTATGGGGGACCTAGAAAGACACTCTTGCCCAATGGTCTTCAATGATCAG 600
DB 592 ATACTGGTATGGGGGACCTAGAAAGACACTCTTGCCCAATGGTCTTCAATGATCAG 651
QY 601 AGAGTAATATGACATTTCCATCCAAAATATGATTTGTGTCTCGAAGATTTTATGAG 660
DB 652 AGAGTAATATGACATTTCCATCCAAAATATGATTTGTGTCTCGAAGATTTTATGAG 711
QY 661 AAGAGTTGATTAAGGAAATTTGTGATCTTATTAAGAAAAAGTCACTTGGTGGATGAC 720
DB 712 AAGAGTTGATTAAGGAAATTTGTGATCTTATTAAGAAAAAGTCACTTGGTGGATGAC 771
QY 721 TTGGCTCACTTCAAAAGAGCTTCGGGACCTTGCTGATGGAAGAAAAATATTTGCTGTC 780
DB 772 TTGGCTCACTTCAAAAGAGCTTCGGGACCTTGCTGATGGAAGAAAAATATTTGCTGTC 831
QY 781 TTGATGATGTTTGAATGAAGATCAAGATTAAGTGGCTTAAGTTTAAACAAGCTTGAAG 840
DB 832 TTGATGATGTTTGAATGAAGATCAAGATTAAGTGGCTTAAGTTTAAACAAGCTTGAAG 891
QY 841 GTTGAAGCAAGTGGCGCTTCTGTTCTAACCACTACTGCTTGAAAAAGTTGATCAATT 900

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DB 892 GTTGAAGCAAGTGGCGCTTCTGTTCTAACCACTACTGCTTGAAGAGTTGATCAATT 951
QY 901 ATGGGAACATTGCAACCAATATGAATTTGTCATGAAGAAAGATTTGTTGTTTG 960
DB 952 ATGGGAACATTGCAACCAATATGAATTTGTCATGAAGAAAGATTTGTTGTTTG 1011
QY 961 TTCAATGCAAGTGCATTTGGGACCAAGAGAAATTAATCTTAATCTTTGGGCTATGGA 1020
DB 1012 TTCAATGCAAGTGCATTTGGGACCAAGAGAAATTAATCTTAATCTTTGGGCTATGGA 1071
QY 1021 AAGAGATTTGAAAAAATGTTGTGTGCTCTAGAGCTTAAACCTTGAGATATT 1080
DB 1072 AAGAGATTTGAAAAAATGTTGTGTGCTCTAGAGCTTAAACCTTGAGAGATTT 1131
QY 1081 TTGCGCTTTAAGAGAGAAAGACAGTGGGAAACATGTGAGAGATTAAGATTTGGAAA 1140
DB 1132 TTGCGCTTTAAGAGAGAAAGACAGTGGGAAACATGTGAGAGATTAAGATTTGGAAA 1191
QY 1141 TTGCTCAAGAGAAAGTTCTATTCCTGCTGCTGAGCTTGAATTCATCACTTCCA 1200
DB 1192 TTGCTCAAGAGAAAGTTCTATTCCTGCTGCTGAGCTTGAATTCATCACTTCCA 1251
QY 1201 CTGATTTGAGACAAATGCTTTACATATTTGTCAGATATTCCTCAAGAGATTCGA 1260
DB 1252 CTGATTTGAGACAAATGCTTTACATATTTGTCAGATATTCCTCAAGAGATTCGA 1311
QY 1261 AAGGGAATCTAATCTCTCTGAGATGCAATGTTTATTTTATGAAAGAACTTG 1320
DB 1312 AAGGGAATCTAATCTCTCTGAGATGCAATGTTTATTTTATGAAAGAACTTG 1371
QY 1321 GAGCTAGAGATGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1380
DB 1372 GAGCTAGAGATGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 1431
QY 1381 GAGATTAAGATTAATCTGCTCAAACTTATTTAAGATGATGATGATGATGATGATG 1440
DB 1432 GAGATTAAGATTAATCTGCTCAAACTTATTTAAGATGATGATGATGATGATGATG 1491
QY 1441 GCAACATCTCTATTTTTCGGAACCAATCAAGAGCAATTCGGAAGAAATTAAGTGA 1500
DB 1492 GCAACATCTCTATTTTTCGGAACCAATCAAGAGCAATTCGGAAGAAATTAAGTGA 1551
QY 1501 AATTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
DB 1552 AATTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1611
QY 1561 CACTTGCAAGATTTGTCTGTTGAGGGTGTAAATCTAAGTGAACATTAAGCAG 1620
DB 1612 CACTTGCAAGATTTGTCTGTTGAGGGTGTAAATCTAAGTGAACATTAAGCAG 1671
QY 1621 TTACGCTCTTCAATTTGAGATCTAAGTGAACATTAAGTGAACATTAAGTGAAC 1680
DB 1672 TTACGCTCTTCAATTTGAGATCTAAGTGAACATTAAGTGAACATTAAGTGAAC 1731
QY 1681 AGTATTCGATGCTTCCAAACGATTATGCAAGCTTCAAAATCTGCAAGCTGATCTA 1740
DB 1732 AGTATTCGATGCTTCCAAACGATTATGCAAGCTTCAAAATCTGCAAGCTGATCTA 1791
QY 1741 CATGCTGCTCATCTACTTTGTTTGCAGAAAGAAACAGCAAACTTGTGTCTTGA 1800
DB 1792 CATGCTGCTCATCTACTTTGTTTGCAGAAAGAAACAGCAAACTTGTGTCTTGA 1851
QY 1801 AATCTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1860
DB 1852 AATCTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1911
QY 1861 ACATGCTTTAAGACTCTAAGATTTGTGTGGAAATTCAGAAAGAAAGTTGTCAACT 1920
DB 1912 ACATGCTTTAAGACTCTAAGATTTGTGTGGAAATTCAGAAAGAAAGTTGTCAACT 1971
QY 1921 GGTGAATTAAGAACTGAAATCTTAATGCTCAATTTGAATCAAGCATTTGAGAGATG 1980
DB 1972 GGTGAATTAAGAACTGAAATCTTAATGCTCAATTTGAATCAAGCATTTGAGAGATG 2031

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Qy	1981	AAAGATGATATGATATGCAAAAGAACCCATTATCTGCAAAAGAAAATCTGCATTCCTTA	2045
Dp	2032	AAGATATGATATGATATGCAAAAGAACCCATTATCTGCAAAAGAAAATCTGCATTCCTTA	2093
Qy	2041	AGCATGAAATGGGATGACGATGAACGTCACGATATATATGATACGAAAAAGTTGAAGTG	2100
Dp	2092	AGCATGAAATGGGATGACGATGAACGTCACGATATATGATACGAAAAAGTTGAAGTG	2151
Qy	2101	CTTGAAAGCTCTCAAAACAACCTCCAACTGCACTTGTTAAACAATCAGGGGCTTCAGAGGA	2166
Dp	2152	CTTGAAAGCTCTCAAAACAACCTCCAACTGCACTTGTTAAACAATCAGGGGCTTCAGAGGA	2211
Qy	2161	ATCCGCTCCCAAGACTGATGATGAATCACTCAGTTTGGAAAAATGTTGTCTCTATTGAAATC	2228
Dp	2212	ATCCGCTCCCAAGACTGATGATGAATCACTCAGTTTGGAAAAATGTTGTCTCTATTGAAATC	2271
Qy	2221	ATCAGTTGCAAAAACTGCTCATGCTTTACCAACCTTGGTAGCTGCTTGTCTAAAAAGT	2280
Dp	2272	ATCAGTTGCAAAAACTGCTCATGCTTTACCAACCTTGGTAGCTGCTTGTCTAAAAAGT	2331
Qy	2281	CTAAGATTGATGAGGGGGCTCTGCGGAATGGAAGTATGTTGAATTCGGAATCCATCAAGA	2340
Dp	2332	CTAAGATTGATGAGGGGGCTCTGCGGAATGGAAGTATGTTGAATTCGGAATCCATCAAGA	2391
Qy	2341	AGAAAGTTTCCATCTCTGAGAAAACTTAAATATACGCAATTTGGTAATCTGAAAGAAATTG	2400
Dp	2392	AGAAAGTTTCCATCTCTGAGAAAACTTAAATATACGCAATTTGGTAATCTGAAAGAAATTG	2451
Qy	2401	CTGAAAAAGAAAGAGAGAGAGCAATGCCCTGTCTTGAAGATATAGATTAAATGTTGC	2460
Dp	2452	CTGAAAAAGAAAGAGAGAGAGCAATGCCCTGTCTTGAAGAGATATAGATTAAATGTTGC	2511
Qy	2461	CCTAATGTTTGTATATCCAAACCTTCTCTGTCAAGAAATGATAGTATAGGGGGAACAAG	2520
Dp	2512	CCTAATGTTTGTATATCCAAACCTTCTCTGTCAAGAAATGATAGTATAGGGGGAACAAG	2571
Qy	2521	TCAGATGCAATAGGTTTCAAGTTCATATCTAATCTCATGAGCTCTTACTTCCCTCAAAAT	2580
Dp	2572	TCAGATGCAATAGGTTTCAAGTTCATATCTAATCTCATGAGCTCTTACTTCCCTCAAAAT	2631
Qy	2581	CGCTATACAAAGAAAGATGCTTCACTCCCAAGAGAGATGTTCAAAAGCTTGCAAATCTC	2640
Dp	2632	CGCTATATCAAAAGAAAGATGCTTCACTCCCAAGAGAGATGTTCAAAAGCTTGCAAATCTC	2691
Qy	2641	AAATATCTGAATATCTCTTTTAACTTGAATGTTAAAGCGTCCATACAGCTGGCTAGT	2700
Dp	2692	AAATATCTGAATATCTCTTTTAACTTGAATGTTAAAGCGTCCATACAGCTGGCTAGT	2751
Qy	2701	CTCAATGCTTTGAAGACATCTGGAAATTCATATGTTGTTATGCACTAGAGAGCTCCCGAG	2760
Dp	2752	CTCAATGCTTTGAAGACATCTGGAAATTCATATGTTGTTATGCACTAGAGAGCTCCCGAG	2811
Qy	2761	GAAAGTGTGAAGGTTTAAATTTCACTCACTACAAGTTATCATATCAATCTGTGAATGCTA	2820
Dp	2812	GAAAGTGTGAAGGTTTAAATTTCACTCACTACAAGTTATCATATCAATCTGTGAATGCTA	2871
Qy	2821	CAATGTTTACCGAGGGAGATGACAGACTTAACAGCCCTCAAAATTAATCAGTTGAGTTT	2880
Dp	2872	CAATGTTTACCGAGGGAGATGACAGACTTAACAGCCCTCAAAATTAATCAGTTGAGTTT	2931
Qy	2881	TGTCCAACACTGGCCCAAGCGGTGTGAGAGGGAAATAGGAGAAAGACTGGTACAAAAATGCT	2940
Dp	2932	TGTCCAACACTGGCCCAAGCGGTGTGAGAGGGAAATAGGAGAAAGACTGGTACAAAAATGCT	2991
Qy	2941	CACATTCCTCGTGCTTAAATTAATTAG 2967	
Dp	2992	CACATTCCTCGTGCTTAAATTAATTAG 3018	

RESULT 2
ADK98518
ID ADK98518 standard; DNA; 3595 BP.

XX	ADK98518;
AC	
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	S Bulbocastanum Shu11 gene genomic DNA sequence SeqID3.
XX	
KW	plant disease resistance polypeptide; solanaceous plant; potato;
KW	late blight disease; fungus; Phytophthora infestans;
KW	conferring pathogen resistance; Shu11; gene; db.
XX	
OS	Solanum bulbocastanum.
XX	
FH	Key Location/Qualifiers
FT	CD5 57..3432
FT	/tag= a
FT	/product= "S Bulbocastanum Shu11 protein"
FT	Intron 488..899
FT	/tag= b
XX	
PN	WO2004020594-A2.
XX	
PD	11-MAR-2004.
XX	
PX	28-AUG-2003; 2003WO-US027045.
XX	
PR	29-AUG-2002; 2002US-0407100P.
XX	
PR	20-AUG-2003; 2003US-00547268.
XX	
PA	(USDA) US SEC OF AGRIC.
XX	
PA	(DRYC-) DRY CREEK LAB.
XX	
PI	Osumi T, Belknap WR, Rockhold DR, Maccree MW;
XX	
XX	WPI; 2004-239179/22.
DR	P-PSDB; ADK98519.
PT	New isolated Solanum bulbocastanum late blight resistance nucleic acid
PT	molecule encoding a plant disease resistance polypeptide, useful for
PT	confering pathogen resistance to phytophthora infestans in plants.
XX	
PS	Claim 1; SEQ ID NO 3; 103pp; English.
XX	
CC	This invention relates to a novel isolated nucleic acid molecule encoding
CC	a plant disease resistance polypeptide. The preferred plant is a
CC	solanaceous plant that is potato. The resistance is to late blight
CC	disease, caused by the fungus Phytophthora infestans. The invention is
CC	useful for confering pathogen resistance in plants using a Solanum
CC	bulbocastanum late blight resistance gene. The present sequence is the S
CC	bulbocastanum gene sequence of the invention.
XX	
SO	Sequence 3595 BP; 1139 A; 614 C; 737 G; 1105 T; 0 U; 0 Other;
Query Match	85.7%; Score 2541.8; DB 12; Length 3595;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2538; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Dy	428 CAGGTTTGTCTTAATGAACCAACAAGTTTATGGAAGAACAAGAAAGCAGATAG 487
Dd	896 CAGGTTTTGTTTTAATGAACCAACAAGTTTATGGAAGAACAAGAAAGCAGATAG 955
Dy	488 TGAATAATCTGATTAACAATGTTTAGCATATGCCAACCAACTTCAGTCTCCCAATACTTG 547
Dd	956 TGAATAATCTGATTAACAATGTTTAGCATATGCCAACCAACTTCAGTCTCCCAATACTTG 1015
Dy	548 GTATGGGGGGACTTAGAAAAGCAGCTTTGGCCCAATGCTTTCAATGATCAAGAGATTAA 607
Dd	1016 GTATGGGGGGACTTAGAAAAGCAGCTTTGGCCCAATGCTTTCAATGATCAAGAGATTAA 1075
Dy	608 TTGAGCAATTTCCAAATCCCAAATATGATTTGTGCTCGGAAGATTTTAATGAGAAAGGT 667
Dd	1076 TTGAGCAATTTCCAAATCCCAAATATGATTTGTGCTCGGAAGATTTTAATGAGAAAGGT 1135

Qy	668	TGATAAAGAAATTGAGATCTAATTGAAGAAAGCACTGGTGCATGCACTTGCGTC	727
Db	1136	TGATAAAGAAATTGAGATCTAATTGAAGAAAGCACTGGTGCATGCACTTGCGTC	1195
Qy	728	CACCTCAAAAGAGCTTCGGGACTTCGTATGGAATAAATATTGTCTCGCTTAGATG	787
Db	1196	CACCTCAAAAGAGCTTCGGGACTTCGTATGGAATAAATATTGTCTCGCTTAGATG	1255
Qy	788	ATGTTTGGAAATGAAAGTCAAAGTAAGTGGGCTTAAGTAAACAAGCTTTGAAGTTGGAG	847
Db	1256	ATGTTTGGAAATGAAAGTCAAAGTAAGTGGGCTTAAGTAAACAAGCTTTGAAGTTGGAG	1315
Qy	848	CAAGTGGCGCTTCGTCTTAACCACTACTCGTTGAAAGGTTGGATCAATTATGGAA	907
Db	1316	CAAGTGGCGCTTCGTCTTAACCACTACTCGTTGAAAGGTTGGATCAATTATGGAA	1375
Qy	908	CATTGCAACATATGAAATTGTCAAAATTGTCTCAGAGAGATTGTTGTGTTGTTCAATGC	967
Db	1376	CATTGCAACATATGAAATTGTCAAAATTGTCTCAGAGAGATTGTTGTGTTGTTCAATGC	1435
Qy	968	AACGTCATTTTGGGCAACAGAAGAAATAAATCTTAATCTTGCTGGCTPATCGGAAAGAGA	1027
Db	1436	AACGTCATTTTGGGCAACAGAAGAAATAAATCTTAATCTTGCTGGCTPATCGGAAAGAGA	1495
Qy	1028	TTGTGAAAAATGTGGTGTGTGCTCTAGCAGCTPAAACTCTTGGAGATATTTTGGCT	1087
Db	1496	TTGTGAAAAATGTGGTGTGTGCTCTAGCAGCTPAAACTCTTGGAGATATTTTGGCT	1555
Qy	1088	TTTAAAGAGAAAGAAAGACAGTGGGAACATGAGAGATAGTGAATTTGSAATTTGGCTC	1147
Db	1556	TTTAAAGAGAAAGAAAGACAGTGGGAACATGAGAGATAGTGAATTTGSAATTTGGCTC	1615
Qy	1148	AAGAGAAAAGTTCTAATCTTGCTGCTCGCTGAGACTTAGTAAACATCACCTTGCATTGATT	1207
Db	1616	AAGAGAAAAGTTCTAATCTTGCTGCTCGCTGAGACTTAGTAAACATCACCTTGCATTGATT	1675
Qy	1208	TGAGACAATGCTTTCATATTGTGAGATATCCCAAGAATACCGGAAATGGAAGGGAA	1267
Db	1676	TGAGACAATGCTTTCATATTGTGAGATATCCCAAGAATACCGGAAATGGAAGGGAA	1735
Qy	1268	ATCTAATCTCTCTGAGATGGCAATGGTTTTATTATTCGAAAGAAACTTGGAGCTAG	1327
Db	1736	ATCTAATCTCTCTGAGATGGCAATGGTTTTATTATTCGAAAGAAACTTGGAGCTAG	1795
Qy	1328	AATAATGATGTAATAAGCTATGGAATGAAATTAATCTTGAAGTCTTTCTTCACAGATTG	1387
Db	1796	AATAATGATGTAATAAGCTATGGAATGAAATTAATCTTGAAGTCTTTCTTCACAGATTG	1855
Qy	1388	AAGTTAAATCTGGTCAAACTTATTTCAAGATGACATGATCTCAATCATGATCTGGCAAT	1447
Db	1856	AAGTTAAATCTGGTCAAACTTATTTCAAGATGACATGATCTCAATCATGATCTGGCAAT	1915
Qy	1448	CTCTATTTTTCCGCAAGCAATCAGACGCAATATCCAGAAATATTGTGAAATTTACA	1507
Db	1916	CTCTATTTTTCCGCAAGCAATCAGACGCAATATCCAGAAATATTGTGAAATTTACA	1975
Qy	1508	TACATATGATGTCATTTGATTTCACTAAAGGATATCTTCTTACTCTCTTCCACTGTC	1567
Db	1976	TACATATGATGTCATTTGATTTCACTAAAGGATATCTTCTTACTCTCTTCCACTGTC	2035
Qy	1568	AGAAATTTGTCTCGTTAGGGGTGCTTAATCTAAGTGCATATAAACTTMAACAGTTAACCGT	1627
Db	2036	AGAAATTTGTCTCGTTAGGGGTGCTTAATCTAAGTGCATATAAACTTMAACAGTTAACCGT	2095
Qy	1628	CTTCATTTGGAGATCTAGTACTTAAGATATCCATAAATCTGTCTGGGAATATCTAGATATTC	1687
Db	2096	CTTCATTTGGAGATCTAGTACTTAAGATATCCATAAATCTGTCTGGGAATATCTAGATATTC	2155
Qy	1688	GTAAGCTTTCCAAACAGTTATGCAAGCTTCAAAATCGCAGACTTGTGATCTACATGGCT	1747
Db	2156	GTAAGCTTTCCAAACAGTTATGCAAGCTTCAAAATCGCAGACTTGTGATCTACATGGCT	2215
Qy	1748	GTCATATCATTTGTGTTTGCCAAAAGAAACAGCAAACTTGGTACTGTTCCAAATCTTT	1807

Db	2216	GTCAATCACTTTGTTGTTGGCCAAAGAAACAAACAACTTGGTAAGCTTTCGAATCTTT	2275
Qy	1808	TACTGATAGTGTGCTATGATATTTGACTTGTATGCCACCAAGGATAGATCTTTGACATGCC	1867
Db	2276	TACTGATAGTGTGCTATGATTTGACTTGTATGCCACCAAGGATAGATCTTTGACATGCC	2335
Qy	1868	TTTAAGACTCTAAGTAGATTTGTGGGAATTCAGAGAAAGTTGTCAACTTGTGTAAT	1927
Db	2336	TTTAAGACTCTAAGTAGATTTGTGGGAATTCAGAGAAAGTTGTCAACTTGTGTAAT	2395
Qy	1928	TACGAAACCTGAATCTCTATGGCTCAATGTGAATACGCATCTTGAGAGGTGAAGATG	1987
Db	2396	TACGAAACCTGAATCTCTATGGCTCAATGTGAATACGCATCTTGAGAGGTGAAGATG	2455
Qy	1988	ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAAATTCGACTCTTTAAGCATGA	2047
Db	2456	ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAAATTCGACTCTTTAAGCATGA	2515
Qy	2048	AATGGAGTAGAGTAGAAGCTCCACGTATATATGAAATACGAAAAGTTGAAGTCTTGAAG	2107
Db	2516	AATGGAGTAGAGTAGAAGCTCCACGTATATATGAAATACGAAAAGTTGAAGTCTTGAAG	2575
Qy	2108	CTCTCAAAACCACTCCATCTGACTTGTTTAACAATCAAGGGCTTCAGAGAACTCCCTC	2167
Db	2576	CTCTCAAAACCACTCCCAATCTGACTTGTTTAACAATCAAGGGCTTCAGAGAACTCCCTC	2635
Qy	2168	TCCGAGCTGGAGTGAATACATCGAGTTTGGAAAATGTGTCTATTTGAAATCATCGATT	2227
Db	2636	TCCGAGCTGGAGTGAATACATCGAGTTTGGAAAATGTGTCTATTTGAAATCATCGATT	2695
Qy	2228	GCAAAAACCTGCTCAAGCTTACCAACCCCTTGGTAGCTGCTTGCTAAAAAAGCTAGAGT	2287
Db	2696	GCAAAAACCTGCTCAAGCTTACCAACCCCTTGGTAGCTGCTTGCTAAAAAAGCTAGAGT	2755
Qy	2288	TGTGAGAGGGGCTCTGCCAAGTGAATGTATTTCTGATTCCTTACAGAGAAGGT	2347
Db	2756	TATGAGAGGGGCTCTGCCAAGTGAATGTATTTCTGATTCCTTACAGAGAAGGT	2815
Qy	2348	TTCCATCTCTGAGAAAACCTTAATATACGCGAATTTGTGTATCGAAAGGATTCGAAAA	2407
Db	2816	TTCCATCTCTGAGAAAACCTTAATATACGCGAATTTGTGTATCGAAAGGATTCGAAAA	2875
Qy	2408	AGAGAAGAGAAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTGCCCTATGT	2467
Db	2876	AGAGAAGAGAAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTGCCCTATGT	2935
Qy	2468	TTGTTATTCACACCCCTTTCCTGTCAAGAAATTTGTATGTAGTTGGGGCAAGTCAGATG	2527
Db	2936	TTGTTATTCACACCCCTTTCCTGTCAAGAAATTTGTATGTAGTTGGGGCAAGTCAGATG	2995
Qy	2528	CAATAGGTTCAAGTCCATATCTAATCTCATGGCTCTTACTTCCCTCCAAATTCGCTATA	2587
Db	2996	CAATAGGTTCAAGTCCATATCTAATCTCATGGCTCTTACTTCCCTCCAAATTCGCTATA	3055
Qy	2588	ACAAAGAAAGTGTTCATCTCCAGAGAGAAATGTCAAAAAGCTTGTCAATCTCAAAATCT	2647
Db	3056	ACAAAGAAAGTGTTCATCTCCAGAGAGATGTCAAAAAGCTTGTCAAAATCTCAAAATCT	3115
Qy	2648	TGAATATCTCTTTTACTTCAATCTTAAAGACGTGCTACACAGCTGTGCTAGTCAATG	2707
Db	3116	TGAATATCTCTTTTACTTCAATCTTAAAGACGTGCTACACAGCTGTGCTAGTCAATG	3175
Qy	2708	CTTTGGAAGCATCTGGAATATTCATAGTTGTATTAGCACTAGAGAGTTCCTCCAGAGAGGTG	2767
Db	3176	CTTTGGAAGCATCTGGAATATTCATAGTTGTATTAGCACTAGAGAGTTCCTCCAGAGAGGTG	3235
Qy	2768	TGAAGAGTTAATTTCACTCACACAGTTATCATTAACCTAGTAAGTGTCAACAATTTT	2827
Db	3236	TGAAGAGTTAATTTCACTCACACAGTTATCATTAACCTAGTAAGTGTCAACAATTTT	3295
Qy	2828	TACCGAGGAGTTGACGACCTTAACAGCCCTCACAAATTTATCAAGTTGATTTGTCCAA	2887

Db 3396 TACCGAGGATTCAGACCACTTAACAGCCCTCAAAATTATCACTGAGTTTGTCCAA 3355
QY 2888 CACTGCGCCAGACGGTGTGAGAGAGGATAGAGAACTGTGTACAAATGTCTCAATTG 2947
Db 3356 CACTGCGCCAGACGGTGTGAGAGAGGATAGAGAACTGTGTACAAATGTCTCAATTG 3415
QY 2948 CTGCTGTGTTTATTTATTTAG 2967
Db 3416 CTCGTGTGTTTATTTATTTAG 3435

RESULT 3
ADK98524
ID ADK98524 standard; DNA; 5028 BP.
XX
AC ADK98524;
DT 03-JUN-2004 (first entry)
DE S Bulbocastanum Sbul protein-related chimeric transgene SeqID9.
XX plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
KW conferring pathogen resistance; gene; ds; transgenic; Ubi 3 promoter.
XX Solanum bulbocastanum.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1029..4404
FT /*tag= a
FT /*product= "S Bulbocastanum Sbul protein"
FT Intron 1460..1871
FT /*tag= b

XX MO2004020594-A2.
XX 11-MAR-2004.
XX 28-AUG-2003; 2003WO-US027045.
XX 29-AUG-2002; 2002US-0407100P.
XX 20-AUG-2003; 2003US-00647268.
XX (USDA) US SEC OF AGRIC.
XX (DRYC-) DRY CREEK LAB.
XX PA
XX PI Osumi T, Belknap WR, Rockhold DR, Maccree NM;
XX WPI: 2004-239179/22.
XX P-PSDB; ADK98525.

XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX molecule encoding a plant disease resistance polypeptide, useful for
XX conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Claim 1; SEQ ID NO 9; 103bp; English.

XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum
XX bulbocastanum late blight resistance gene. The present sequence is that
XX of a chimeric transgene (Sbul gene with a potato Ubi1 promoter sequence)

XX Sequence 5028 BP; 1647 A; 847 C; 958 G; 1576 T; 0 U; 0 Other;
XX
XX Query Match 85.7%; Score 2541.8; DB 12; Length 5028;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 CAGGTTTTTTTGAATGAAACCAAGTTTATGGAAGACAAAGAAAGACGATAG 487
Db 1868 CAGGTTTTTTTGAATGAAACCAAGTTTATGGAAGACAAAGAAAGACGATAG 1927
QY 488 TGAATATCTGTATTAACAATGTTAGCAATGCCCAACCTCCAGTCTCCCAATACTTG 547
Db 1928 TGAATATCTGTATTAACAATGTTAGCAATGCCCAACCTCCAGTCTCCCAATACTTG 1987
QY 548 GTATGGGGGACTAGAAAAGACGACTCTTGCCCAATGCTTCAATGATCAGAGATGA 607
Db 1988 GTATGGGGGACTAGAAAAGACGACTCTTGCCCAATGCTTCAATGATCAGAGATGA 2047
QY 608 TTGAGCATTTCCATCCCAAAATATGATTTGTGTCGGAAAGATTTATGAGAAAGCT 667
Db 2048 TTGAGCATTTCCATCCCAAAATATGATTTGTGTCGGAAAGATTTATGAGAAAGCT 2107
QY 668 TGAATTAAGAAATTTGTAGAAATCTATTTGAAAGAAAGTCACTTGTGGCATGGAAGTCTG 727
Db 2108 TGAATTAAGAAATTTGTAGAAATCTATTTGAAAGAAAGTCACTTGTGGCATGGAAGTCTG 2167
QY 728 CACTTCAAAAAGACCTTCGGGACTTGCTGATGAGAAAAAATATTTGCTGCTTAGATG 787
Db 2168 CACTTCAAAAAGACCTTCGGGACTTGCTGATGAGAAAAAATATTTGCTGCTTAGATG 2227
QY 788 ATGTTTGAATGAATCAAGATTAAGTGGGCTTAAGTAAACAAGCTTTGAAGTTGAG 847
Db 2228 ATGTTTGAATGAATCAAGATTAAGTGGGCTTAAGTAAACAAGCTTTGAAGTTGAG 2287
QY 848 CAAATGGCGCTTCTGTTCTTAACCACTACTGCTCTTGAAGAAAGTTGATCAATTATGGAA 907
Db 2288 CAAATGGCGCTTCTGTTCTTAACCACTACTGCTCTTGAAGAAAGTTGATCAATTATGGAA 2347
QY 908 CATTGCAACCATGAATGTCAAATTTGTCGAAGAAGATTTGTTGTTGTTCAATGC 967
Db 2348 CATTGCAACCATGAATGTCAAATTTGTCGAAGAAGATTTGTTGTTGTTCAATGC 2407
QY 968 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGGCTATCGAAAGAGAA 1027
Db 2408 AACGTGATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGGCTATCGAAAGAGAA 2467
QY 1028 TTGTGAAAAAATGTGTGTGTGCTCTAGCAAGCTAAACCTTTGAGAGTATTTTGGCCT 1087
Db 2468 TTGTGAAAAAATGTGTGTGTGCTCTAGCAAGCTAAACCTTTGAGAGTATTTTGGCCT 2527
QY 1088 TTAAGAGAAAGAAAGACAGTGGGAACGTGAGAGATGAGATTTGAAATTTGCTC 1147
Db 2528 TTAAGAGAAAGAAAGACAGTGGGAACGTGAGAGATGAGATTTGAAATTTGCTC 2587
QY 1148 AAGAAAGAAAGTTCTATTCTGTGCTGCCCTGAGACTTAATTACATCACCTTCACCTGAT 1207
Db 2588 AAGAAAGAAAGTTCTATTCTGTGCTGCCCTGAGACTTAATTACATCACCTTCACCTGAT 2647
QY 1208 TGAACAAATGCTTTACATATTGTGCAATTTCCAAAGGATACCGAAATGGAAGGAA 1267
Db 2648 TGAACAAATGCTTTACATATTGTGCAATTTCCAAAGGATACCGAAATGGAAGGAA 2707
QY 1268 ATCTAATCTCTCTGATGAGCAATGCTTTATTTATGGAAGAAACCTTGAGCTAG 1327
Db 2708 ATCTAATCTCTCTGATGAGCAATGCTTTATTTATGGAAGAAACCTTGAGCTAG 2767
QY 1328 AGAATGATAGTAATGATAGATGATGATGATGATGATGATGATGATGATGATGATG 1387
Db 2768 AGAATGATAGTAATGATAGATGATGATGATGATGATGATGATGATGATGATG 2827
QY 1388 AAGTTAAATCTGTGCAAACTTATTCAAGATGATGATGATGATGATGATGATGAT 1447
Db 2828 AAGTTAAATCTGTGCAAACTTATTCAAGATGATGATGATGATGATGATGATGAT 2887
QY 1448 CTCTATTTTGGGCAAGACATCAAGACGCAATACCGAGAAATATGTAAGAAATTA 1507
Db 2888 CTCTATTTTGGGCAAGACATCAAGACGCAATATCCGAGAAATATGTAAGAAATTA 2947
QY 1508 TACATATGATGTCATTTGTTCACTAAAGTGTATCTTCTTACTCTCTTCCACTTGC 1567


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Db      2948 TACATATGATGTCATTTGTTTCTACTAAAGGTATCTTTTACTCTCTTCCACTTGC 3007
Qy      1568 AGAAGTTGTCTGTTGAGGGTCTTAATCTAAGACATAAACTTAAGACATTACCGT 1627
Db      3008 AGAAGTTGTCTGTTGAGGGTCTTAATCTAAGACATAAACTTAAGACATTACCGT 3067
Qy      1628 CTTCATATGAGATCTAGTACATTTAAGATACCTAACTGTGCGCAATCTAGTATTC 1687
Db      3068 CTTCATATGAGATCTAGTACATTTAAGATACCTAACTGTGCGCAATCTAGTATTC 3127
Qy      1688 GTAGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGACAGCTTTGATCTACATGCT 1747
Db      3128 GTAGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGACAGCTTTGATCTACATGCT 3187
Qy      1748 GTCAATCACTTTGTTGTTGCAAAAGAAACAAGCAAACTTGTAAGTCTTGAATCTTT 1807
Db      3188 GTCAATCACTTTGTTGTTGCAAAAGAAACAAGCAAACTTGTAAGTCTTGAATCTTT 3247
Qy      1808 TACTTGATGGTGTGCTAATGATTTGACTTGTACCGCAAGATAGATCTTTGACATGCC 1867
Db      3248 TACTTGATGGTGTGCTAATGATTTGACTTGTACCGCAAGATAGATCTTTGACATGCC 3307
Qy      1868 TTAAGACTTAAAGTATGATTTGTGTGGGAATTCAGAAAGAAAGTTGCACTTGAT 1927
Db      3308 TTAAGACTTAAAGTATGATTTGTGTGGGAATTCAGAAAGAAAGTTGCACTTGAT 3367
Qy      1928 TAGAAAACCTGAATCTCTAATGGCTCAATTTGAATACAGCACTTGAGAGTGAAGATG 1987
Db      3368 TAGAAAACCTGAATCTCTAATGGCTCAATTTGAATACAGCACTTGAGAGTGAAGATG 3427
Qy      1988 ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGCATGA 2047
Db      3428 ATATGATGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGCATGA 3487
Qy      2048 AATGGATGACGATGAAAGCTCCACGTATATATGATCAAGAAAGTTGAAGTCTTGAAG 2107
Db      3488 AATGGATGACGATGAAAGCTCCACGTATATATGATCAAGAAAGTTGAAGTCTTGAAG 3547
Qy      2108 CTCTCAAAACCACTCAATCTGATCTTTTAACAATCAAGGGGCTTCAAGGAATCCGTC 2167
Db      3548 CTCTCAAAACCACTCAATCTGATCTTTTAACAATCAAGGGGCTTCAAGGAATCCGTC 3607
Qy      2168 TCCCAAGCTGATGATCACTCACTGATTTTGAAGAAATGTGTCTCTAATGAATCATCAGT 2227
Db      3608 TCCCAAGCTGATGATCACTCACTGATTTTGAAGAAATGTGTCTCTAATGAATCATCAGT 3667
Qy      2228 GCAAAAATCTGCTCATGCTTACACCTTTGGTGAAGTGTCTGTCTAAGAAAGTCTAGAGT 2287
Db      3668 GCAAAAATCTGCTCATGCTTACACCTTTGGTGAAGTGTCTGTCTAAGAAAGTCTAGAGT 3727
Qy      2288 TGTGAGAGGGGGTCTGCGGAAGTGAAGTATGTGATTTGCGATTCCTCAAGAAAGAGGT 2347
Db      3728 TATGAGAGGGGGTCTGCGGAAGTGAAGTATGTGATTTGCGATTCCTCAAGAAAGAGGT 3787
Qy      2348 TTCCATCTCTGAGAAAACTTAATATACGCAATTTGGTAATCTGAAAGATTTGCTGAAAA 2407
Db      3788 TTCCATCTCTGAGAAAACTTAATATACGCAATTTGGTAATCTGAAAGATTTGCTGAAAA 3847
Qy      2408 AGGAAGAGAGAGCAATGCCCTGTGCTTGAAGAGATAGAGATTAATTTGGCCCTATGT 2467
Db      3848 AGGAAGAGAGAGCAATGCCCTGTGCTTGAAGAGATAGAGATTAATTTGGCCCTATGT 3907
Qy      2468 TTGTTATTTCCAAACCTTTCTTCTGTCAAGAAATTTGATTTAGTGGGAGCAAGTCAGATG 2527
Db      3908 TTGTTATTTCCAAACCTTTCTTCTGTCAAGAAATTTGATTTAGTGGGAGCAAGTCAGATG 3967
Qy      2528 CAATAGGTTTCAGTTCCATATCTAATCTCATGGCTTACTTCCCTCCAAATTCGCTATA 2587
Db      3968 CAATAGGTTTCAGTTCCATATCTAATCTCATGGCTTACTTCCCTCCAAATTCGCTATA 4027
Qy      2588 ACAAGAGATGCTTCACTCCCAAGAGATTTCAAAAGCCTTGCAAAATCTCAAAATCT 2647

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Db      4028 ACAAGAGATGCTTCACTCCCAAGAGATGTTCAAAAGCCTTGCAAAATCTCAAAATCT 4087
Qy      2648 TGAATATCTCTTTTACTTGAATCTTAAAGAGCTGCTTACAGCTGCTAGTCTCAATG 2707
Db      4088 TGAATATCTCTTTTACTTGAATCTTAAAGAGCTGCTTACAGCTGCTAGTCTCAATG 4147
Qy      2708 CTTTGAAGCATCTGGAATTCATAGTTGTTATGACATAGAGAGTCTCCGAGAGAGTGT 2767
Db      4148 CTTTGAAGCATCTGGAATTCATAGTTGTTATGACATAGAGAGTCTCCGAGAGAGTGT 4207
Qy      2768 TGAAGGTTTAAATTTCACTCAACAGTTATTCATATACATACCTGTGAATGCTCAATGTT 2827
Db      4208 TGAAGGTTTAAATTTCACTCAACAGTTATTCATATACATACCTGTGAATGCTCAATGTT 4267
Qy      2828 TACCGAGGATTTGACACCTTAAACAGCTTCAAAATTTATCACTGAGTTGTGCA 2887
Db      4268 TACCGAGGATTTGACACCTTAAACAGCTTCAAAATTTATCACTGAGTTGTGCA 4327
Qy      2888 CACTGCGCAAGCGGTGAGAGAGGAATAGAGAGACTGTACAAATTTGCTCACATTC 2947
Db      4328 CACTGCGCAAGCGGTGAGAGAGGAATAGAGAGACTGTACAAATTTGCTCACATTC 4387
Qy      2948 CTGCTGTTTATTTATTAG 2967
Db      4388 CTGCTGTTTATTTATTAG 4407

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RESULT 4
ADK98520
ID ADK98520 standard; DNA; 3347 BP.
XX
AC ADK98520;
XX
DT 03-JUN-2004 (first entry)
XX
DE S Bulbocastanum Sbul2 gene sequence SegID5.
XX
KW plant disease resistance polypeptide; solanaceous plant; potato;
late blight disease; fungus; Phytophthora infestans;
confering pathogen resistance; Sbul2; gene; ds.
XX
OS Solanum bulbocastanum.
XX
FH Key Location/Qualifiers
FT 57..3344 /*tag= a
FT CDS /*product= "S Bulbocastanum Sbul2 protein"
FT intron /*tag= b
FT FT
PN MO2004020594-A2.
XX
PD 11-MAR-2004.
XX
PE 28-AUG-2003; 2003MO-US027045.
XX
PR 29-AUG-2002; 2002US-0407100P.
PR 20-AUG-2003; 2003US-00647268.
XX
PA (USDA) US SEC OF AGRIC.
PA (DRC-) DRY CREEK LAB.
PI Oseum T, Belknap WR, Rockhold DR, Macree MM;
XX
XX WPI: 2004-239179/22.
DR P-PSDB; ADK98521.
XX
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
PT molecule encoding a plant disease resistance polypeptide, useful for
PT conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Example; SEQ ID NO 5; 103bp; English.
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This invention relates to a novel isolated nucleic acid molecule encoding a plant disease resistance polypeptide. The preferred plant is a solanaceous plant that is potato. The resistance is to late blight disease, caused by the fungus *Phytophthora infestans*. The invention is useful for conferring pathogen resistance in plants using a *Solanum bulbocastanum* late blight resistance gene. The present sequence is the *S bulbocastanum* Sbul 2 gene sequence which was used in the exemplification of the invention.

Sequence 3347 BP; 1070 A; 577 C; 693 G; 1007 T; 0 U; 0 Other;

Query Match 77.8%; Score 2309; DB 12; Length 3347;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2773; Conservative 0; Mismatches 190; Indels 330; Gaps 2;

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QY 1 ATGGCTGAAGCTTCCTCAAGTCTGTAGCATCGACTGTGTTTCATCCAGGGGAA 60
DB 57 ATGGCTGAAGCTTCCTCAAGTCTGTAGCATCGACTGTGTTTCATCCAGGGGAA 116
QY 61 CTGGATTGATTTCTTGTGTTTAAAGATGATTCGAAAAGCTTCAAGACGTTTACTACA 120
DB 117 GTTGATTTGATTTCTTGTGTTTAAAGATGATTCGAAAAGCTTCAAGACATTTTACTACA 176
QY 121 ATCCAGCTGTGCTAGAGATGCTCAGAAAGCAATTGAAAGACAGCAAGCAATGAAAT 180
DB 177 ATCCAGCTGTGCTAGAGATGCTCAGAAAGCAATTGAAAGACAGCAATGAAAT 236
QY 181 TGGTTGCGAAGATCTAATGCTGCTGATATGAGGCTGATGACATCTTGGAGAAATGAAA 240
DB 237 TGGTTGCGAAGATCTAATGCTGCTGATATGAGGCTGATGACATCTTGGAGAAATGAAA 296
QY 241 ACTGAGGACCAATTAGACAGAAAGAAACAATATGAGTGTATCATCCAAAGCTTATC 300
DB 297 ACTGAGGACCAATTAGACAGAAAGAAACAATATGAGTGTATCATCCAAAGCTTATC 356
QY 301 ACTTTTCTCAAGATTTGGGAAAAGATGAAAGAAAGATTATGAGAAATCTAGATGTAAT 360
DB 357 GCTTCCGTCACAAAGATTTGGGAAAAGATGAAAGAAAGATTATGAGAAATCTAGATGTAAT 416
QY 361 GCACGCGAAGCAATTAATTTTCAATTTGATGAAAGCAATAGAGACAGATTTGCTACA 420
DB 417 GCACGCGAAGCAATTAATTTTCAATTTGATGAAAGCAATAGAGACAGATTTGCTACA 476
QY 421 CGCCAAA----- 427
DB 477 CGCCAAAAGGTGCTCATCTTGAATTTTCTAAAAAAGCCTTATATCATGAAT 536
QY 428 ----- 427
DB 537 CATGTGTGTTGGGATTTTCTAATCTAATGTTGTCTCAAGCTTAAAGTAGATAGTG 596
QY 428 ----- 427
DB 597 ATCCAGATTGATATATATATATATATATATATATATATATATATATATATATATAT 656
QY 428 ----- 427
DB 657 AAAGCTGAGTTGTTTGAACATTAATTAACAATGATTAATGGAATTCAAAAAA 716
QY 428 ----- 427
DB 717 GTGATATATGCTGCTGCTCTCAAGCTTATCATGTTCTTTATATGCAAAATTTCTC 776
QY 428 ----- 427
DB 777 TTGCTTTTGTGCTACTCTACTAGAGCTTGAACAGGTTTGTGTTTAAAGAACCAAA 836
QY 454 GTTATGAGAGACAAAGAAAGAGACAGATAGTGAATCTGATTAACATAGTTAGC 513
DB 837 GTTATGAGAGACAAAGAAAGAGATAGTGAATCTGATTAACATAGTTAGC 896
QY 514 AATGCCCAACATTCAGTCTCCCAATACCTTGGTATGGGGGAGCTAGAAAGACGACT 573
DB 514 AATGCCCAACATTCAGTCTCCCAATACCTTGGTATGGGGGAGCTAGAAAGACGACT 573
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DB 897 GATGCCCAACATTCAGTCTCCCAATACCTTGGTATGGGGGAGCTAGAAAGACGACA 956
QY 574 CTTCGCCCAATATGCTTCAATGATCAGAGTAATGATGCAATTCATCCCAAAATATG 633
DB 957 CTTCGCCCAATATGCTTCAATGATCAGAGTAATGATGCAATTCATCCCAAAATATG 1016
QY 634 ATTTGTCTCGGAAGATTTTATGAGAAAGGTTGTAAGAAATTTGTAATCTAAT 693
DB 1017 ATTTGTCTCGGAAGATTTTATGAGAAAGGTTGTAAGAAATTTGTAATCTAAT 1076
QY 694 GAAGAAAGTCACTTGTGCGATGAGACTTGGCTCCATTCAAAGAACTTCGGGACTTG 753
DB 1077 GAAGAAAGTCACTTGTGCGATGAGACTTGGCTCCATTCAAAGAACTTCAGAGACTTG 1136
QY 754 CTGAATGAAAAAATATATGCTGCTGCTTGAATGATGTTGGAATGAGATCAAGATTA 813
DB 1137 CTGAATGAAAAAATATATGCTGCTGCTTGAATGATGTTGGAATGAGATCAAGATTA 1196
QY 814 TGGCTAAGTTAAGACAACTTGAAGGTTGAGCAAGTGGCGCTTGTCTTAACACT 873
DB 1197 TGGCTAAGTTAAGACAACTTGAAGGTTGAGCAAGTGGCGCTTGTCTTAACACT 1256
QY 874 ACTGCTCTGAAAAAGTTGGATCAATTAAGGAAATTTGCAACATATGATTTGCAAT 933
DB 1257 ACTGCTCTGAAAAAGTTGGATCAATTAAGGAAATTTGCAACATATGATTTGCAAC 1316
QY 934 TTGTCTAAGAAATGTTGGTGTGTTGATGACAGTGATTTGGGACCAAGAAAGAA 993
DB 1317 TTGTCTAAGAAATGTTGGTGTGTTGATGACAGTGATTTGGGACCAAGAAAGAA 1376
QY 994 ATTAATCTTAATCTTGTGCTATCGAAGAGAAATGTTGAAAAATGTTGTGTGTGCT 1053
DB 1377 ATTAATCTTAATCTTGTGCTATCGAAGAGAAATGTTGAAAAATGTTGTGTGTGCT 1436
QY 1054 CTAGACCTAATACTTGGAGGTAATTTGGCTTTAAGAGAAAGAAAGCAAGTGGGAA 1113
DB 1437 CTAGACCTAATACTTGGAGGTAATTTGGCTTTAAGAGAAAGAAAGCAAGTGGGAA 1496
QY 1114 CATGTGAGATGATGATTTGGAATTTGCTCAAGAAAGTCTATTTCTGCTGCC 1173
DB 1497 CATGTGAGATGATGATTTGGAATTTGCTCAAGAAAGTCTATTTCTGCTGCC 1556
QY 1174 CTGAGACTTATGATCACTTCACTTCACTTGAATTTGAGCAATGCTTATATATGCA 1233
DB 1557 CTGAGACTTATGATCACTTCACTTGAATTTGAGCAATGCTTATATATGCA 1616
QY 1234 GATTTCCCAAGATACCGAAATGGAAGGAAATCTAATCTCTCTGAGTGGCAAT 1293
DB 1617 GATTTCCCAAGATACCGAAATGGAAGGAAATCTAATCTCTCTGAGTGGCAAT 1676
QY 1294 GCTTTATTTTATCGAAGAACTTGGAGCTAGAGAAATGATGATATGAAATGGAAT 1353
DB 1677 GCTTTATTTTATCGAAGAACTTGGAGCTAGAGAAATGATGATATGAAATGGAAT 1736
QY 1354 GAATTTACTTGAAGTCTTCTTCAAGAGATGAAATCTGCTCAAACTTATTTCC 1413
DB 1737 GAATTTACTTGAAGTCTTCTTCAAGAGATGAAATCTGCTCAAACTTATTTCC 1796
QY 1414 AAGATGATATCTCATATGATCTGCAACATCTCTATTTTGGCAAGCAATCAAGC 1473
DB 1797 AAGATGATATCTCATATGATTTGGCTATCTCTATTTTGGCAAGCAATCAAGC 1856
QY 1474 AGCAATATCGGAGAAATATGTAAGAAATTAACAATATGATGATGATGATGATGAT 1553
DB 1857 AGCAATATCGGAGAAATATGTAAGAAATTAACAATATGATGATGATGATGATGAT 1916
QY 1534 AAGTGTATCTTCTTACTCTTCTTCCACTTGCAGAAATTTGCTGAGGATGCT 1593
DB 1917 AAGTGTATCTTCTTACTCTGCTTCTTCCAAAGTTTGTCTGATTAAGGATGCT 1976
QY 1594 AATCTAAGTACATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 1653
DB 1977 AATCTAAGTACATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA 2036
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QY 1654 AGATACCTAACTTGTCTGGCAATATCTAGTAATTCGTAATCTTCCAAACGAGTTATGCAAG 1713
 DB 2037 AGATACCTAACTTGTCTAGCAATATATAGATTCGTAATCTTCCAAACGAGTTATGCAAG 2096
 QY 1714 CTTCAAATCTGAGACTCTTATGATCAATGCTGATCACTCTTGTGTTGCAAAA 1773
 DB 2097 CTTCAAATCTGAGACTCTTATGATCAATGCTGATCACTCTTGTGTTGCAAAA 2156
 QY 1774 GAAACAGCAACTTGTGATCTTGAATCTTTATCTGATGTTGTAATGATGATGAT 1833
 DB 2157 GAAACAGCAACTTGTGATCTTGAATCTTTATCTGATGTTGTAATGATGATGATGAT 2216
 QY 1834 TGTATGCCACCAAGATAGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 1893
 DB 2217 TGTATGCCACCAAGATAGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 2276
 QY 1894 GGAATTCAGAAAGAAAGTTGTAATCTTGAATCTTGAATCTTGAATCTTGAATCT 1953
 DB 2277 GGAATTCAGAAAGAAAGTTGTAATCTTGAATCTTGAATCTTGAATCTTGAATCT 2333
 QY 1954 ATTGAATTCAGCACTCTGAGAGATGAAATGATGATGATGATGATGATGATGATGAT 2013
 DB 2334 ATTGAATTCAGCACTCTGAGAGATGAAATGATGATGATGATGATGATGATGATGAT 2393
 QY 2014 TCTGCAAAAGAAAGTTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 2073
 DB 2394 TCTGCAAAAGAAAGTTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 2453
 QY 2074 ATATATGATCAAGAAAGTTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 2133
 DB 2454 AGATATGATCAAGAAAGTTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAAT 2513
 QY 2134 TGTATTCAGATCAGGAGCTTCAAGAAATGCTGCTCCAGATGATGATGATGATGATGAT 2193
 DB 2514 TGTATTCAGATCAGGAGCTTCAAGAAATGCTGCTCCAGATGATGATGATGATGATGAT 2573
 QY 2194 TTGAAATATGTTGTTCTTATGAAATCAATCAATGCAAAATCTGCTCAATGCTCAATCC 2253
 DB 2574 TTGAAATATGTTGTTCTTATGAAATCAATCAATGCAAAATCTGCTCAATGCTCAATCC 2633
 QY 2254 TTTGGTGAAGTCCCTTGTCTTAAAGTCTAAGATGTTGAGAGGAGGAGGAGGAGGAGGAG 2313
 DB 2634 TTTGGTGAAGTCCCTTGTCTTAAAGTCTAAGATGTTGAGAGGAGGAGGAGGAGGAGGAG 2693
 QY 2314 TATGTTGATCTGATGATCTTCAAGAAAGATGTTGATCTTCAAGAAAGATGTTGAT 2373
 DB 2694 TATGTTGATCTGATGATCTTCAAGAAAGATGTTGATCTTCAAGAAAGATGTTGAT 2753
 QY 2374 CGGCAATTTGTTATCTGAAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2433
 DB 2754 CGGCAATTTGTTATCTGAAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2813
 QY 2434 CTTCGAAGATGATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2493
 DB 2814 CTTCGAAGATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2873
 QY 2494 AAGCAATTTGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2553
 DB 2874 AAGCAATTTGTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2933
 QY 2554 CTGATGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2613
 DB 2934 CTGATGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2993
 QY 2614 GAGATGTTCAAAAGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 2673
 DB 2994 GAGATGTTCAAAAGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 3053
 QY 2674 AAGAGCTGCTTCAAGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 2733
 DB 3054 AAGAGCTGCTTCAAGCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCT 3113

QY 2734 TGTATGCACTAGAGAGCTCTCCGAGAGAGTGTGAAGGTTAATTTACTCAGACAG 2793
 DB 3114 TGTATGCACTAGAGAGCTCTCCGAGAGAGTGTGAAGGTTAATTTACTCAGACAA 3173
 QY 2794 TTATCCATTAATCTGTAAGTGTGAATGTTTAACTGAGAGGATGAGACCTTACA 2853
 DB 3174 TTATCCATTAATCTGTAAGTGTGAATGTTTAACTGAGAGGATGAGACCTTACA 3233
 QY 2854 GCCCTCAAAATTTATGAGTTGAGTTTGTTCACAACCTGCGCAAGCGGTGTGAGAGGA 2913
 DB 3234 GCCCTCAAAATTTATGAGTTGAGTTTGTTCACAACCTGCGCAAGCGGTGTGAGAGGA 3293
 QY 2914 ATAGAGAGAGCTGTGCAAAATGTTCTCAATCTCTGTTGTTATTTATTA 2966
 DB 3294 ATAGAGAGAGCTGTGCAAAATGTTCTCAATCTCTGTTGTTATTTATTTA 3346
 RESULT 5
 ADF17759
 ID ADF17759 standard; DNA; 2913 BP.
 XX
 AC ADF17759;
 DT 12-FEB-2004 (first entry)
 DE Solanum bulbocastanum Rpi-b1b DNA sequence.
 KW gene, ds; Rpi-b1b, Rpi-b1b gene cluster; growth regulator;
 KM oomycete infection; introgression breeding; plant; late blight.
 OS Solanum bulbocastanum.
 FH Key
 FT 1. 2913
 FT CDS
 FT /tag= a
 FT /product= "Rpi-b1b protein"
 XX
 XX BP1334979-A1.
 XX
 PD 13-AUG-2003.
 XX
 PF 08-FEB-2002; 2002EP-00075565.
 XX
 PR 08-FEB-2002; 2002EP-00075565.
 XX
 PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
 XX
 PI Van Der Voosen EAG, Allefs JHM;
 XX
 DR WPI; 2003-714439/68.
 DR P-PSDB; ADF17765.
 XX
 PT New resistance gene conferring resistance against an oomycete pathogen,
 PT useful for producing plants, especially potatoes and tomatoes, resistant
 PT against oomycete pathogens such as Phytophthora infestans.
 XX
 PS Example 5; SEQ ID NO 35; 86pp; English.
 XX
 CC This invention relates to novel isolated polynucleotides that confer
 CC resistance against late blight caused by the oomycete pathogen
 CC Phytophthora infestans, which threatens both tomato and potato crops.
 CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
 CC leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
 CC and which cause disease resistance to bacteria, fungi, nematodes etc.
 CC These R genes, namely Rpi-b1b, RGCI-b1b, RGCI-b1b and RGCI-b1b, can be
 CC described as plant growth regulators. They are useful in providing
 CC resistance to Phytophthora infestans, especially in Solanum tuberosum
 CC (potato) plants to protect against oomycete infection or to demonstrate
 CC disease susceptibility. Resistance can be conferred by transformation of
 CC existing potato and tomato cultivars with the gene, a procedure that is
 CC more straightforward and faster than conventional introgression breeding.
 CC This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b DNA of
 CC the invention.

XX Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;
SQ Query Match 70.0%; Score 2077.2; DB 10; Length 2913;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 2495; Conservative 0; Mismatches 388; Indels 105; Gaps 8;

QY 1 ATGCTGAGCTTCTTCAAGTCTGTGATGCAATCTGACTGTTGATCCAGGGGAA 60
DB 1 ATGCTGAGCTTCTTCAAGTCTGTGATGCAATCTGACTGTTGATCCAGGGGAA 60
QY 61 CTGATGCTGTTTGGGTTTCAAGATGATGCTTCAAGCTTCAAGCATGTTTCTACA 120
DB 61 CTGATGCTGTTTGGGTTTCAAGATGATGCTTCAAGCTTCAAGCATGTTTCTACA 120
QY 121 ATCCAGCTGCTAGAGATGCTCAGAGAGCAATGGAAGCAGAGCAATGAAAT 180
DB 121 ATCCAGCTGCTAGAGATGCTCAGAGAGCAATGGAAGCAGAGCAATGAAAT 180
QY 121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAGCAATGGAAGCAGAGCAATGAAAT 180
DB 121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAGCAATGGAAGCAGAGCAATGAAAT 180
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATGATGAGCTGATGATCTTGAAGATGTA 240
DB 181 TGGTTGCAAGAACTCAATGCTGCTGATGATGAGCTGATGATCTTGAAGATGTA 240
QY 181 TGGTTGCAAGAACTCAATGCTGCTGATGATGAGCTGATGATCTTGAAGATGTA 240
DB 181 TGGTTGCAAGAACTCAATGCTGCTGATGATGAGCTGATGATCTTGAAGATGTA 240
QY 241 ACTGAGCAACCAATGAGCAGAGAGCAATATGAGGTTATCATCCAAAGTTATC 300
DB 241 ACTGAGCAACCAATGAGCAGAGAGCAATATGAGGTTATCATCCAAAGTTATC 300
QY 241 ACTGAGCAACCAATGAGCAGAGAGCAATATGAGGTTATCATCCAAAGTTATC 300
DB 241 ACTGAGCAACCAATGAGCAGAGAGCAATATGAGGTTATCATCCAAAGTTATC 300
QY 301 ACTTTTGTCTCAAGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 301 ACTTTTGTCTCAAGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 298 CTTTTCGCTCAAGAGTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
DB 298 CTTTTCGCTCAAGAGTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
QY 361 GCAGCGAG 420
DB 361 GCAGCGAG 420
QY 358 GCTAG 417
DB 358 GCTAG 417
QY 421 CGCCAAACAGGTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 CGCCAAACAGGTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 418 CGGAG 477
DB 418 CGGAG 477
QY 481 GAGATGAG 540
DB 481 GAGATGAG 540
QY 478 GAGATGAG 537
DB 478 GAGATGAG 537
QY 541 ATACTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 ATACTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 538 ATACTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
DB 538 ATACTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
QY 601 AGAGTAAATGAG 660
DB 601 AGAGTAAATGAG 660
QY 598 AGAGTAAATGAG 657
DB 598 AGAGTAAATGAG 657
QY 661 AAGAGTTGATGAG 717
DB 661 AAGAGTTGATGAG 717
QY 658 AAGAGTTGATGAG 717
DB 658 AAGAGTTGATGAG 717
QY 718 GACTTGTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
DB 718 GACTTGTCTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
QY 778 GCTTATGATGATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
DB 778 GCTTATGATGATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
QY 838 AAGGTTGAG 897
DB 838 AAGGTTGAG 897
QY 898 ATTAAGGAG 957
DB 898 ATTAAGGAG 957
QY 958 TTGTTTCATGCAAGCTGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017
DB 958 TTGTTTCATGCAAGCTGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017

DB 958 TTGTTTCATGCAAGCTGATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1017
QY 1018 GGAAG 1077
DB 1018 GGAAG 1077
QY 1078 ATTTTGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1137
DB 1078 ATTTTGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1137
QY 1138 AATTTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197
DB 1138 AATTTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197
QY 1198 CCACTGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
DB 1198 CCACTGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
QY 1258 GAAAG 1317
DB 1258 GAAAG 1317
QY 1318 TTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
DB 1318 TTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1377
QY 1378 CAAGAGATGAG 1437
DB 1378 CAAGAGATGAG 1437
QY 1438 CTGGCAACATCTCTATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
DB 1438 CTGGCAACATCTCTATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
QY 1498 GAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
DB 1498 GAAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
QY 1558 TCCCATGAG 1617
DB 1558 TCCCATGAG 1617
QY 1618 CAGTTACGCTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677
DB 1618 CAGTTACGCTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677
QY 1678 ACTAGATGAG 1737
DB 1678 ACTAGATGAG 1737
QY 1735 CTACATGAG 1794
DB 1735 CTACATGAG 1794
QY 1798 CGAATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1857
DB 1798 CGAATCTTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1857
QY 1858 TTGACATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1917
DB 1858 TTGACATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1917
QY 1918 CTTGAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1977
DB 1918 CTTGAGATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1977
QY 1978 GGAAGATGAG 2037
DB 1978 GGAAGATGAG 2037
QY 2038 TTAAGCATGAG 2097
DB 2038 TTAAGCATGAG 2097
QY 2032 TTAAGCATGAG 2088
DB 2032 TTAAGCATGAG 2088

QY	2098	GTGCTGGAAGCTCTCAACCAACA	CTCCATCTGACTTGTTAACA	CATGAGGGCTTCAGA	2157
Db	2089	GTGCTGGAAGCCCTCAACCAACA	CACTCCATCTGACTTCTTTAA	AATCTATGCTTCAGA	2148
QY	2158	GGATCCGCTCCAGACTGATGAA	TGACTAGTTTGAAAATGTTGCTATATGA		2217
Db	2149	GGATTCATCTCCAGAGTGGATG	ATCACTAGATATGAAAATATGTCTTATCTTA		2208
QY	2218	ATCATCAGTTGCAAAAAC	TGCTCATGCTTACACCCCTTGTGAGCTGCTGTAAA		2277
Db	2209	ATTAGCAACTTCAGAAACTG	CTCATGCTTACACCCCTTGTGATCTGCTGTCTGAA		2268
QY	2278	AGCTTAGAGTGTGGAGGGGG	CTCGGAATGGAGATGTTG-----		2320
Db	2269	AGCTTAGAGTTTCACTGGGG	GTCTCGGATGGAGATGTTGGAAGATGATTTGAT		2328
QY	2321	----ATTGAGATCCCTTCAGA	AGAAAGATTCATCTGAGAAA	CTTAATATAGC	2376
Db	2329	GTTCATCTCGAATCTCCCA	CANAGATTAAGTTTCCATCTTGAGGAACTTGATATATG		2388
QY	2377	GAATTTGGTATCTGAAAAG	ATGTGCTGAAAAAGAGAGAAAGCAATGCCCTGTGCTT		2436
Db	2389	GACTTTGGTAGTCTGAAAAG	ATGTGCTGAAAAAGAGAGAAAGCAATGCCCTGTGCTT		2448
QY	2437	GAAAGATAGAGATTAAT	ATGTTGCCCTATGTTTGATTCACACCTTTCTTCTGTCAAG		2496
Db	2449	GAAAGATAGATTAATCA	GAGAGTGCC-----TTTTCGACCCCTTTCTT-----		2490
QY	2497	AAATGTAGTATAGTGGGAG	ACAAGTCAGATCAATAGGTTCA	GTTCCATATCTAATCTC	2556
Db	2491	-----TCTAATCTT			2499
QY	2557	ATGCTCTTACTTCCCTC	CAAAATTGCTATTAACAAGAAGATGCTCACTCCAGAAAG		2616
Db	2500	AGGCTCTTACTTCCCTC	AGAAATTTGCTATTAATAGCTACTTCACTCCAGAAAG		2559
QY	2617	ATGTTCAAAAGCCTTG	CAAAATCTCAAAATCTGSAATATCTTTTTCCTTCATATCTTAAA		2676
Db	2560	ATGTTCAAAAACCTTG	CAAAATCTCAAAATCTGSAATATCTCTGGTCAATATCTCAAA		2619
QY	2677	GAGCTGCCCTAC	CAGCCTGGCTAGTCTCAATGCTTTGGAAGCATCTGAAATTCATAGTTGT		2736
Db	2620	GAGCTGCCCTAC	CAGCCTGGCTAGTCTCAATGCTTTGGAAGCATTCATATTCATATTTGTGT		2679
QY	2737	TATGCACTAGAGATCT	CCCCGAGAGAGGTGTGAAGGTTTAATTCATCTCACACATTA		2796
Db	2660	TGCGACACTAGAGATCT	CCCCGAGAGAGGTGTGAAGGTTTAATTCATCTCACACAGATTA		2739
QY	2797	TCCATTAACATCTG	TGAAATGCTCAATGTTTACCGAGGGATTTGAGACACCTTAACAGCC		2856
Db	2740	TTTGTGTGAACCT	TATACATGCTTAATGTTTACAGAGGGAATTTGACACCTTAACAGCC		2799
QY	2857	CTCACAAAATTTAT	CAGTTGAGTTTGTCCAAAC	CTGAGCCAGCGGTGTGAGAGGGAGATA	2916
Db	2800	CTCACAAGATTTAA	AAAAATTCGGGAGATGTCCACA	CTGATCAAGCGGTGTGAGAGGGAGATA	2859
QY	2917	GGAGAACA	CTGTACAAAATTTGCTCACATTCCTCGTGTGTTAT		2964
Db	2860	GGAGAACA	CTGTGCACAAAATTTCTCACTTCTTAATGTGATATATAT		2907

KM	Rpi-blb protein; plant; late blight; Solanaceae; potato; tomato; gene;
XW	ds.
XX	Solanum bulbocastanum.
OS	
PN	US2003221215-A1.
XX	
PD	27-NOV-2003.
XX	
PF	07-FEB-2003; 2003JUS-00360522.
XX	
PR	07-FEB-2003; 2003JUS-00360522.
XX	
PA	(KWEB-) KWECK EN RESEARCHBEDRIJF AGRICO BV.
XX	
PI	Alliefs JHM, Van Der Vossen EAG;
XX	
DR	WI; 2004-010903/01.
XX	P-PADB; ADHS1537.
XX	
PT	New isolated or recombinant Rpi-blb nucleic acids and proteins, useful
PT	for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX	with resistance against oomycete infection.
XX	
PS	Claim 6; SEQ ID NO 48; 98bp; English.
XX	
CC	This invention relates to a novel DNA sequence in the field of plant
CC	disease, in particular oomycete infections. The DNA sequence encodes a
CC	protein which may provide a plant or its progeny with at least partial
CC	resistance against an oomycete infection caused by Phytophthora
CC	infestans. The invention may be useful for the development of compounds
CC	with a fungicide activity. The DNA sequence of the invention encodes an
CC	Rpi-blb protein comprising 970 amino acids. The nucleic acid, vector,
CC	cell, protein or binding molecule is useful for providing a plant or its
CC	progeny with resistance against an oomycete infection such as late blight
CC	(a disease of major importance to production of Solanaceae such as potato
CC	and tomato cultivars). The present sequence is that of the S
CC	bulbocastanum Rpi-blb gene of the invention.
XX	
SEQ	Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;
Query Match	70.0%; Score 2077.2; DB 12; Length 2913;
Best Local Similarity	83.5%; Pred. No. 0;
Matches 2495; Conservative	0; Mismatches 388; Indels 105; Gaps 8
QY	1 ATGCGCTGAAGCTTTCCTCAAGTTCTGTGACAAATGTGACTTGTCATCCAAGGGGAA 60
DB	1 ATGCGCTGAAGCTTTCATTCAAGTTCTGTGACAAATCTCACTTTCTCAAAGGGGAA 60
QY	61 CTGTGATGTAATCTGTGTTTTAAAGATGATGCAGAAAAGCTTCAAGCAGCTTACTACA 120
DB	61 CTGTGATGTCCTTTTCGGTTTTCAAGATGAGATTCAAAGGCTTTCAGAGCATGTTTCTACA 120
QY	121 ATCCAGACTGTGCTTAGAAGATGCTCAGAGAAGCAATTGAGAGCAAGCAATTAATAAT 180
DB	121 ATTCAAGCGGTCCTTGAAGATGCTCAGAGAAACCACTAACACAAAGCTCTAGAAAAAT 180
QY	181 TGGTTCAGAAACTCAATGCTGCTGATAGAGGCTGATGACATCTTGGACGATGTAAA 240
DB	181 TGGTTCAGAAAATCAATGCTGCTGATAGATGAGTGTGATGATGATTAATAATAA 240
QY	241 ACTGAGGCAACCAATTAGACAGAGAGAACCAATATGSGTGTATCATCAAAAGCTTATC 300
DB	241 ACCAAGGGCACAA--AAATTTCTCCCAAGTCTGAATATAGGCCGCTTATCATCAAAAGCTTATC 297
QY	301 ACTTTTGCTCAAGATTTGGGAAAAGGATGAATAAGATTATAGAGAAACTGATGTTAAT 360
DB	298 CCTTTCCTGTCACAAAGTCTGGGAAAAGATGACCAAGTATGATAAAAACTAAGGCAAT 357
QY	361 GAGAGGAAAGCAATTAAAGTTCAATTTGGATGAAGAAAGCACTATAGAGAGCAAGTTGCTACA 420
DB	358 GCTAGGAAAGAAAGAAATTTTCATTTTGCAACGAAAAATGTGTGACAGCAAGCTTTTGA 417

421 GCCCAACAGGTTTGTGTTGAATGACCAAGATTATGAAAGACAAAGAAAGAC 480
418 CCGGAAACAGTTCGTGTATTAACCGAACCGAGTTTATGAAAGACAAAGAAAGAT 477
481 GAGATAGTGAATTCCTGATTAACAATGTACCAATGCCAAACCTTCAGTCTCCCA 540
478 GAGATAGTGAATTCCTGATTAACAATGTAGAGTCCCAACCTTCAGTCTCCCA 537
541 ATACTTGTGATGGGGGACCTAGAAAGACAGCTCTTGCCCAATGGTCTTCAATGAC 600
538 ATACTTGTGATGGGGGACCTAGAAAGACAGCTCTTGCCCAATGGTCTTCAATGAC 597
601 AGAGTATAGTGAATTCCTGATTAACAATGTAGAGTCCCAACCTTCAGTCTCCCA 660
598 AGAGTATAGTGAATTCCTGATTAACAATGTAGAGTCCCAACCTTCAGTCTCCCA 657
661 AGAGTATAGTGAATTCCTGATTAACAATGTAGAGTCCCAACCTTCAGTCTCCCA 717
658 AGAGTATAGTGAATTCCTGATTAACAATGTAGAGTCCCAACCTTCAGTCTCCCA 717
718 GACTTGGCTCAGCTTCAAAAGAGCTTGGGGCTTGGCTGATGAAAGAAATATTTGCTC 777
718 GACTTGGCTCAGCTTCAAAAGAGCTTGGGGCTTGGCTGATGAAAGAAATATTTGCTC 777
778 GTCTTAGATGATGTTTGAATGAAAGATCAAGATTAAGTGGCTTAAGTGAACAGTCTG 837
778 GTCTTAGATGATGTTTGAATGAAAGATCAAGATTAAGTGGCTTAAGTGAACAGTCTG 837
838 AAGTTTGAAGCAAGTGGCTTCTGTCTTCAACCACTACTGCTTGAAGAAAGTGGATCA 897
838 AAGTTTGAAGCAAGTGGCTTCTGTCTTCAACCACTACTGCTTGAAGAAAGTGGATCA 897
898 ATTATGGGAACTTGAACCATATGAAATTTGCTCAAGAAATGTTGGTTG 957
898 ATTATGGGAACTTGAACCATATGAAATTTGCTCAAGAAATGTTGGTTG 957
958 TTGTTCACTGACAGTGGCTTGGGCAACCAAGAAATTAATCTTAATCTTGGCTATC 1017
958 TTGTTCACTGACAGTGGCTTGGGCAACCAAGAAATTAATCTTAATCTTGGCTATC 1017
1018 GGAAGAGAGATTTGTGAAAAATGTGGTGTGCTTGAACCTTAATCTTGGCTATC 1077
1018 GGAAGAGAGATTTGTGAAAAATGTGGTGTGCTTGAACCTTAATCTTGGCTATC 1077
1078 AATTGGCTTGAAGAGAAAGAAAGACAGTGGGAACTTGAAGATGAGATTTGG 1137
1078 AATTGGCTTGAAGAGAAAGAAAGACAGTGGGAACTTGAAGATGAGATTTGG 1137
1138 AAATTTGCTCAAGAGAAAGTCTATCTGCTGCTGAGACTTGAATCCATGACCTT 1197
1138 AAATTTGCTCAAGAGAAAGTCTATCTGCTGCTGAGACTTGAATCCATGACCTT 1197
1198 CCACCTGATTTGAAACCAATGCTTTCGATATGTGGGAGTTCCTCAAGAGATCCAAATG 1257
1258 GAAAAGGAAATCTATCTCTCTGAGAGAGCAATGTTTTATTTATTCGAAAGAAAC 1317
1258 GAAAAGGAAATCTATCTCTCTGAGAGAGCAATGTTTTATTTATTCGAAAGAAAC 1317
1318 TTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1318 TTGAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
1378 CAAGAGATTTGAATTTGCTGCAACTTATTTCAAGATGATGATGATGATGATGATGAT 1437
1378 CAAGAGATTTGAATTTGCTGCAACTTATTTCAAGATGATGATGATGATGATGATGAT 1437
1438 CTGGGAACATCTCTATTTTGGGCAAGCAATCAAGCAAGCAATTCGGAAGAAATTTGTA 1497
1438 CTGGGAACATCTCTATTTTGGGCAAGCAATCAAGCAAGCAATTCGGAAGAAATTTGTA 1497
1498 GAAAATTCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557

1498 CACAGTTCACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
1558 TCCCACTTGAAGATTTGCTGCTGAGAGGAGCTTAATCTTAAGTGAACATTAAGCTTAAG 1617
1558 TCCCACTTGAAGATTTGCTGCTGAGAGGAGCTTAATCTTAAGTGAACATTAAGCTTAAG 1617
1618 CAGTACCGTCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
1618 CAGTACCGTCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
1618 AAGTACCATCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1674
1675 AAGTACCATCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1674
1738 CTACATGCTGATCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1797
1738 CTACATGCTGATCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1797
1735 CTACATGCTGATCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1794
1798 CGAATCTTCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857
1795 CGAATCTTCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
1858 TTGACATGCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1917
1858 TTGACATGCTTCACTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
1918 CTGCTGATTAATGCAAAACCTTAATCTTGAAGATGATGATGATGATGATGATGATGAT 1977
1912 CTGCTGATTAATGCAAAACCTTAATCTTGAAGATGATGATGATGATGATGATGATGAT 1971
1978 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2037
1972 GTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2031
2038 TTAAGCATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
2032 TTAAGCATGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2088
2088 GTGCTTGAAGCTTCAAAACCTTAATCTTGAAGATGATGATGATGATGATGATGATGAT 2157
2088 GTGCTTGAAGCTTCAAAACCTTAATCTTGAAGATGATGATGATGATGATGATGATGAT 2148
2158 GGAATCCGCTTCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2217
2149 GGAATCCGCTTCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2208
2218 ATCATCACTTCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2277
2209 ATTAGCAACTTCCAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2268
2278 AGCTAGAGTGTGAGAGGAGGCTTGGGAGTGAAGTGTG----- 2320
2269 AGCTAGAGTGTGAGAGGAGGCTTGGGAGTGAAGTGTG----- 2328
2321 ----ATTCTGATTTCCCAAGAAAGAGTTCATCTGAGAAACCTTAATTAAGC 2376
2329 GTTCACTTGAATTTCCCAAGAAAGAGTTCATCTGAGAAACCTTAATTAAGC 2388
2377 GAATTTGATTAATCTGAAGAGTTCCTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2436
2389 GACTTGTGATGCTGAAGAGTTCCTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2448
2449 GAAGAGATGATTAATCTGAGAGAGTTCCTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 2490
2497 AAATTTGATTAATGAG 2556
2491 ----TCAATCTT 2499
2557 ATGCTTACTTCCCTCCAAATTCGCTATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 2616

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Dh 2500 AGGGCTTACTTCCCTCAGAAATTGCTATATAAAGTAGTACTTCAATCCACAGAG 2559
Qy 2617 ATGTTCAAAAAGCTTGCAAAATCTCAAAATCTGAAATATCTTTTACTTCAATCTTAA 2676
Db 2560 ATGTTCAAAAAGCTTGCAAAATCTCAAAATCTGAAATATCTTTTACTTCAATCTTAA 2619
Qy 2677 GAGCTCCTACAGAGCTGAGTCTCAGAGCTTGAACATCTGAAATTCATAGTTGT 2736
Db 2620 GAGCTCCTACAGAGCTGAGTCTCAGAGCTTGAACATCTGAAATTCATAGTTGT 2679
Qy 2737 TATGCACTAGAGAGTCTCCCGAGAGAGGTGAAGTTTAATTCATCAACAGTTA 2796
Db 2680 TGGGCACTAGAGAGTCTCCCGAGAGAGGTGAAGTTTAATTCATCAACAGTTA 2739
Qy 2797 TCCATACATCTGCAATATGCTCAATTTTACCGAGAGAGTTGACAGCTTAACAGCC 2856
Db 2740 TTTGTTGAACACTGTAACATGCTAAATTTTACCAAGAGAGTTGACAGCTTAACACC 2799
Qy 2857 CTCACAAATTTATCAGTTGAGTTTGTCCACACACTGCGCAGCGGTGAGAGAGGAATA 2916
Db 2800 CTCACAAATTTTAAATTTGGGGAGTGTCCACACACTGATCAAGCGGTGAGAGAGGAATA 2859
Qy 2917 GGAGAAAGCTGTGACAAAATTTCTCAATCTCTCGTGTGTTTAT 2964
Db 2860 GGAGAAAGCTGTGACAAAATTTCTCAATCTCTATGTAATATAT 2907
```

RESULT 7

ADFI17763

ID ADFI17763 standard; DNA; 3971 BP.

XX ADFI17763;

DT 12-FEB-2004 (first entry)

DE S_bulbocastanum RGC3-b1b coding DNA containing an intronic sequence.

XX gene; ds; RGC3-b1b; Rpi-b1b gene cluster; growth regulant;
KM oomycete infection; introgression breeding; plant; late blight.

XX Solanum bulbocastanum.

FH Key Location/Qualifiers

FT CDS 1..3971

FT /*tag= a

FT /product= "RGC3-b1b protein"

FT /note= "this coding sequence contains one intron"

FT /transl_except= (pos: 1459..14560, aa: Gly)

FT intron 428..1458

FT /*tag= b

FT /number= 1

XX EPI334979-A1.

XX 13-AUG-2003.

XX 08-FEB-2002; 2002EP-00075565.

XX 08-FEB-2002; 2002EP-00075565.

XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

XX Van Der Vossen EAG, Allefs JHM;

XX WPI; 2003-714339/68.

XX P-PSDB; ADFI17766.

PT New resistance gene conferring resistance against an oomycete pathogen,
PT useful for producing plants, especially potatoes and tomatoes, resistant
PT against oomycete pathogens such as Phytophthora infestans.

XX Example 5; SEQ ID NO 39; 86pp; English.

CC This invention relates to novel isolated polynucleotides that confer
CC resistance against late blight caused by the oomycete pathogen
CC Phytophthora infestans, which threatens both tomato and potato crops.
CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
CC and which cause disease resistance to bacteria, fungi, nematodes etc.
CC These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
CC described as plant growth regulants. They are useful in providing
CC resistance to Phytophthora infestans, especially in Solanum tuberosum
CC (potato) plants to protect against oomycete infection or to demonstrate
CC disease susceptibility. Resistance can be conferred by transformation of
CC existing potato and tomato cultivars with the gene, a procedure that is
CC more straightforward and faster than conventional introgression breeding.
CC This polynucleotide sequence is the Solanum bulbocastanum RGC3-b1b coding
CC DNA containing an intronic sequence in an exemplification of the
CC invention.

SQ Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;

Query Match 63.4%; Score 1880.8; DB 10; Length 3971;

Best Local Similarity 85.5%; Pred. No. 0;

Matches 2173; Conservative 0; Mismatches 342; Indels 27; Gaps 6;

Qy 426 AACAGTTTTTTTGAATGACACCAAGTTTANGAGAGACAAAGAAAGACAGAT 485
Db 1454 ACCAGTTCTGTGTTAACTGAACCAAGTTTANGAGAGACAAAGAAAGATGAGAT 1513

Qy 486 AGTAAATTCCTGATTAACCAATGTAGCAATGCCAAACCTTCAGTCTCCAAATCT 545
Db 1514 AGTAAATTCCTGATTAACCAATGTAGTATGCCAAACCTTCAGTCTCCAAATCT 1573

Qy 546 TGGTATGCGGGGACCTGAGAAAGACGCTCTGCCAAATGCTTCAATATATAGAGAT 605
Db 1574 TGGTATGCGGGGACCTGAGAAAGACGCTCTGCCAAATGCTTCAATATATAGAGAT 1633

Qy 606 AATTGAGCATTTTCATCCCAATATGATGATTTGTCTCGAGAAATTTTAATGAGAG 665
Db 1634 AACTGAGCGTTTCTATCCCAATATGATGATTTGTCTCGAGATTTTATGAGAGAG 1693

Qy 666 GTTGATTAAGAAATTTGAGATCTATTGAAGAAAGTCACTTGTCGATGAGCTTGGC 725
Db 1694 GTTGATTAAGAAATTTGAGATCTATTGAAGAGAGTCCCTCAGTGAATGAGCTTGGC 1753

Qy 726 TCCATTTCAAAAGACCTCGGAGCTTGCTGAATGAGAAATATTTCTGTCTTAA 785
Db 1754 TCCATTTCAAAAGACCTCGAGTGTCTGAATGAGAAATATTTCTGTCTTAA 1813

Qy 786 TGAATTTGGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGCAAGCTTGAAGGTTGG 845
Db 1814 TGAATTTGGAATGAAGATCAAGATTAAGTGGCTAATTTAAGGAGAGCTTGAAGGTTGG 1873

Qy 846 AGCAAGTGGCGCTTCTGTTCTAACCACTACTGCTTGAAAGGTTGATCAATATGGG 905
Db 1874 AGCAAGTGGCGATTTGTTCTTAACCTACTGCTTGAAAGGTTGATCAATATGGG 1933

Qy 906 AACATTGCAACCAATGAAATTTGCAAAATTTGCTCAAGAAATGTTGGTTGTTCAT 965
Db 1934 AACATTGCAACCAATGAAATTTGCAAAATTTGCTCAAGAAATGTTGGTTGTTCAT 1993

Qy 966 GCAACGTGATTTGGGACCAAGAAATTAATCTTAATCTTGCTATCGAAGAGA 1025
Db 1994 GCAACGTGATTTGGACCAAGAAATTAATCTTAATCTTGCTATCGAAGAGA 2053

Qy 1026 GATTGGAATAAATGAGTGTGCTCTGACACTAAATCTTGAAGGATTTTGGCG 1085
Db 2054 GATTGGAATAAATGAGTGTGCTCTGACACTAAATCTTGAAGGATTTTGGCG 2113

Qy 1086 CTTTAAGAGAGAAAGACAGTGGAAATGATGAGATGATGATTTGGAATTTGCC 1145
Db 2114 CTTTAAGAGAGAAAGACAGTGGAAATGATGAGATGATGATTTGGAATTTGCC 2173

Qy 1146 TCAAGAAAGTTTATTTGCTGCTGCTGAGACTTATGTTACATCACTTCCACTTGA 1205
Db 1146 TCAAGAAAGTTTATTTGCTGCTGCTGAGACTTATGTTACATCACTTCCACTTGA 1205

Db 2174 TCAGATGAAAGTCTATTCCTGCTGCCCTGAGGCTTAGTACATCATCTTCCACTTGA 2233
Qy 1206 TTGAGACAATGCTTTACATATTTGTGACATATTTCCAAAGATACCAAAATGAAAGG 1265
Db 2234 TTTGAGACAATGCTTTGTGATATTTGCGGTAATTTCCAAAGACACCAAAATGCAAGGA 2293
Qy 1266 AAATCTAATCTCTCTGAGATGCAATGCTTTTATTTTATGAAAGAACTTGGAGCT 1325
Db 2294 AAATCTAATGCTTTTGGATGCGACATGCTTTTCTTTATTCGAAAGAAATTTGGAGCT 2353
Qy 1326 AGAGAAATGAGTATGAGATGAGAAATTAATTAATCTGAGTCTTTCTCCAGATAT 1385
Db 2354 AGAGATATGAGTATGAGATGAGAAATTAATTAATCTGAGTCTTTCTCCAGATAT 2413
Qy 1386 TGAATTAATCTGATCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAC 1445
Db 2414 TGAATTAATCTGATCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAC 2473
Qy 1446 ATCTCTATTTTGGGAGACATCAAGACATATTCGAGAAATTAATGTAAGAAATTA 1505
Db 2474 ATCTCTATTTTGGGAGACATCAAGACATATTCGAGAAATTAATGTAAGAAATTA 2533
Qy 1506 CATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
Db 2534 TGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
Qy 1566 GAGAGATTTGCTGAGGAGTCTTAATCTAGATGATCAATTAAGATGATGATGATGAT 1625
Db 2594 GAGAGATTTGCTGAGGAGTCTTAATCTAGATGATCAATTAAGATGATGATGATGAT 2653
Qy 1626 GTCTTCCATGAGATCTAGATCAATTAAGATCAATTAAGATCTGAGATCTGAGAT 1685
Db 2654 ATCTTCCATGAGATCTAGATCAATTAAGATCAATTAAGATCTGAGATCTGAGAT 2713
Qy 1686 TGTGATGATTTTCCAAACCAATTAAGATCAATTAAGATCTGAGATCTGAGAT 1745
Db 2714 TGTGATGATTTTCCAAACCAATTAAGATCAATTAAGATCTGAGATCTGAGAT 2773
Qy 1746 CTGATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805
Db 2774 TTGGAATCT 2833
Qy 1806 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
Db 2834 TTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2890
Qy 1866 CCTTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1925
Db 2891 CCTTACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2947
Qy 1926 ATTACGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1985
Db 2948 ACTAATAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3007
Qy 1986 TGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
Db 3008 AGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3067
Qy 2046 GAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
Db 3068 GAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3115
Qy 2106 AGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2165
Db 3116 AGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3175
Qy 2166 TGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2225
Db 3176 TGTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3235
Qy 2226 TTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2285
Db 3236 TTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3295

Qy 2286 GTTGTGAGAGGAGTCTGCGAAGTGAAGTGAATGTTGATTTCTGATTTCCCTACAAAGAG 2345
Db 3286 GTTGTGAGAGGAGTCTGCGAAGTGAAGTGAATGTTGATTTCTGATTTCCCTACAAAG 3352
Qy 2346 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2405
Db 3353 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3412
Qy 2406 AAAG 2465
Db 3413 AAAG 3472
Qy 2466 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2525
Db 3473 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3526
Qy 2526 TGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2585
Db 3527 TGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3586
Qy 2586 TTAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2645
Db 3587 TTAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3646
Qy 2646 CTGGAATATCTCTTTTACTTCAATCTTAAGAGCTGCTCAAGCTGCTGCTGCTGCTGCT 2705
Db 3647 CTGGAATATCTCTTTTACTTCAATCTTAAGAGCTGCTCAAGCTGCTGCTGCTGCTGCT 3706
Qy 2706 TGTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2765
Db 3707 TGTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3766
Qy 2766 TGTGAAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2825
Db 3767 GGTGAAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3826
Qy 2826 TTTACCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2885
Db 3827 TTTACCGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3886
Qy 2886 AACACTGCGCAGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2945
Db 3887 AATAGTATTAAGCGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3946
Qy 2946 TCTCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2967
Db 3947 TCTCTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3968

RESULT 8
ADH51535
ID ADH51535 standard; DNA; 3971 BP.
XX
AC ADH51535;
XX
XX 25-MAR-2004 (first entry)
DE
DE S bulbocactanum RGC3-b1b gene SegID52.
XX
XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW de; RGC3-b1b.
XX
OS Solanum bulbocactanum.
XX
XX US2003221215-A1.
XX
XX 27-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
PR

XX (KME-) KMEK EN RESEARCHBEDRIJF AGRICO BV.
PA Allefs JHM, Van Der Vossen EAG;
PI WPI, 2004-010903/01.
XX

PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX

PS Claim 6; SEQ ID NO 52; 98pp; English.

XX This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
XX protein which may provide a plant or its progeny with at least partial
XX resistance against an oomycete infection caused by Phytophthora
XX infestans. The invention may be useful for the development of compounds
XX with a fungicide activity. The DNA sequence of the invention encodes an
XX Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX cell, protein or binding molecule is useful for providing a plant or its
XX progeny with resistance against an oomycete infection such as late blight
XX (a disease of major importance to production of Solanaceae such as potato
XX and tomato cultivars). The present sequence is that of the S
XX bulbocactanum RG3-b1b gene which is related to the invention.

XX Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;

Query Match 63.4%; Score 1880.8; DB 12; Length 3971.

Best Local Similarity 85.5%; Pred. No. 0;
Matches 2173; Conservative 0; Mismatches 342; Indels 27; Gaps 6;

QY 426 AACAGGTTTGTGTTGAATGAACCAAGTTATGAGAGAGACAAAGAAAGACGAGAT 485
DB 1454 ACCAGGTTCTGTGTTAACTGAACCAAGTTATGAGAGAGACAAAGAAAGATGAGAT 1513
QY 486 AGTGAATTCCTGAATGAACCAAGTTATGAGAGAGACCAAGTTATGAGAGAT 545
DB 1514 AGTGAATTCCTGAATGAACCAAGTTATGAGAGAGACCAAGTTATGAGAGAT 1573
QY 546 TGTATGAGGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
DB 1574 TGTATGAGGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1633
QY 606 AATTGAGATTTCATCCCAAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
DB 1634 AACTGAGGTTTCTATCCCAAAATATGAGAGAGAGAGAGAGAGAGAGAGAG 1693
QY 666 GTTATGAAGAGAGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
DB 1694 GTTATGAAGAGAGATGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1753
QY 726 TCCACTTCAAAAGAGGTTGCGGAGTCTGAGATGAGAGAGAGAGAGAGAGAG 785
DB 1754 TCCACTTCAAAAGAGGTTGCGGAGTCTGAGATGAGAGAGAGAGAGAGAGAG 1813
QY 786 TGAATGTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 845
DB 1814 TGAATGTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 1873
QY 846 AGCAAGTGGGCTCTGTTCAACCACTACCTGCTGAGAGAGAGAGAGAGAGAG 905
DB 1874 AGCAAGTGGGCTCTGTTCAACCACTACCTGCTGAGAGAGAGAGAGAGAGAG 1933
QY 906 AACATGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 965
DB 1934 AACATGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1993
QY 966 GCAAGGCAATTTGGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1025
DB 1994 GCAAGGCAATTTGGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2053
QY 1026 GATTTGAGAAAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1085

DB 2054 GATTTGAGAAAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2113
QY 1086 CTTTAAAG 1145
DB 2114 CTTTAAAG 2173
QY 1146 TCAAG 1205
DB 2174 TCAAG 2233
QY 1206 TTTGAGCAATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1265
DB 2234 TTTGAGCAATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 2293
QY 1266 AATCTATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1325
DB 2294 AATCTATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2353
QY 1326 AG 1385
DB 2354 AG 2413
QY 1386 TGAAGTTAAATCTGATCAATCTATGATGATGATGATGATGATGATGATGAT 1445
DB 2414 TGAAGTTAAATCTGATCAATCTATGATGATGATGATGATGATGATGATGAT 2473
QY 1446 ATCTATATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1505
DB 2474 ATCTATATTTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2533
QY 1506 CATACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
DB 2534 TGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
QY 1566 GCAAGAGTTGTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1625
DB 2594 GCAAGAGTTGTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 2653
QY 1626 GTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1685
DB 2654 ATCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2713
QY 1686 TCGTATGTTTCCAAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1745
DB 2714 TCGTATGTTTCCAAACCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2773
QY 1746 CTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805
DB 2774 CTGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2833
QY 1806 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
DB 2834 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2890
QY 1866 CCTTAAAGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGAT 1925
DB 2891 CCTTAAAGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGAT 2947
QY 1926 ATTAAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1985
DB 2948 ACTTAAAGAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3007
QY 1986 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
DB 3008 AGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3067
QY 2046 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
DB 3068 GAGTTGGGAGCTTGAATGATAA---ACATGATATGATGATAA---GAAATCTTGA 3115
QY 2106 AGCTTCAAAACCACTTCAATGATGATGATGATGATGATGATGATGATGATGAT 2165

Db 3116 AGCCCTCAACCACTCCCAATCTGAAATATTAGAAATCAATGGCTTCGAGAAATCCG 3175
 Qy 2166 TCTCCCAAGATGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 2225
 Db 3176 TCTCCCAAGATGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 3235
 Qy 2226 TTGCAAAATGCTGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 2285
 Db 3226 TTGCAAAATGCTGATGATCACTCAGTTTGGAAAAATGTTGCTCTATTTGAATCATCAG 3295
 Qy 2286 GTTGGAGAGGGGCTGCGGAAAGTGAATGTTGATTTGGATTTCCCTCAAGAAAGAG 2345
 Db 3296 GTTGGAGAGGGGCTGCGGAAAGTGAATGTTGATTTGGATTTCCCTCAAGAAAGAG 3352
 Qy 2346 GTTTCATCTCTGAGAAATTAATATACGGAAATTTGATATCGAAAGATTTGCTGAA 2405
 Db 3353 GTTTCATCTCTGAGAAATTAATATACGGAAATTTGATATCGAAAGATTTGCTGAA 3412
 Qy 2406 AAAGGAGAGAGAGCAATGCTGCTGCTGAGAGATAGAGATTAATGTTGCTGAT 2465
 Db 3413 AAAGGAGAGAGAGCAATGCTGCTGCTGAGAGATAGAGATTAATGTTGCTGAT 3472
 Qy 2466 GTTGTATATCCAACTCTTCTCTGCTCAAGAAATTTGATTTGGAGGAGCAAGTCA 2525
 Db 3473 GTTGTATATCCAACTCTTCTCTGCTCAAGAAATTTGATTTGGAGGAGCAAGTCA 3526
 Qy 2526 TGCAATAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2585
 Db 3527 TGCAATAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3586
 Qy 2586 TAAAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2645
 Db 3587 TAAAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3646
 Qy 2646 CTGGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2705
 Db 3647 CTGGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3706
 Qy 2706 TGCTTTGAGAGATCGAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2765
 Db 3707 TGCTTTGAGAGATCGAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 3766
 Qy 2766 TGTGAAAGATTTATTTCTACTCAGACAGATTTTCAATACATCTGTAATGCTTCAATG 2825
 Db 3767 GGTGAAGATTTATTTCTACTCAGACAGATTTTCAATACATCTGTAATGCTTCAATG 3826
 Qy 2826 TTTACCGGAGGATTTGAGACCTTACAGCCCTCAAAATTTATCAGTTGAGTTTGTCC 2885
 Db 3827 TTTACCGGAGGATTTGAGACCTTACAGCCCTCAAAATTTATCAGTTGAGTTTGTCC 3886
 Qy 2886 AACACTGGCCCAAGGGGTGTGAGAGAGAGATTTGAGAGAGATTTGCTCAGAT 2945
 Db 3887 AATGATATTTCAAGGGGTGTGAGAGAGAGATTTGAGAGAGATTTGCTCAGAT 3946
 Qy 2946 TCCTCGTGTGTTTATTTATTTAG 2967
 Db 3947 TCCTCGTGTGTTTATTTATTTAG 3968
 RESULT 9
 ADF17760
 ID ADF17760 standard; DNA; 3592 BP.
 AC ADF17760;
 XX 12-FEB-2004 (first entry)
 DE Solanum bulbocastanum Rpi-b1b genomic DNA.
 XX Solanum bulbocastanum Rpi-b1b gene cluster; growth regulator;
 KM oomycete infection; introgression breeding; plant; late blight.
 XX Solanum bulbocastanum.
 OS

XX Key Location/Qualifiers
 FH CDS 1..3592
 FT 1..3592
 FT /*tag= a
 FT /product= "Rpi-b1b protein"
 FT /note= "this coding sequence contains one intron"
 FT /transl_except= (pos: 1107..1108, aa: Gly)
 FT intron 428..1106
 FT /*tag= b
 FT /number= 1
 XX
 XX EP1334979-A1.
 XX
 XX 13-AUG-2003.
 XX
 XX 08-FEB-2002; 2002EP-00075565.
 XX
 XX 08-FEB-2002; 2002EP-00075565.
 XX
 XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
 XX
 XX Van Der Vossen ENG, Allefs JHM;
 XX
 XX WPI; 2003-714439/68.
 DR P-PSDB; ADF17765.
 XX
 PT New resistance gene conferring resistance against an oomycete pathogen,
 PT useful for producing plants, especially potatoes and tomatoes, resistant
 PT against oomycete pathogens such as Phytophthora infestans.
 XX
 XX Example 5; SEQ ID NO 36; 86bp; English.
 PS
 CC This invention relates to novel isolated polynucleotides that confer
 CC resistance against late blight caused by the oomycete pathogen
 CC Phytophthora infestans, which threatens both tomato and potato crops.
 CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
 CC leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
 CC and which cause disease resistance to bacteria, fungi, nematodes etc.
 CC These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
 CC described as plant growth regulators. They are useful in providing
 CC resistance to Phytophthora infestans, especially in Solanum tuberosum
 CC (potato) plants to protect against oomycete infection or to demonstrate
 CC disease susceptibility. Resistance can be conferred by transformation of
 CC existing potato and tomato cultivars with the gene, a procedure that is
 CC more straightforward and faster than conventional introgression breeding.
 CC This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b genomic
 CC DNA of the invention.
 CC
 XX
 SQ Sequence 3592 BP; 1129 A; 659 C; 734 G; 1070 T; 0 U; 0 Other;
 Query Match 60.9%; Score 1805.8; DB 10; Length 3592;
 Beet Local Similarity 84.2%; Pred. No. 0;
 Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
 Qy 426 AACAGTTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
 Db 1102 ACCAGTTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
 Qy 486 AGTGAATATCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
 Db 1162 AGTGAATATCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1221
 Qy 546 TGTGATGAGGAGCTAG 605
 Db 1222 TGTGATGAGGAGCTAG 1281
 Qy 606 AATTGACATTTCCATCCCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 665
 Db 1282 TACTGACATTTCCATCCCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1341
 Qy 666 GTTGATTAAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 722
 Db 1342 GTTATATAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401

QY	723	GGCTCCAC	TTTCAAAAGAGCTTCGGGACTTGC	TGAAATGAAAAAAATATTTGCTGC	CTC	782
Db	1402	GGCTCCAC	TTTCAAAAGAGCTTCAGGAGTTGC	TGAATGAAAAAGATCTTGCTGTCT	CTC	1461
QY	783	AGATGATG	TTTGGAAAGATCAAGATATGATG	GGCTAGTTAAAGCAAGCTTTGAAGT		842
Db	1462	AGATGATG	TTTGGAAAGATCAAGATATGATG	GGCTAGTTAAAGCAAGCTTTGAAGT		1521
QY	843	TGGAGCAAG	TGGCGCTTCTGTTCTAACCACTAC	TACTGCTTTGAAAAGTTGATCAATAT		902
Db	1522	TGGAGCAAG	TGGCGCTTCTGTTCTAACCACTAC	TACTGCTTTGAAAAGTTGATCAATAT		1581
QY	903	GGGAATATTG	CAACCAATATGATTTGCTCAGAGAA	ATGTTGTTGTTGTT		962
Db	1582	GGGAATATTG	CAACCAATATGATTTGCTCAGAGAA	ATGTTGTTGTTGTT		1641
QY	963	CATGCAAC	TGCAATTTGGGACCAAGAAATTAAT	CTTATCTTGNGGCTATCCGAAA		1022
Db	1642	CATGCAAC	TGCAATTTGGGACCAAGAAATTAAT	CTTATCTTGNGGCTATCCGAAA		1701
QY	1023	GGAGATTGT	GAATAAAATGTGTGTGCTCTACAG	CTTAAACTCTTGAGGGTATTTT		1082
Db	1702	GGAGATTGT	GAATAAAATGTGTGTGCTCTACAG	CTTAAACTCTTGAGGGTATTTT		1761
QY	1083	GGGCTTTAA	GAGAGAAAGACAGTGGGACATGTGA	GAGATGATGATTTGAAATT		1142
Db	1762	GGGCTTTAA	GAGAGAGAAAGAGAGACATGTGA	GAGATGATGATTTGAAATT		1821
QY	1143	GGCTCAAG	AAGAAAGTTCTATTTCTGCTCCG	CCCTGAGACTTATGATCACTTCCACT		1202
Db	1822	GGCTCAAG	AAGAAAGTTCTATTTCTGCTCCG	CCCTGAGACTTATGATCACTTCCACT		1881
QY	1203	TGATTTGAG	CAATGCTTTACATATTTGCAATTC	CCAAAGATACCGAATGAGAAA		1262
Db	1882	TGATTTGAG	CAATGCTTTACATATTTGCAATTC	CCAAAGATACCGAATGAGAAA		1941
QY	1263	GGGAATCT	AAATCTCTCTGCGATGGGACATGAT	TTTATTTATGGAAGGAACTTGA		1322
Db	1942	GGGAATCT	AAATCTCTCTGCGATGGGACATGAT	TTTATTTATGGAAGGAACTTGA		2001
QY	1323	GCTAGAGA	ATGTAGTAAATGAAATGGAATGAA	TTATCTTGAGGCTCTTCTTCCAGA		1382
Db	2002	GCTAGAGA	ATGTAGTAAATGAAATGGAATGAA	TTATCTTGAGGCTCTTCTTCCAGA		2061
QY	1383	GATGAAGT	TAATCTGGTGCAACTTATTTTCAAG	ATGCAATGATCTCATGATCTGGC		1442
Db	2062	GATGAAGT	TAATCTGGTGCAACTTATTTTCAAG	ATGCAATGATCTCATGATCTGGC		2121
QY	1443	AACATCTCT	ATTTTTCGGCAAGACATCAAGCAG	CAATATCCGAGAAATATTTGAGAAA		1502
Db	2122	AACATCTCT	ATTTTTCGGCAAGACATCAAGCAG	CAATATCCGAGAAATATTTGAGAAA		2181
QY	1503	TTAATATCA	TATGATGTCACATTTGGTTTCACT	AAATGATGATCTTCTCTTTTCCCA		1562
Db	2182	TTAATATCA	TATGATGATGTCACATTTGGTTTCA	CTTAACTCTTCCCCC		2241
QY	1563	CTTGCAAA	AGTTTGTCTCGTTGAGGGGCTTAAT	CTTAAGGACATATAAATCTTAAGAGTT		1622
Db	2242	CTTGCAAA	AGTTTGTCTCGTTTAAAGATGCTTA	ATCTTAAGGATTCGACATTTAATAAGTT		2301
QY	1623	ACCGTCTT	CCATTGAGATCTAAGTCAATTTAAG	ATACCTAACTTGCGCAATCTAAG		1682
Db	2302	ACCGTCTT	CCATTGAGATCTAAGTCAATTTAAG	ATACCTAACTTGCGCAATCTAAG		2358
QY	1683	TATTCGAT	GCCTTCCAAACAGATTAAGGACGCT	TCCAAATCTGCGACACTCTGATCTTACA		1742
Db	2359	CATGCGAT	GCCTTCCAAACAGATTAAGGACGCT	TCCAAATCTGCGACACTCTGATCTTACA		2418
QY	1743	TGGCTGTC	ATCTCACTTGTGTGTGTGCGCAAA	AGAAACAAGCAAACTTGATGATCGAAA		1802
Db	2419	ATATTTGCA	CAAGCTTTGTTGTTTGGCAAAAGAA	CAAGTAACTTGGTATGCTCGAAA		2478

QY	1803	TCCTTTACCTTGAATGCGTGTGTATGAAATTTGA	CTTTGATGCGACCGAAGATGAGATCTTTGAC	1862
Db	2479	TCCTTTTACTTGATGATGAGCGACGTCACTTGA	CTTGATATGCGACCAAGATGAGATCAATTGAC	2538
QY	1863	ATGCGCTTAAGACCTTAAGTAGATTTGTGATGG	AGAAATTCAGAAAGAAATTTGCAACTTGG	1922
Db	2539	ATGCGCTTAAGACCTTAAGTAGATTTGTGATGG	AGAAAGATTTATCAACTTGG	2595
QY	1923	TGAATTAAGAAACCTGAATCTCTATATGCTCA	ATTGAATTCACGCACTTGGAGAGTGAA	1982
Db	2596	TGAACCTAGGAAACCTTAATCTCTATATGCTCA	ATTGAATTCGCACTTGGAGAGTGAA	2655
QY	1983	GAAATGATGATGATGCGAAAGAAAGCCAAATTA	TTATCTGCGAAGAAAGAAATTCGCACTTTAG	2042
Db	2656	GAAATGATGATGATGCGAAAGAAAGCCAAATTA	TTATCTGCGAAGAAAGAAATTCGCACTTTAG	2715
QY	2043	CATGAAATGCGATGACGATGAAACGTCCACGTA	TATATGAAATCAGAAAAAGTTGAAAGTCT	2102
Db	2716	CATGAGTTGGAATTAATCTTTG---GACCA	CATATATATGAAATCAGAAAGATTAAGTCT	2772
QY	2103	TGAACCTCCTCAACACACATCTGCAATCTGAT	CTTTGTTAAATCAGAGGGCTTCAGAGAAAT	2162
Db	2773	TGAACCTCCTCAACACACATCTGCAATCTGAT	CTTTGTTAAATCAGATGAGCTTCAGAGAAAT	2832
QY	2163	CCGTCCTCCACAGCTGATGAAATCACTCAGTTT	TGAAAAATGTTGTCTCTATTTGAAATCAT	2222
Db	2833	CCATCTCCACAGCTGATGAAATCACTCAGTTT	TGAAAAATGTTGTCTCTATTTGAAATGAG	2892
QY	2223	CAGTTGCAAAAATGCTCTATGCTTTACCA	CGCTTTGAGCTGCTTGTCTAAAGATCT	2282
Db	2893	CAACTTCAGAAACCTGCTCATGCTTTACCA	CGCTTTGAGCTGCTTGTCTAAAGATCT	2952
QY	2283	AGAGTTTGAGAGGGGGCTGCGAGAGTAGATAT	GTGTG-----A	2321
Db	2953	AGAGTTTACCTGGGGGCTTGGGATATGAGATAT	GTGTGAAAGATGAGATTTGATGTTTCA	3012
QY	2322	TTCTGGAATTCCTTACAGAAAGAAAGTTTCCAT	CTCTGAGAAAATTTAATATACGCGAATTT	2381
Db	3013	TTCTGGAATTCCTTACAGAAATTAAGTTTCCAT	CTCTGAGAAAATTTAATATATGAGACTTT	3072
QY	2382	TGCTATATCTGAAAGAGATTTGCTGAAAAA	AGAAAGAAAGCAATGCGCTGTCTTGAAATA	2441
Db	3073	TGCTATATCTGAAAGAGATTTGCTGAAAAA	AGAAAGAAAGCAATTCCTGTGTCTTGAAATA	3132
QY	2442	GATAGAGATTTAATATGTTGCCCCCTATGTTT	TTATTTCAACCCCTTTCTTGTCAAGAAATTT	2501
Db	3133	GATATATATTCACAGAGTGCCC-----	TTTCTGAGCCCTTTCT-----	3169
QY	2502	GCTAGTTAATGAGGGAGCAATGCAATGCAAT	AGATTTCAATTCATATCTAATCTATGCGC	2561
Db	3170	-----	-----TCTAATCTTAAAGGCG	3183
QY	2562	TCCTACTTCCCTCCAAATTCGTATATAACA	AGAAAGATGCTTCACCTCCAGAGAGATGTT	2621
Db	3184	TCCTACTTCCCTCCAAATTCGTATATAACA	AGATGCTTCATTCATTCCTCCAGAGAGATGTT	3243
QY	2622	CAAAAGCCTTGCAAAATCTCAAAATCTGTAAT	ATATCTCTTTTATCTTCAATCTTAAAGAGCT	2681
Db	3244	CAAAAGCCTTGCAAAATCTCAAAATCTGTAAT	ATATCTCTCTCGTCCAAATATCTCAAAAGAGCT	3303
QY	2682	GCGTACAGAGCTGGCTAGTCTCAATGCTTTGA	AGCATCTGCGAAATTCATATAGTGTGTAATGC	2741
Db	3304	GCGTACAGAGCTGGCTAGTCTCAATGCTTTGA	AGCATCTGCGAAATTCATATAGTGTGTGCGC	3363
QY	2742	ACTPAGAGAGTCTCCCGAGAGAGGTGTGA	AGAGTTAATTTCACTCAACAGTTATTCAT	2801
Db	3364	ACTPAGAGAGTCTCCCGAGAGAGGTGTGA	AGAGTTATTTATCTTACTCAACAGATTTATTTGT	3423
QY	2802	AACATATCTGGAATATGCTCAATGTTTAC	CCGAGAGAGATTCAGAGCATTAACGCTCTAC	2861
Db	3424	TGAACCTGTAACATGCTAAATATGTTTAC	CAAGAGGATTCAGCACTTAAACACCTCTAC	3483
QY	2862	AAATTTATCAGTTGAGTTTGTTCACCA	CTGCGCCAGAGGAGGTGTGAGAGGGAAT	2921

Db 3484 AAGTTAAAAATTCGGGAGATGCCAACATGATCAAGCGGTGTGAGAGGAAATGAGAGA 3543
QY 2922 AGACTGTACAAATTCGTCATTCCTCGTGTGTTATTTAT 2964
Db 3544 AGACTGGCAAAATTTCTCACATTCCTAAATGTGAATATAT 3586

RESULT 10
ADH51532
ID ADH51532 standard; DNA; 3592 BP.
XX
XX ADH51532;
AC ADH51532;
XX
XX 25-MAR-2004 (first entry)
DT
XX
DE S bulbocaezanum Rpi-b1b gene SeqID49.
XX
XX plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW de.
XX
OS Solanum bulbocaezanum.
XX
XX US2003221215-A1.
XX
XX 27-NOV-2003.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX 07-FEB-2003; 2003US-00360522.
XX
XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Allefs JHM, Van Der Vossen BAG;
PI WPI; 2004-010903/01.
XX
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
XX Claim 6; SEQ ID NO 49; 98bp; English.
XX
XX This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of the S
CC bulbocaezanum Rpi-b1b gene which is related to the invention.
XX
XX Sequence 3592 BP; 1129 A; 659 C; 734 G; 1070 T; 0 U; 0 Other;

Query Match 60.9%; Score 1805.8; DB 12; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;

QY 426 AACGAGTTTGTGTAATGACCAACAGTTTATGAGAGACAAAGAAAAGACGAGAT 485
Db 1102 ACCAGGTTCTGTATTAACCGAACCGAGTTTATGAGAGACAAAGAAAAGATGAGAT 1161
QY 486 AGTGAATTCCTGATTAACATGTTAGCAATGCCCAACACTTCAGTCCCTCCAAATCT 545
Db 1162 AGTGAATTCCTGATTAACATGTTAGTATGCCCAACACTTCAGTCCCTCCAAATCT 1221
QY 546 TGGTATGGGGGAGATGAGAAAGACACTTGTGCCCAATGCTTCAATGATCAGAGAGT 605

Db 1222 TGGTATGGGGGAGATGAGAAAGACACTTGTGCCCAATGCTTCAATGATCAGAGAGT 1281
QY 606 AATTGAGCATTTCCATCCCAAAATATGAAATTTGTCTCGGAGATTTTAATGAGAGAG 665
Db 1282 TACTGAGCATTTCCATTCCAAAAATATGAAATTTGTCTCGGAGAGATTTTAATGAGAGAG 1341
QY 666 GTTGATTAAGAAATTTGTAGAAATCTATTTGAAGAAAGTC--ACTGTGGCATGAGACTT 722
Db 1342 GTTAATTAAGCAATTTGATGAAATCTATTTGAAGAGAGCACTACTTGTGTGATGAGACTT 1401
QY 723 GGCCTCACTTCAAAAGAGCTTGGGACTTCTGTGAATATGAGAAAAAATTTGTCTGCTT 782
Db 1402 GGCCTCACTTCAAAAGAGCTTGGGAGTGTCTGAATATGAGAAAAAAGATCTGTCTGCTT 1461
QY 783 AGATGATGTTTGAATGAAGATCAAGATTAAGTGGGCTAAGTTAAGACAAAGCTTGAAGGT 842
Db 1462 AGATGATGTTTGAATGAAGATCAAGATTAAGTGGGCTAAGTTAAGACAAAGCTTGAAGGT 1521
QY 843 TGGAGCAAGTGGCGCTTCTGTCTAACCACTACTGCTTGTGAAAAAGTTGGATCAATAT 902
Db 1522 TGGAGCAAGTGGCGCTTCTGTCTAACCACTACTGCTTGTGAAAAAGTTGGATCAATAT 1581
QY 903 GGGAACTTGGCAACATATGATTTGCAAAATTTGTCTCAAGAGATTTGTTGTTGTT 962
Db 1582 GGGAACTTGGCAACATATGATTTGCAAAATTTGTCTCAAGAGATTTGTTGTTGTT 1641
QY 963 CATGCAACGTGCAATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGGCTATCGGAA 1022
Db 1442 CATGCAACGTGCAATTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGGCTATCGGAA 1701
QY 1023 GGAATTTGTGAAAAAATGTGGTGTGCTCTAGACAGCTTAAACCTTGTGAGGTATTTT 1082
Db 1702 GGAATTTGTGAAAAAATGTGGTGTGCTCTAGACAGCTTAAACCTTGTGAGGTATTTT 1761
QY 1083 GCGCTTTAAGAGAGAGAAAGACAGTGGAAACATGTGAAGATGTGAATTTGAAATT 1142
Db 1762 GTGCTTCAAGAGAGAAAGAGAGATGGGAAACATGTGAAGAGCTCGAATTTGAAATTT 1821
QY 1143 GCCCAAGAAAGAAAGTCTAATCTGCGCTGCGCTGAGACTTATGATCACTCCCTCACT 1202
Db 1822 GCCCAAGAAAGAAAGTCTAATCTGCGCTGCGCTGAGACTTATGATCACTCCCTCACT 1881
QY 1203 TGATTTGAGCAATGCTTTTACATATTTGTGAGATTTCCCAAGAGATCCGAATGAGAAA 1262
Db 1882 TGATTTGAGCAATGCTTTTACATATTTGTGAGATTTCCCAAGAGATCCGAATGAGAAA 1941
QY 1263 GGGAAATCTAATCTCTCTGTGATGSCACATGTTTATTTATTCGAAAGAAAATTGGA 1322
Db 1942 AGAAATCTAATCTCTCTGTGATGSCACATGTTTATTTATTCGAAAGAAAATTGGA 2001
QY 1323 GCTAGAGAAATGTAAGTAAAGATGAAATGAAATTAATCTGAGAGCTTCTTCCAGA 1382
Db 2002 GCTAGAGAAATGTAAGTAAAGATGAAATGAAATTAATCTGAGAGCTTCTTCCAGA 2061
QY 1383 GATTGAAGTTAAATCTGTGCAAACTTATTTCAAGATCATGATCTCAATGATCTGGC 1442
Db 2062 GATTGAAGTTAAATCTGTGCAAACTTATTTCAAGATCATGATCTCAATGATTTGGC 2121
QY 1443 AACATCTTAATTTGGCAAGACATCAAGCAGCAATATCCGAGAAATTAATTTAGAAA 1502
Db 2122 AACATCTTAATTTGGCAAGACATCAAGCAGCAATATCCGAGAAATTAATTTAGAAA 2181
QY 2182 TTACACACATATATATGTCATGCTTGTGCGGAGATGATTTTATTTTCACTCTCCCC 2241
QY 1563 CTTCGAGAAATTTGTCTGTGAGGGGTCTTAATCTTAAGTACATAAACTTAAGCAGTT 1622
Db 2242 CTTCGAGAAATTTATCTGTGTAAGAGTCTTAATCTTAAGTATTCGACATTTAATAGTT 2301
QY 1623 ACCGTTCTTCATTTGAGATCTAATGATCTTAATTAAGATCTTAATCTTGTGCAATATCTAG 1682
Db 2302 ACCATCTTCCATTTGAGATCTAATGATCTTAATTAAGATCTTAATCTTGTGCAATATCTAG 2358

1683 TATTGGAGTCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTGCAGACTTGTATCA 1742
1743 TGGCTGTCACTTCCTTGTGTGTCACCAAGCAAGCAAACTGTGTATCTTGAAA 1802
1803 TCTTTTACTGATAGTGTGCTATGATGATGATGATGATGATGATGATGATGAT 1862
1803 TCTTTTACTGATAGTGTGCTATGATGATGATGATGATGATGATGATGATGAT 1862
2479 TCTTTTACTGATAGTGTGCTATGATGATGATGATGATGATGATGATGATGAT 2538
1863 ATGCTTTAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGAT 1922
2539 ATGCTTTAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGAT 2595
1923 TGAATTAACAACCTGAATCTCTATGATGATGATGATGATGATGATGATGAT 1982
2596 TGAATTAACAACCTGAATCTCTATGATGATGATGATGATGATGATGATGAT 2655
1983 GAATGATTAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2042
2656 GAATGATTAAGTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2715
2043 CATGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
2716 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2772
2103 TGAAGCTCTCAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2162
2773 TGAAGCTCTCAACCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2832
2163 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
2833 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2892
2223 CAGTTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2282
2893 CAGTTGCAAAAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2952
2283 AGAGTGTGAG 2321
2953 AGAGTGTGAG 3012
2322 TTCTGATTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2381
3013 TTCTGATTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3072
2382 TGTGATTTGAG 2441
3073 TGTGATTTGAG 3132
2442 GATAGAGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2501
3133 GATAGAGATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3169
2502 GGTAGTATGAG 2561
3170 GGTAGTATGAG 3183
2562 TCTTACTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2621
3184 TCTTACTTCCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243
2622 CAAAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2681
3244 CAAAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3303
2682 GCTTACCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2741
3304 GCTTACCAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 3363

2742 ACTAGAGAGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2801
3364 ACTAGAGAGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3423
2802 AACATCTGTAATGCTCAAGATGTTTACCGAGAGAGAGAGAGAGAGAGAGAG 2861
3424 TGAACATCTGTAATGCTCAAGATGTTTACCGAGAGAGAGAGAGAGAGAGAG 3483
2862 AAATTTATCAAGTGAAGTGTGCTCAACACTGCGAGAGAGAGAGAGAGAGAG 2921
3484 AAGTTTAAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3543
2922 AGACTGTGCAAAATTTGCTCAATCTCTCGTGTGTTATTTAT 2964
3544 AGACTGTGCAAAATTTGCTCAATCTCTCGTGTGTTATTTAT 3586

RESULT 11
ADH51533
ID ADH51533 standard; DNA; 5191 BP.
XX
AC ADH51533;
XX
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum Rpi-b1b partial gene SeqID50.
XX
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
XX
OS Solanum bulbocastanum.
XX
PN US2003221215-A1.
XX
PD 27-NOV-2003.
XX
PF 07-FEB-2003; 2003US-00360522.
XX
PR 07-FEB-2003; 2003US-00360522.
XX
PA (KWE-) KWEER EN RESEARCHBEDRIJF AGRICO BV.
XX
PI Allefs JHM, Van Der Voessen EAG;
XX
DR WPI; 2004-010903/01.
XX
PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
PS Claim 6; SEQ ID NO 50; 98bp; English.
XX
CC This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a fragment of the
CC S bulbocastanum Rpi-b1b protein which is related to the invention.
XX
SQ Sequence 5191 BP; 1673 A; 877 C; 941 G; 1700 T; 0 U; 0 Other;

Query Match 60.9%; Score 1805.8; DB 12; Length 5191;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
426 AACAGTTTGTGTTGATGAAACCAAGTTTATGAAAGAGACAAAGAAAGAGAGAT 485

Db 2292 ACCAGGTTCTGATTAACCGAAGCCGAGGTTATGGAAGACAAAGGAAGATGAGAT 2351
Qy 486 AGTGAATTCGATTAACCAATGTTAGCAATGCCAACAACCTCCAGTCCCAATCT 545
Db 2352 AGTGAATTCGATTAACCAATGTTAGCAATGCCAACAACCTCCAGTCCCAATCT 2411
Qy 546 TGGTATGGGGGGAAGTGAAGAACGACTCTTGCCCAATGCTCTCAATGATCAGAGT 605
Db 2412 TGGTATGGGGGGAAGTGAAGAACGACTCTTGCCCAATGCTCTCAATGATCAGAGT 2471
Qy 606 AATTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATGAGAAG 665
Db 2472 TACTAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAGATTTTATGAGAAG 2531
Qy 666 GTTGAATAAGAAATTTGATGATCTAATGGAAGAAAGC---ACTGTGCGATGAGCT 722
Db 2532 GTTATTAAGGCAATTTGATGATCTAATGGAAGAAAGCCTACTTGTGTGAGATGAGCT 2591
Qy 723 GGCCTCACTTCAAAGAAGCTTCGGGACTTGCTGAATGGAAGAAATATTTGCTGCTT 782
Db 2592 GGCCTCACTTCABAAAGAGCTTCAGAGATGCTGAATGGAAGAAATATTTGCTGCTT 2651
Qy 783 AGATGATGTTGGAATGAAGATCAAGATPAAGTGGCTAAGTTAGACAAGTCTTGAGGT 842
Db 2652 AGATGATGTTGGAATGAAGATCAAGAGTGGCTAATTTAGAGAGCTTGAGAGT 2711
Qy 843 TGGAGCAAGTGGCGCTTCTGTTCTAACAATCTGCTTGGAAGATTTGATCAATAT 902
Db 2712 TGGAGCAAGTGGTGTCTGTTCTAACAATCTGCTTGGAAGATTTGATCAATAT 2771
Qy 903 GGAACATTTGCAACCATATGATTTGTCAAAATTTGTCTGAAGATTTGATGTTGTT 962
Db 2772 GGAACATTTGCAACCATATGATTTGTCAAAATTTGTCTGAAGATTTGATGTTGTT 2831
Qy 963 CATGCAACGTGATTTGGGCAACCAAGAAATAAATCTTAATCTTGTGCTATCGAAA 1022
Db 2832 CATGCAACGTGATTTGGGCAACCAAGAAATAAATCTTAATCTTGTGCTATCGAAA 2891
Qy 1023 GGAATTTGTGAAGAAATGTTGTGTGTGCTCTAGCACTAATACTTTGAGATTTT 1082
Db 2892 GGAATTTGTGAAGAAATGTTGTGTGTGCTCTAGCACTAATACTTTGAGATTTT 2951
Qy 1083 GCGCTTTAAGAGAGAAAGACAGTGGGAAATGAGAGATGATGATTTGGAAT 1142
Db 2952 GTGCTTCAAGAGAGAAAGACAGTGGGAAATGAGAGATGATGATTTGGAAT 3011
Qy 1143 GCGCTCAAGAAAGTTCTATTTCTGCTGCTGCGCTGAGACTTATACATCACTTCCACT 1202
Db 3012 GCGCTCAAGATGAAGTTCTATTTCTGCTGCTGCGCTGAGACTTATACATCACTTCCACT 3071
Qy 1203 TGAATTTGACATATGCTTTACATATTTGTCAGATTTCCCAAGATACCGAAATGGA 1262
Db 3072 TGAATTTGACATATGCTTTGCTGATATTTGCGGTGTTCCCAAGATACCGAAATGGA 3131
Qy 1263 GGGAAATCTAATCTCTCTGGAATGCGCATGTTTATTTTATGGAAGAAACTTGA 1322
Db 3132 AGAAATGCTAATCTCTCTGGAATGCGCATGTTTATTTTATGGAAGAAACTTGA 3191
Qy 1323 GCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
Db 3192 GCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3251
Qy 1383 GATTGAATTAATCTGCTCAACTTATTTCAAGATGATGATGATGATGATGATGAT 1442
Db 3252 GATTGAATTAATCTGCTCAACTTATTTCAAGATGATGATGATGATGATGATGAT 3311
Qy 1443 AACATCTGATTTTGGGAGAGACATCAAGAGCAATTCGAGAAATATTTGAGAAA 1502
Db 3312 AACATCTGATTTTGGGAGAGACATCAAGAGCAATTCGAGAAATATTTGAGAAA 3371
Qy 1503 TTACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562

Db 3372 TTACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3431
Qy 1563 CTGAGAGATTTGCTGCTGAGGAGCTTAATCTAATGATACATTAAGCACTT 1622
Db 3432 CTGAGAGATTTGCTGCTGAGGAGCTTAATCTAATGATACATTAAGCACTT 3491
Qy 1623 ACCGCTTCCATTGAGATCTAGTACATTTTAAGATCTTAATCTTGTGCGCAATCTAG 1682
Db 3492 ACCATCTTCCATTGAGATCTAGTACATTTTAAGATCTTGAACCTGTATGCG---AGTGG 3548
Qy 1683 TATTCGTAGTCTTCCAAACGATTAATGACAGCTTCAAAATGTCGAGACTTGAATCTCA 1742
Db 3549 CATCGATAGTCTTCCAAACGATTAATGACAGCTTCAAAATGTCGAGACTTGAATCTCA 3608
Qy 1743 TGGCTGATCATTCATTTGTTGTTGCGCAAAAGAAACAAACCTTGTAGTCTTGA 1802
Db 3609 ATATTTGACCAAGCTTGTGTTGTTGCGCAAAAGAAACAAACCTTGTAGTCTTGA 3668
Qy 1803 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
Db 3669 TCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3728
Qy 1863 ATGCTTTAAGACTTAAAGTATGATTTGTGTGGAAATTCAGAGAAAGTGTCAACTGG 1922
Db 3729 ATGCTTTAAGACTTAAAGTATGATTTGTGTGGAA---GGAAGAAAGTTATCAACTGG 3785
Qy 1923 TGAATTAAGAACTGATCTATGCTCAATGGAATCAAGCATCTGAGAGATGAA 1982
Db 3786 TGAATTAAGAACTGATCTATGCTCAATGGAATCAAGCATCTGAGAGATGAA 3845
Qy 1983 GAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
Db 3846 GAATGATATGAGAGCAAGAAAGCAATTTATCTGCAAAAGGAATGCACTTTTAAG 3905
Qy 2043 CATGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
Db 3906 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3962
Qy 2103 TGAAGCTCTGAAACCACTCTCAATCTGATGTTTAACATCAAGGGCTTCAAGGAT 2162
Db 3963 TGAAGCTCTCAACCACTCTCAATCTGATGTTTAACATCTGATGTTCAAGGAT 4022
Qy 2163 CCGTCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
Db 4023 CCACTCTCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4082
Qy 2223 CAGTTGAAAACTGCTCATGCTTACCAACCTTGTGTGAGTGTGCTTGAAGTCT 2282
Db 4083 CAACTTCAAGAACTGCTCATGCTTACCAACCTTGTGTGAGTGTGCTTGAAGTCT 4142
Qy 2283 AGATTTGTGAGAGGGGTCTGCGGAAGTGAATGTTG-----A 2321
Db 4143 AGATTTGTGAGAGGGGTCTGCGGAAGTGAATGTTG-----A 2381
Qy 2322 TTCTGATATCCCTTCAAGAGAGATTTTCAATCTGAGAGAACTTAATATCCGAAT 2381
Db 4203 TTCTGATATCCCTTCAAGAGATTTTCAATCTGAGAGAACTTAATATCCGAAT 4282
Qy 2442 GATGAGATTAATATGTTGCTTATGTTTATTTTCAACCTTCTCTGTGCAAGAAAT 2501
Db 4203 GATGAGATTAATATGTTGCTTATGTTTATTTTCAACCTTCTCTGTGCAAGAAAT 4359
Qy 2502 GGTAGTTAGTGGGACAAGTCAGATGCAATAGTTTCAATCTAATCTCATGCG 2561
Db 4360 -----TCTAATCTTAAGGC 4373
Qy 2562 TCTTACTTCCCTCAAAATGCTATTAACAAGAAAGATGCTTCACTCCAGAGAGATGTT 2621
Db 4374 TCTTACTTCCCTCAAAATGCTATTAATAAGTACTTCAATCTTCCAGAGAGATGTT 4433

XX MPI: 2003-714439/68.
DR P-PSDB; ADP17767.
XX
PT New resistance gene conferring resistance against an oomycete pathogen,
PT useful for producing plants, especially potatoes and tomatoes, resistant
PT against oomycete pathogens such as Phytophthora infestans.
XX
PS Example 5; SEQ ID NO 38; 86pp; English.

CC This invention relates to novel isolated polynucleotides that confer
CC resistance against late blight caused by the oomycete pathogen
CC Phytophthora infestans, which threatens both tomato and potato crops.
CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC leucine-rich repeat (LRR) proteins identified in Solanum tuberosum,
CC and which cause disease resistance to bacteria, fungi, nematodes etc.
CC These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
CC described as plant growth regulators. They are useful in providing
CC resistance to Phytophthora infestans, especially in Solanum tuberosum
CC (potato) plants to protect against oomycete infection or to demonstrate
CC disease susceptibility. Resistance can be conferred by transformation of
CC existing potato and tomato cultivars with the gene, a procedure that is
CC more straightforward and faster than conventional introgression breeding.
CC This polynucleotide sequence is the Solanum tuberosum RGC1-b1b coding
CC DNA containing an intronic sequence in an exemplification of the
CC invention.

Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;

Query Match 59.7%; Score 1771.6; DB 10; Length 3260;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 389; Indels 54; Gaps 7;

QY 426 AACAGTGTGTTGTAAGAACACCAAGTTTGAAGAGACAAAGAAAGAGAGAT 485
DB 704 ACGAGTTTGTGTTTAACTGACCCAAAGTTTATGAGAGAAAGAGAGATGAT 763
QY 486 AGTGAATTCCTGATTAACATGTTAGCAATGCCCAACACTTCCAGTCTCCCAACT 545
DB 764 AGTGAATTCCTGATTAACATGTTAGTTATCCAGAGAGATCCAGTCTCCCAACT 823
QY 546 TGTGATGGGGGACCTAGAGAAAGACACTCTTCCCAATGCTTCAATGATCAGAGAT 605
DB 824 TGTGATGGGGGACCTAGAGAAAGACACTCTAGCCCAATGCTTCAATGATCAGAGAT 883
QY 606 AATTGACATTTCCATCCCAAAATATGATTTGTGTCGGAAGTTTAAATGAGAGAG 665
DB 884 TACTGAGCATTTCAATCTAAAGATATGGGTTGTGTCTCAATATATTTTATGAGAGAG 943
QY 666 GTTGAATAAGAAATTTGATATCTATTTGAAGAAAGTCACTTGTGATGATGATGAT 725
DB 944 GTTGAATAAGCAATTTGATATCTATTTGAAGAAAGTCACTTGTGATGATGATGAT 1003
QY 726 TCCACTTCAAAAGAGCTTCGGACCTTCCGTAATGAGAAAGAAATTTGCTGCTTGA 785
DB 1004 TCCCTCTCAAGAAAGCTTCAGAGGTTGTAATGAGAAAGAAATTTCTTGTGTTGA 1063
QY 786 TGATGTTTGAATGAAGATCAAGATTAAGTGGCTAAGTTAAGCAAGCTTGAAGTTGG 845
DB 1064 TGATGTTTGAATGAAGATCAAGAAAGTGGGATTAATCTTGAAGATTAAGTTGG 1123
QY 846 AGCAAGTGGGCTTCTGTTCTAACCACTACTGCTTGTGAAGAGGTTGATCAATTAAT 905
DB 1124 AGCAAGTGGGCTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1183
QY 906 AACATTCACCAATATGAATTTGCTCAAGAGATTTGTTGTTGTTGAT 965
DB 1184 AACATTCACCAATATGAATTTGCTCAAGAGATTTGTTGTTGTTGAT 1243
QY 966 GCAACGTGCAATTTGGGACCAAGAAATTAATCTTATCTTGTGCTATCGGAAAGGA 1025
DB 1244 GCAACGTGCAATTTGGCACCAAGAAATTAATCTTATGGAATTCGAAAGGA 1303

QY 1026 GATTGTGAAAAATGTGGTGTGTCCTCTAGCACTTAAACCTTTGGAGGATTTTGGC 1085
DB 1304 GATTGTGAAAAATGTGGGTTGTGCTCTAGCACTTAAACCTTTGGAGGCTTTTACG 1363
QY 1086 CTTTAAAGAGAAAGAAAGACAGTGGGAAACATGTAGAGATGTGTGATTTTGAATTTGCC 1145
DB 1364 CTTCAAGAGGAAAGAAAGTGAATGGAAACATGTAGAGATGTGTGATTTTGAATTTACC 1423
QY 1146 TCAAGAAAGAAAGTTCTATTTCTGCTGCTGCTGAGACTTAATTAATCAATCACTTCACTGA 1205
DB 1424 TCAAGATGAAGAAATTTCTGTTTCTGCTGCTGAGGCTGATATATCATCTTCCACTGA 1483
QY 1206 TTTGAGCAATGCTTTACATTTTGTGAGATATCCCAAGAGATCCGAATTTGAAGAGG 1265
DB 1484 TTTGAGCAATGTTTGTGATATTTGCGATATTTCCCAAGAGACCAAAATGAGAAAGGA 1543
QY 1266 AATCTATCTCTCTGATGAGACATGTTGTTTATTTATTCGAAAGAAAGAACTTGAGCT 1325
DB 1544 ATATCTATGCTCTCTGATGAGACATGTTTCTTTATCAAGAAAGAAAGATGAGCT 1603
QY 1326 AGAATGATGATATGATATGATATGAAATTAATTAATCTTGAAGTCTTTTCCAGAGAT 1385
DB 1604 AGAATGATGAGCAATGATATGAAATTAATTAATCTTGAAGTCTTTTCCAGAGAT 1663
QY 1386 TGAAGTTAAATCTGATCAAACTTATTTCAAGATGATCTCATTCATGATCTGGCAAC 1445
DB 1664 TGAAGTTAAATCTGATTAACCTTATTTCAAGATGATCTCATTCATGATCTGGCTAC 1723
QY 1446 ATCTTATTTTGGCAAGACATCAAGACCAATATCCGAAATA----- 1491
DB 1724 ATCTATGTTTTCAGCAAGCCCATCAAGCAGATATACGCAATTAATGAAAGATGA 1783
QY 1492 -----ATTGTAAGAAATTAATCAATATGATATGATATGATATGATATGATATGAT 1535
DB 1784 TGAAGATGATGATCTCATTTGTAACAAATTAATTAATGATATGATATGATATGATATGAT 1843
QY 1536 AGTGTATCTTCTTACTCTCTTCCACTGCAAGATTTGTCTGTTGAGGTTGCTTAA 1595
DB 1844 AGTGTATCTTCTTACT 1903
QY 1596 TCTAAGTACATTAATCTTAAGCAATTTACCGTCTTCCATTTGAGATCTAGTACATTTAAG 1655
DB 1904 TCTAAGTACATCTGAATTTGAAACAGTATACCGTCTTCCGTTGAGATCTAGTACATTTAAG 1963
QY 1656 ATACCTTAATCTTCTGAGCAATCTAGTATTTGCTATCTTCAACACAGTATGCAAGCT 1715
DB 1964 ATACCTTACCTCTCTGATTAATAA---ATTGTATCTTCTCAAGAGGTTGTGCAAGCT 2020
QY 1716 TCAAAATCTGACACCTTGTATCTACATGAGCTGTCAATCACTTGTGTTGCAAAAGA 1775
DB 2021 TCAAAATCTGACACCTTGTATCTATTAATGCAATGCACTTGTGTTGCAAAAGA 2080
QY 1776 AACAGCAATCTGATGCTTGAATCTTGAATCTTGAATGCTTGAATGATGATGATGAT 1835
DB 2081 AACAGCAATCTTGTATGCTGCTGCAATCTTGAATCTTGAATGATGATGATGATGAT 2137
QY 1836 TATGACCAAGAGATGATCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1895
DB 2138 TATGACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2197
QY 1896 AATTCAGAAAGAAAGTTGTCAACTTGTGTAATTAAGAAAGCTGAATCTCTATGCTCAAT 1955
DB 2198 ---CGAGAGAAAGGTTATCAACTTGTGTAATTAAGAAAGCTGAGTCAAT 2254
QY 1956 TGAATTCACGCAATCTTGAAGAGTGAAGATGATATGATGCAAAAGAAAGCAATTTATC 2015
DB 2255 TGAATTCACGCAATCTTGAAGAGTGAAGATGATATGATGCAAAAGAAAGCAATTTATC 2314
QY 2016 TCAAAAGAAAGTCTGATCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2075
DB 2315 TCAAAAGAAAGTCTGATCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2365
QY 2076 ATATGATTCAGAAAGGTTGAAGTCTTGAAGTCTTCAACCAAGCACTCAATCTGACTTG 2135

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Db      2366 ATATGAATCCGAAGAAGTTAAAGTCTGAAGCCCTCAACCAACCAATCCCAATCTGAAATA 2425
Oy      2136 TTTAACAATCCAGGGCTTCAAGGAATCCCTCTCCAGCTGGAGAAATCCAGTTT 2195
Db      2426 TTTAACAATCCAGGGCTTCAAGGAATCCCTCTCCAGCTGGAGAAATCCAGTTT 2485
Oy      2196 GAAAAATGTTGCTCTAATGAATCATGATGCAAAAACTGCTATGCTTACCACTT 2255
Db      2486 GAAAAATGTTGCTCTAATGAATCATGATGCAAAAACTGCTATGCTTACCACTT 2545
Oy      2286 TGTGAGCTGCTTCTTAAAAAGTCTAGAAGTGTGAAGGGGCTCTGCGGAAGTGAATA 2315
Db      2546 TGTGAGCTGCTTCTTAAAAAGTCTAGAAGTGTGAAGGGGCTCTGCGGAAGTGAATA 2605
Oy      2316 TGTT---GATTCGATTCCTTCAACAAGAAAGTTTCCATCTCTGAGAAAACTTAAT 2372
Db      2606 TGTGAAAGATTCCTGATTCCTCAACAAGAAAGTTTCCATCTCTGAGAAAACTTAAT 2665
Oy      2373 ACGCAATTTGGTAAATCTGAAGAATGCTGAAGAAAGAAAGAAAGCAATGCGCTGT 2432
Db      2666 AGTGGCTTTTGTATCTGAAGAATGCTGAAGAAAGAAAGAAAGCAATGCGCTGT 2725
Oy      2433 GCTTGAAGATAGAGATTTAAATGTTGCCCTAATGTTTGTATTCACCTTTCTTCTGT 2492
Db      2726 GCTTGAAGATAGAGATTTGCGATTTGCCCTAATGTTTGTATTCACCTTTCTTCTGT 2785
Oy      2493 CAAAGAAATTTGATTAAGTGGGGAACAATGCAATGCAATGATTCATCTCATCTTA 2552
Db      2786 CAAAGAAATTTGATTAAGTGGGGAACAATGCAATGCAATGATTCATCTCATCTTA 2842
Oy      2553 TCTGATGCTCTTACTTCCCTCCCAATTCGCTATTAACAAGAAAGTCTGACCTCCAGA 2612
Db      2843 TCTGATGCTCTTACTTCCCTCCCAATTCGCTATTAACAAGAAAGTCTGACCTCCAGA 2902
Oy      2613 AGAGATGTTCAAAAGCTTGCATAATCTCAAAATCTGAATATCTTTTACTTCAATCT 2672
Db      2903 AGAGATGTTCAAAAGCTTGCATAATCTCAAAATCTGAATATCTTTTACTTCAATCT 2962
Oy      2673 TAAAGAGCTGCTTACCAAGCTTGGCTAGTCTCAATGCTTGAAGCAATCTGAATCAT 2732
Db      2963 CAAAGAGCTGCTTACCAAGCTTGGCTAGTCTCAATGCTTGAAGCAATCTGAATCAT 3022
Oy      2733 TTGTTATGCTAGAGAGTCTCCCGAGGAAGGTGAAGGTTAATTTACTCTGACACA 2792
Db      3023 TTGTTATGCTAGAGAGTCTCCCGAGGAAGGTGAAGGTTAATTTACTCTGACACA 3082
Oy      2793 GTTATCATTAACATATCTGTAATGCTCAATGTTTACCGAGGAGTTCAGCACTTAAC 2852
Db      3083 GTTATCATTAACATATCTGTAATGCTCAATGTTTACCGAGGAGTTCAGCACTTAAC 3142
Oy      2853 AGCCCTCAAAATTTATCAAGTGTGATTTTTCACAACCTGCGCAAGCGGTGAGAGGG 2912
Db      3143 AACCTTCAAAAGTTTAAATTCGGGGAATGTCACAACCTGCAAGCGGTGAGAGGG 3202
Oy      2913 AATAGGAAGAAGCTGTAACAAATGCTCACTTCTGCTGCTTATTTAT 2964
Db      3203 AATAGGAAGAAGCTGTAACAAATGCTCACTTCTGCTGCTTATTTAT 3254

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RESULT 14
ADH51534

ID ADH51534 standard; DNA; 3260 BP.

XX AC ADH51534;

XX DT 25-MAR-2004 (first entry)

XX DE S bulbocastanum RGL1-b1b gene SeqID51.

XX KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
de; RGL1-b1b.

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XX OS Solanum bulbocastanum.
XX US US2003221215-A1.
XX PD 27-NOV-2003.
XX PF 07-FEB-2003; 2003US-00360522.
XX PR 07-FEB-2003; 2003US-00360522.
XX PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX PI Allele JHM, Van Der Vossen EAG;
XX DR WPI; 2004-010903/01.
XX PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
XX for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX with resistance against oomycete infection.
XX BS Claim 6; SEQ ID NO 51; 98pp; English.
XX CC This invention relates to a novel DNA sequence in the field of plant
XX disease, in particular oomycete infections. The DNA sequence encodes a
XX protein which may provide a plant or its progeny with at least partial
XX resistance against an oomycete infection caused by Phytophthora
XX infestans. The invention may be useful for the development of compounds
XX with a fungicide activity. The DNA sequence of the invention encodes an
XX Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX cell, protein or binding molecule is useful for providing a plant or its
XX progeny with resistance against an oomycete infection such as late blight
XX (a disease of major importance to production of Solanaceae such as potato
XX and tomato cultivars). The present sequence is that of the S
XX bulbocastanum RGL1-b1b gene which is related to the invention.
SQ Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;

Query Match      59.7%; Score 1771.6; DB 12; Length 3260;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 389; Indels 54; Gaps 7;

Oy      426 AACAGTTTGTGTTGAATGAACCAAGTTTATGAAAGACAAAGAAAGACGAGAT 485
Db      704 AGCAGTTTGTGTTTAACTGAGCCAAAGTTTATGAAAGGAAAGAGAGATGAT 763
Oy      486 AGTAAATCTGATTAACAAATGTTAGCAATGCCAAACACTTCAGTCTCCCAATCT 545
Db      764 AGTAAATCTGATTAACAAATGTTAGTATTCGAAAGAGTTCCAGTACTCCCAATCT 823
Oy      546 TGTATGGGGGACTTAGAAAGAGACTCTTCCCAATGCTTCAATGATCAGAGAT 605
Db      824 TGTATGGGGGACTTAGAAAGAGAGACTCTTCCCAATGCTTCAATGATCAGAGAT 883
Oy      606 AATGAGATTTCCATCCCAAAATATGATTTGTCTCGGAATTTTAAATGAAAGAG 665
Db      884 TACTGAGATTTCAATCAAAAGATGAGTTTGTCTCAGATATTTGATGAGAGAG 943
Oy      666 GTTATTAAGGAATTTGATGATCTATTTGAAGAAAGTCACTTGTGTCATGAGACTTGGC 725
Db      944 GTTATTAAGGAATTTGATGATCTATTTGAAGAAAGTCACTTGTGTCATGAGACTTGGC 1003
Oy      726 TCCACTTCAAAAGAGCTTGGGACTTGCCTGAATGGAAGAAATTAATTTGCTGCTTGA 785
Db      1004 TCCCTTCCAGAAAGCTTCAAGAGTTGTGAATGGAAGAAAGATATCTTCTGTTTGA 1063
Oy      786 TGATGTTGAGATGAATCAAGATTAAGTGGCTTAAGTTAAGACAGCTTGAAGTTGG 845
Db      1064 TGATGTTGAGATGAATCAAGATTAAGTGGCTTAAGTTAAGACAGATTTGAAGATGG 1123
Oy      846 AGCAGTGGCGCTTCTGTTTACCACTACTGCTTGAAGAAAGTTGATCAATTAATGG 905
Db      1124 AGCTAGTGGTCTTCAATTTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1183

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QY 906 AACATTGCAACCATGAAATGTGCAAAATTTGCTCAAGAAAGATGTTGTTGTTCAAT 965
DB 1184 AACTTTGCAATATATATCACTTATCAAAATTTGCTCAAGAAAGATGTTGTTGTTCA 1243
QY 966 GCAACGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGCTGCTATCGAAAGGA 1025
DB 1244 GCAACGTGATTTGGGCAACCAAGATCTTAATCTTAAGAAATCGAAAGGA 1303
QY 1026 GATTGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1085
DB 1304 GATTGGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1363
QY 1086 CTTTAAAGAGAAAGAAAGACAGTGGGAAATGATGAGATGATGAGATTTGGAAATTTGCC 1145
DB 1364 CTTCAAGAGGAAAGAAAGATGATGAGATGATGAGATGATGAGATTTGGAAATTTACC 1423
QY 1146 TCAGAGAAAGATTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205
DB 1424 TCAGAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1483
QY 1206 TTTGAGACATGCTTTATCATATTTGACAGTATTTCCAAAGATTCGAAATGGAAGG 1265
DB 1484 TTTGAGACATGCTTTGCAATTTGCGAGATTTCCAAAGACACCAAAATGAAAGGA 1543
QY 1266 AATCTAATCTCTCTGATGAGCAATGCTTTTATTTATGAAAGAACTTGGAGCT 1325
DB 1544 ATATCTCATGCTCTCTGATGAGCAACAGTTTCTTTATCAAAAGAAATGAGACT 1603
QY 1326 AGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
DB 1604 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
QY 1386 TGAAGTAAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGATGATG 1445
DB 1664 TGAAGTAAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGATGATG 1723
QY 1446 ATCTCTATTTTGGGAGCAATCAAGAGCAATATCCAGAAATTA----- 1491
DB 1724 ATCTATGTTTTCAGAGACGATCAAGAGCAATATCCAGAAATTAAGATGA 1783
QY 1492 -----ATTGTAAGAAATTAATCAATGATGATGATGATGATGATGATGATGATG 1535
DB 1784 TGAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1843
QY 1536 AGTGTATCTTCTTACTCTCTTCCACTGACAGAAATTTGCTGTTGAGAGGCTTAA 1595
DB 1844 AGTGTATCTTCTTACTCTCTTCCACTGACAGAAATTTGCTGTTGAGAGGCTTAA 1903
QY 1596 TCTTAAGTACATTAATCTTAAGCAATGCTGCTTCCATTTGAGATCTAATCAATTTAAG 1655
DB 1904 TCTTAAGTACATCAAAATTTGAACAGTTACCGTCTTCCGTTGAGATCTAATCAATTTAAG 1963
QY 1656 ATATCTTAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1715
DB 1964 ATATCTTAAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2020
QY 1716 TCAAAATCTGCAACTCTTGAATCTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1775
DB 2021 TCAAAATCTGCAACTCTTGAATCTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2080
QY 1776 AACAAGCAAACTTGTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 1835
DB 2081 AACAAGCAAACTTGTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 2137
QY 1836 TATGCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1895
DB 2138 TATGCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2197
QY 1896 AATTCAAGAAAGATTTGCTCAATGCTGATGATGATGATGATGATGATGATGATGATG 1955
DB 2198 ----CGAGAGAAAGGTTATCAACTTGTGAACTACGAATTTAACTCGTGTGGAAT 2254

QY 1956 TGAATCAGCATCTTGAGAGATGAGAAATGATGATGATGATGATGATGATGATGATGATG 2015
DB 2255 TTAATCACAATCTTGAGAGATGAGAAATGATGATGATGATGATGATGATGATGATGATG 2314
QY 2016 TGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2075
DB 2315 TGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2365
QY 2076 ATATGATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2135
DB 2366 ATATGATCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2425
QY 2136 TTTAACAATCAGGAGCTTCAAGAGATCCGCTCCAGATGATGATGATGATGATGATGATG 2195
DB 2426 TTTAACAATCAGGAGCTTCAAGATCCGCTCCAGATGATGATGATGATGATGATGATGATG 2485
QY 2256 TGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2315
DB 2486 GAAAAATGTTGCTCTAATCTTAATTTAGCGGTTGAAAACTGCTCGTTACACCTT 2545
QY 2256 TGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605
DB 2546 TGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2605
QY 2316 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2372
DB 2606 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2665
QY 2373 ACGGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2432
DB 2666 ACGGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2725
QY 2433 GCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2492
DB 2726 GCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2785
QY 2493 CAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2552
DB 2786 CAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2842
QY 2553 TCTCAGCTGCTTACTTCTTCCCTCAAAATTTGCTATTAACAAAGAAATGCTTCACTCCAG 2612
DB 2843 TCTCAGCTGCTTACTTCTTCCCTCAAAATTTGCTATTAACCAACAGTCACTTCACTGGA 2902
QY 2613 AGAGATGTTCAAAAGCTTGAATCTCAAAATCTGAATGATGATGATGATGATGATGATGAT 2672
DB 2903 AGAGATGTTCAAAAGCTTGAATCTCAAAATCTGAATGATGATGATGATGATGATGAT 2962
QY 2673 TAAAGAGCTGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2732
DB 2963 CAAGAGCTGCTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3022
QY 2733 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2792
DB 3023 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3082
QY 2793 GTTATCATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2852
DB 3083 GTTATCATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3142
QY 2853 AGCTTCACAAAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2912
DB 3143 AACCTTCACAAAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3202
QY 2913 AATGAGAGAGAGCTGCTGATCAAAATTTGCTCAATCTGCTGCTGCTGCTGCTGCTGCT 2964
DB 3203 AATGAGAGAGAGCTGCTGATCAAAATTTGCTCAATCTGCTGCTGCTGCTGCTGCTGCT 3254

RESULT 15
ADFL17764
ID ADFL17764 standard; DNA; 3899 BP.
XX

AC ADF17764;
XX 12-FEB-2004 (first entry)
XX
DE S_bulbocastanum RGc4-b1b coding DNA.
XX
KW gene; de; RGc4-b1b; Rpi-b1b gene cluster; growth regulant;
KM oomycete infection; introgression breeding; plant; late blight.
XX
OS Solanum bulbocastanum.
XX
FH Key Location/Qualifiers
FT CDS 1..3899
FT /tag= b
FT /product= "RGc4-b1b protein"
FT /note= "This sequence contains 3 introns and some
FT translation exceptions"
FT 1..433
FT exon /tag= a
FT /number= 1
FT 434..510
FT /tag= c
FT /number= 1
FT 511..542
FT /tag= d
FT /number= 2
FT 543..618
FT /tag= e
FT /number= 2
FT 619..742
FT /tag= f
FT /number= 3
FT 743..1365
FT /tag= g
FT /number= 3
FT 1366..3899
FT /tag= h
FT /number= 4
XX
XX EPI334979-A1.
XX
XX 13-AUG-2003.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX 08-FEB-2002; 2002EP-00075565.
XX
XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
XX Van Der Vossen EAG, Allefs JHM;
XX
XX WPI; 2003-714439/68.
XX
XX P-PSDB; ADF17768.
XX
XX
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX
XX Example 5; SEQ ID NO 40; 86pp; English.
XX
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGc1-b1b, RGc3-b1b and RGc4-b1b, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.

CC This polynucleotide sequence is the Solanum bulbocastanum RGc4-b1b coding
CC DNA containing an intronic sequence in an exemplification of the
CC invention.
XX
XX Sequence 3899 BP; 1186 A; 678 C; 846 G; 1189 T; 0 U; 0 Other;
XX
XX Query Match 59.5%; Score 1736.2; DB 10; Length 3899;
XX Best Local Similarity 82.0%; Pred. No. 0;
XX Matches 2096; Conservative 0; Mismatches 428; Indels 33; Gaps 7;
XX
QY 426 AACGCTTTTGTGTAATGACCAAGATTATGAGAGACAAAGAAAAGCGAGAT 485
DB 1361 AACAGCTTTTGTGTAATGACCAAGATTATGAGAGACAAAGAAAAGCGAGAT 1420
QY 486 AGTAAATTCCTGTAATGACCAAGATTATGAGAGACCAAGATTATGAGAGAT 545
DB 1421 AGTAAATTCCTGTAATGACCAAGATTATGAGAGACCAAGATTATGAGAGAT 1480
QY 546 TGTATGAT 605
DB 1481 TGTATGAT 1540
QY 606 AATTGAGCAATTCATCCCAAAATATGAGATTGTTCTCGAGAGATTATGAGAGAG 665
DB 1541 AACTAGCAATTCATCCCAAAATATGAGATTGTTCTCGAGAGATTATGAGAGAG 1600
QY 666 GTTATAGAGAAATTTAGAAATCTATGAGAGAAAGTCTGAGAGAGAGAGAT 725
DB 1601 GTTATAGAGCAATTTAGAGAAATTTAGAGAAAGTCTGAGAGAGAGAGAT 1660
QY 726 TCCACTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 785
DB 1661 TTGATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1720
QY 786 TGATGTTGAT 845
DB 1721 TGATGTTGAT 1780
QY 846 AGCAGAT 905
DB 1781 AGCAGAT 1840
QY 906 AACATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 965
DB 1841 AACATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1900
QY 966 GCAAGAT 1025
DB 1901 GCAAGAT 1960
QY 1026 GATTTGAT 1085
DB 1961 GATTTGAT 2020
QY 1086 CTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1145
DB 2021 CTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2080
QY 1146 TCAGAT 1205
DB 2081 TCAGAT 2140
QY 1206 TTTGAT 1265
DB 2141 TTTGAT 2200
QY 1266 AATTCATATCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1325
DB 2201 AATTCATATCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2260
QY 1326 AGAT 1385
DB 2261 AGAT 2320

QY 1386 TGAAGTAAATCTGTCGCAACCTTATTTCAAGATGCAATCTCATTCATGATCTGGCAAC 1445
 Db 2321 TGAAGTAAATCGGGTAATCTTATTTCAAGATGCAATCTCATTCATGATGATGCTGAC 2380
 QY 1446 ATCTCTATTTTGGGCAAGCAATCAAGCAATATCCGAAATATATTTGAAATTA 1505
 Db 2381 ATCTCTATTTTGGGCAAGCAATCAAGCAATATCCGAAATATATTTGAAATTA 2440
 QY 1506 CATACATATGATGTCATTTGCTTCACTAAGTGTATTTCTTACTCTCTTCCACTT 1565
 Db 2441 TAAGCATATAGTGTCTATTTGCTTCAAGTGTGTCTTCTTCTCTCTCTCTCT 2500
 QY 1566 GCAGAAATTTGCTCTGTTGAGGGTCTTATCTAATGACATTAATTAAGCAATTAAC 1625
 Db 2501 GAAAGATTTGCTCTGTTAAGGGTCTTATCTAATGACATTAATTAAGCAATTAAC 2560
 QY 1626 GTCTTCCATTTGGAATCTTATGATTAAGATTAATCTTATGCTGCAATTAATTA 1685
 Db 2561 GTCTTCCATTTGGAATCTTATGATTAAGATTAATCTTATGCTGCAATTAATTA 2617
 QY 1686 TGTAGTCTTCCAAACCAATTAAGATTAAGATTAATCTTATGATTAATTAAG 1745
 Db 2618 CCGTATGCTTCCAAACCAATTAAGATTAAGATTAATCTTATGATTAATTAAG 2677
 QY 1746 CTGTCAATCACTTTGTTGTTCCAAAGAAACCAAGCAATCTTATGATTAATTAAG 1805
 Db 2678 TTGCTACTCACTTATTTGTTGTTCCAAAGAAACCAAGCAATCTTATGATTAATTAAG 2737
 QY 1806 TTTACTTGAATGTTTCTATGATTAATGATTAATGATTAATGATTAATGATTAATG 1865
 Db 2738 TTTTGTATGATG---GCTGTCAATGATTAATGATTAATGATTAATGATTAATG 2794
 QY 1866 CCTTAAGACTCTAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATG 1925
 Db 2795 CCTTAAGACTCTAAGTATGATTAATGATTAATGATTAATGATTAATGATTAATG 2851
 QY 1926 ATTACGAAACCTGAATCTCTATGCTCAATGAAATCAAGATCTTGAAGATGAAGAA 1985
 Db 2852 ACTGAAACCTGAATCTCTGCGGCTCAATTTCAATCAACATCTGAGAGATGAAGAA 2911
 QY 1986 TGATATGATGCAAAAGCAATTTATCTGCAAAAGAAATCTGATTTTAAAGAT 2045
 Db 2912 CGATATGATGCAAAAGCAATTTATCTGCAAAAGCAATTTTAAAGAT 2968
 QY 2046 GAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2105
 Db 2969 GAGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3025
 QY 2106 AGCTCTCAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2165
 Db 3026 AGCACTCAACCAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 3085
 QY 2166 TCTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2225
 Db 3086 TTTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3145
 QY 2226 TTGCAAAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2285
 Db 3146 CTGCAAAATCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 3205
 QY 2286 GTTGTGAGAGGGGTCTGCGAAGTGAATGTTG-----ATTCTGATTT 2330
 Db 3206 GTTGTGAGAGGGGTCTGCGAAGTGAATGTTG-----ATTCTGATTT 3265
 QY 2331 CCTTACAAAGAAAGGTTTCCATCTGAGAAATTAATTAAGGATTTGGTAACT 2390
 Db 3266 CTCCAAAGAAAGGTTTCCATCTGAGAAATTAATTAAGGATTTGGTAACT 3325
 QY 2391 GAAAGATTTGCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2450
 Db 3326 GAAAGATTTGCTGAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3385

QY 2451 TAAATGTTCCCTATGTTGTTATTTCCAAACCTTTCTTCTGTCAAGAAATTTGATTAAG 2510
 Db 3386 TTTATATGCTCTGTTGTTTTCCTCAACCTTTCTTCTGTCAAGAAATTTGATTAAG 3445
 QY 2511 TGGGACAAAGTCAATGATGATTAAGTTTCAATTTCAATTTCAATTTCAATTTCA 2570
 Db 3446 CGG---CAAGCAAAACCTGAGAGTTTGAAGTCTCAATTTCAATTTCAATTTCA 3502
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Search completed: April 16, 2005, 14:47:08
 Job time : 1458 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: April 16, 2005, 14:14:21 ; Search time 502 Seconds
(without alignments)
9670.982 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapept 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	208.8	7.0	4465	US-08-930-996A-3	Sequence 3, Appli
2	202.6	6.8	4208	US-09-004-838-1	Sequence 1, Appli
3	201	6.8	4163	US-09-004-838-70	Sequence 70, Appli
4	200.8	6.8	1662	US-09-004-838-6	Sequence 6, Appli
5	196.6	6.6	2352	US-09-004-838-2	Sequence 2, Appli
6	177.8	6.0	4946	US-08-930-996A-1	Sequence 1, Appli
7	104	3.5	644	US-09-387-286-24	Sequence 24, Appli
8	93.6	3.2	1036	US-09-004-838-3	Sequence 3, Appli
9	88.4	3.0	3997	US-08-947-823-2	Sequence 2, Appli
10	88.4	3.0	51952	US-08-947-823-1	Sequence 1, Appli
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12	87.4	2.9	544	US-09-004-838-10	Sequence 10, Appli
13	87.4	2.9	544	US-09-004-838-137	Sequence 137, App
14	82.4	2.8	9870	US-09-245-928A-15	Sequence 15, Appli
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17	75	2.5	475	US-09-004-838-5	Sequence 5, Appli
18	73.6	2.5	475	US-09-004-838-8	Sequence 8, Appli
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21	71.8	2.4	3099	US-09-360-186-2	Sequence 2, Appli
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45	46.2	1.6	1238	2	US-08-414-938A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-3
; Sequence 3, Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval
; APPLICANT: ORI, Naomi
; APPLICANT: PARAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 PUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; NUMBER OF SEQUENCES: 12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4465 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 204..3923
; US-08-930-996A-3
; Query Match 7.0%; Score 208.8; DB 3; Length 4465;
; Best local Similarity 50.8%; Pred. No. 7e-50;
; Matches 675; Conservative 0; Mismatches 622; Indels 33; Gaps 6;

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QY 1390 GTTAAATCTG 1399
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RESULT 2
US-09-004-838-1
; Sequence 1, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; NUMBER OF SEQUENCES: 140
; CONFERRING PEST RESISTANCE IN PLANTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..4208
; OTHER INFORMATION: /note="RLGIA"
; US-09-004-838-1
Query Match 6.8%; Score 202.6; DB 3; Length 4208;
Best Local Similarity 49.2%; Pred. No. 4,4e-48;

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RESULT 3
US-09-004-838-70
; Sequence 70, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmere, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; CONFERRING PEST RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:

LENGTH: 4163 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4163
OTHER INFORMATION: /note="RLG1-E169"
US-09-004-838-70

Query Match 6.8%; Score 201; DB 3; Length 4163;
Best Local Similarity 49.1%; Pred. No. 1.3e-47;
Matches 739; Conservative 10; Mismatches 705; Indels 51; Gaps 7;

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991 GAAATTAATCTTAATCTTGTGCTATGCGAAGAGATGTAAGAAATGATGATGATG 1050
2140 GATTCACATCAACACTAAGGCCACATGAGAGACTGTTTGTGAAGAAATGATGATGCT 2199
1051 CCTTAGCAGCTAAACTCTTGAAGTATTTGCGCTTAAAGAGAAAGAAAGAGCTG 1110
2200 CCTTAGCTTAAAGAACTTGAAGGTTATTAAGCAAAACAGACGAGAAATG 2259
1111 GAACATGAGAGATGATGAGATTTGGAATTTGCAATGCTCAAGAAAGTCTATCTGCT 1170
2260 AAGAGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2316
1171 GCCCTGAGACTTACTACATCACTTCACTTGATTTGAGACATGCTTATATATG 1230
2317 GCTTGAAGCTAAGCTACATGATCTTTGCGCCCTTGAAGCTRTTGTGATATG 2376
1231 GCAATATTTCCAAAGATACCAGAAATGAAAGGAAATCTATCTCTCTGATGCA 1290
2377 TCTTGTGTTCCAAAGACTATGATGATGATGATGATGATGATGATGATGATG 2436
1291 CATGTTTAT---TTATGAAAAGAACTTGAGCTAGAGATGATGATGATGATGATG 1347
2437 GAAGGTTTTTGACCAACAACATTAACAAAGTCAAGAGAGAGAGAGAGAGAGAG 2496
1348 TGGAATTAATTAATCTGAGCTTTCTTCCAAAGATTAAGTAAATCTGATCAACT 1407
2497 TTTTAAAGATTTTGTCAAGTCTTTTCA-----CATGCTCTTAATRCAATCS 2550
1408 TATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467
2551 TTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2610
1468 TCAAG 1472
2611 TCAAG 2615
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RESULT 4
US-09-004-838-6
Sequence 6, Application US/0904838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
TITLE OF INVENTION: Procedures and Materials for
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998

CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/781,734
 FILING DATE: 10-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Einhorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 023070-078810US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1662 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: -
 LOCATION: 1..1662
 OTHER INFORMATION: /note="R1G1F"
 US-09-004-838-6

Query Match 6.8%; Score 200.8; DB 3; Length 1662;
 Best Local Similarity 48.9%; Pred. No. 8.4e-48;
 Matches 720; Conservative 9; Mismatches 695; Indels 47; Gaps 6;

19 CAAGTCTGTTAGACATCTGCTTTTCATCCAAAGGGAACCTTGATGATTTCTGGT 78
 59 CCAGATATCTTTGAAAGAGGCTTCTGAGCTTGAAGAGATCGCGCTTCATCGG 118
 79 TTAAAGATGAGTTCGAAGAGCTTCAAGAGCTTACTACATCCAGCTGCTGTA 138
 119 ATGATTTCTGAGCTCAGAAAGCTGAGAGCTTATTAATCCAGATGATCTGTGCTTAAT 178
 139 GATGCTCAGAAAGAGCAATTTGAGGACAAAGCAATGAAATTTGGTTCAGAAATCTCAAT 198
 179 GATGCTTCTGAGAGGAAATAGTGAAGCTGTTAAAGATGCTGAATGCTGCTCA 238
 199 GCTGCTGATATGAGGCTGATGACATCTTGAAGATGTAATGAGGACCAATTTGA 258
 239 CATTTGCTTACGATAGACGACCTTATGATGATTTGGCAACGAAATATGATGATGCT 298
 259 CAGAAAGAAACAAATATGGGTGTTA-----TCAATC 289
 299 GAGTTGACCCAGGATCTGAGCCCTCCACAGCTTGAAGAAAGTAATCCCAATCTGCTT 358
 290 CAACGTTATCACTTTTCTCACAAGATTTGGGAAAGATGAAAGATTTAGAGAAAC 349
 359 GCAAGATTTCTCACTAAGTAGTAGTACGTTACGATGATGATGATGATGATGATGATGAT 418
 350 TAGATGTAATTCAGCGGACCAATTAAGTTTCAATTTGATGAAAGGACTATAGAGAC 409
 419 TACAAGAACTGTAGAGGAAAAAGATATCTTGGCTTAAGTGAAGAGTGAAGGCCAA 478
 410 AAGTTGCTACGCGCAACAGGTTTGTGTTGA--ATGAACCAAGATTTATGGAAG 466
 479 AACCTACCAAGAGATTTACAGACCTTTGTGATGATGATGATGATGATGATGATGATGAT 538
 467 ACAAGAAAGAGAGAGATGATGAAATCTGATTAACATGATGATGATGATGATGATGATGATGAT 526
 539 AAGGTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 598
 527 TTCCAGTCTCCCAATACCTTGTATGAGGAGGACTAGAAAGAGCACTCTTGGCCCAATG 586
 599 TTAGCATGCTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 658
 587 TCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 646
 659 TGTATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718
 647 AAGATTTTATGAGAAAGGTTGATTAAGAAATTTGATGATGATGATGATGATGATGATGATGATGAT 706

719 ATGAT 778
 707 TTGAT 766
 779 AAGATTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 838
 767 AATATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 826
 839 GATTTCTTTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 898
 827 GACAAGCTTTGAGAGGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 886
 899 CAGCTTCATTTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 958
 887 AGTTGAT 946
 959 CGTTGCTAACCAACTGGGTTACAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1018
 947 ATTTGAT 1003
 1019 ATGCTTTGCTTTATTTCTGTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
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 1064 AAATCTTTGAGAGGATTTTGGCTTTAAG 1123
 1139 TTGACATTTGAGAGGATTTTGAAG 1198
 1124 ATATGAT 1183
 1199 ATATGAT 1255
 1184 GTTACCATCACTTTCACTGATTTGAG 1243
 1256 GCTACATGAT 1315
 1244 AGATACCGAAG 1301
 1316 AAGAT 1375
 1302 -TTATGAG 1360
 1376 ACCAATCAACCAAG 1435
 1436 TGTCAAGAT 1489
 1421 ATGATCTCATGAT 1451
 1490 ATGACCTGAT 1520

RESULT 5
 US-09-004-838-2
 Sequence 2, Application US/09004838
 Patent No. 6350933
 GENERAL INFORMATION:
 APPLICANT: Michellmore, Richard W.
 APPLICANT: Shen, Kathy
 APPLICANT: Meyers, Blake
 TITLE OF INVENTION: Procedures and Materials for
 CONFERRING PEST RESISTANCE IN PLANTS
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..2353
OTHER INFORMATION: /note= "RLG1B"
US-09-004-838-2

Query Match 6.6%; Score 196.6; DB 3; Length 2353;
Best Local Similarity 48.8%; Pred. No. 1.7e-46;
Matches 767; Conservative 1; Mismatches 754; Indels 51; Gaps 7;

QY 10 GCTTCTCTCAAGTCTGTAGACATCTGACTTGTTCATCCAAAGGGAACTTGATG 69
DB 298 GCGTCTTTGGGGTGTCTTTGAAAGCTGCTTGAAGCTTGAAGAGGTTGCTTGC 357
QY 70 ATTCTGTTTAAAGATGATGTAAGAAAGCTTCAAGCAGTTTCTACATCCAACT 129
DB 358 TCCAAAGTAATTCAGAGAGCTCAGAAATGTAATAGCTCATGATCAATATAAGCT 417
QY 130 GTGCTAGAGATGCTCAGAGAGCAATGGAAGCAAGGCAATTAAGAAATGTTGAG 189
DB 418 CTGCTCATGATGCTTCTCAGAGAGAAATTAAGTAAGAGCTTTAAAGAAATGTTGAT 477
QY 190 AAATCTCAATGCTGCTCATATGAGCTGATGACATCTTGAAGAATGTAAATCGAGCA 249
DB 478 GCTCTTCAACATTTGCTTACAGACATAGATGATCTTGGCGATTGGCAACCAAGCT 537
QY 250 CCAATTTAGACAGAGAGAAACAATATGAGGTGTATCATCCAAACGTTATCATTTTCT 309
DB 538 ATCCATGTAATGTTCTCTGAGAAATACGGGCCCAACATCAACAAAGTAACGAATTAAT 597
QY 310 CAC-----AAGATTGGGAAAAGATGAATAAGTTATG 342
DB 598 CCAATCTGTTTCTGATGTTTCTCAAGTATCAAGTATGAGATGCCAAACAGATACATTAATTAAC 657
QY 343 GAGAAATAGATGTAATGTCAGCGCAAGAAATTAAGTTTCAATTTGATGAAGACATATA 402
DB 658 AGCAAGTTTACAAAGATTAATAGAGAGAGAAATATCTTGATATATGTAAGAAATGGTGA 717
QY 403 GAGAGCAAGTTGCTACACGCCCAACAGTTTGTGTTGAATGAACCAAGTTATGGA 462
DB 718 AGCCGAAATCTTGAATTAAGAAATACAGAGACCTCTGCTAGATCCATCTAGATATGTT 777
QY 463 AGAGCAAAAGAAAGAGAGAGATAGTAAATCTCTGATTAACATGTTAGCAATGCCCA 522
DB 778 GAGAGCAAGATTAAGAGAGAGCGTTGCTTCAAGCTATA--TGAACATGATAGTA 834

QY 523 AACCTCCAGTCTCCCAATACTTGATATGGGGGACATAGAAAGACGACTTGGCCA 582
DB 835 AACTTTAGCATCTTGCACATATGTTGTATGGTGGTTAGTAAGACCACTTAAGTAGTA 894
QY 583 ATGCTCTCAATGATCAGAGAGTAATGAGCAATTTCCATCCCAAAATATGATTTGTCT 642
DB 895 CTTTGTATGATTAATAATGCAAGTAAAGATCATTGCAACTCAAGCGGTGTTGTCT 954
QY 643 TCGAAGATTTTAATGAAAGAGGTTGATTAAGAAATGATGATCTTATGTAAGAAAG 702
DB 955 TCTGATGATGTTGATATCTTCGTATTAAGCAAAACATTTTCGATGATAGAGGGGGA 1014
QY 703 TCACCTGTGGCATGAGCTTGAGCTCCAATTCAAAAGAGCTTGGGACCTTGCAATGGA 762
DB 1015 AACCAAGTTTAAAGATTAATATCTGCTTCAAGTGCCTTTAAAGGAAAATCTCAAG 1074
QY 763 AAAAAATATTTGCTGCTTATGATGATGTTGGAATGAGATCAAGATTAAGTGGCTAG 822
DB 1075 AAACGATTTCTGTTGTTCTGATGATGATGAGGAGGCTATATGATTTGGAAATTT 1134
QY 823 TTAAGACAAGCTTGAAGGTTGAGCAAGTGGGCTTCTGTTCAACCACTACTGCTT 882
DB 1135 CTAGAACGTCATTTTACAGAGAGCACAGAAATTAAGTAATCATCACACCCGACAG 1194
QY 883 GAAAAGTTGATCAATTAATGAGCAATGCAACATATGATGTAATTTGCTCA 942
DB 1195 TTGCTGTTGCTAAACCAATTTGGGTCATGATCAACCATATTTGCTGATTTGTCAT 1254
QY 943 GAAGATTTGTTGTTGTTGTTTATGCAACGTCATTTGGGACCAAGAA--GAATTAAT 999
DB 1255 GACATGCTCATCTTAATTTTGTCAACAGCATTTGGTGTAAATAGCTTGAATCAAT 1314
QY 1000 CTTAATCTTGGCTATTCGGAAGAGATTTGGAATAAATGCTGTGCTCTAGCA 1059
DB 1315 CCGATCTTAAACCACTGATGTAAGGTAATTTGAAATAATGATGTTGGCATTGGCT 1374
QY 1060 GCTAAAATCTTGAAGGTAATTTGCGCTTAAAGAGAAAGAAAGACAGTGGAACTGTG 1119
DB 1375 TTGATTTGCACTTGGAGGTTATTAAGAGCAAAAGAGATGAGAAATGAGAAAGTA 1434
QY 1120 AGAGATGATGATTTGGAATTTGCTCAAGAGAAAGTTCTATTTCTGCTGCTGAG 1179
DB 1435 TTGAATGATGATGATGAGGTTAGAGAAAGAGAG--TGAGATTATTCGGGCTTGA 1491
QY 1180 CTTAGTTACCATGACCTTCCATGATTTGAGACATGCTTTATCATATGTCAGATATC 1239
DB 1492 CTAACTATATATATCTTCTGCTCTTTGAGACAGTTGTTGCAATATGCTCTGTTTC 1551
QY 1240 CCAAGGATACCGAAATGAGAAAGGAAATCTAATCTCTCTGATGACATGCTTTT 1299
DB 1552 CCCAAAGACTATGTTTCAACAAAGAGAGGTTGATTTTATGATGACAGAAAGGTTT 1611
QY 1300 ATTTTACGAAAG--AACTTGAAGCTAGAGATGTAAGTATGATAGTAAGTA 1356
DB 1612 TTGCACAAATGAAATACAAACAGATCAATGGAACGCTTGAATTTGAAATTTGACGAC 1671
QY 1357 TTATCTGAGGCTTCTTCTCAAGAGATGAAATTAATCTGTCATTAATTTCAAG 1416
DB 1672 TTGTTGTCAAGGCTATTTTTCACATGACATGACATGAC-----AATGTTGTTGTC 1725
QY 1417 ATGATGATCTCATGATGATCTGCAACATCTCT-----ATTTTGGCAACATCA 1470
DB 1726 GTGCAAGACCTCATGATGATCTTGGCAATCTGTTGAGATTAATTTTAAAGATTA 1785
QY 1471 AGAGCAATATCCGAAATTAATTTGAGAAATTAATCATATGATGATGCTATGTTTC 1530
DB 1786 GACATTTGAATGAAAGAGAGAGCTTGGAAATAACGACATATGATGATTTGTTGTAG 1845
QY 1531 ACTAAGTGTAT 1543
DB 1846 AGTTACATGTTT 1858

APPLICANT: Zhang, Bei
APPLICANT: Swords, Kathy M M
APPLICANT: Yan, Hua
TITLE OF INVENTION: A new method of identifying non-host plant disease
FILE REFERENCE: r gene patent
CURRENT APPLICATION NUMBER: US/09/387,286
EARLIER APPLICATION NUMBER: 60/098,402
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 24
LENGTH: 644
TYPE: DNA
ORGANISM: Nicotiana tabacum
US-09-387-286-24

Query Match 3.5%; Score 104; DB 4; Length 644;
Best Local Similarity 54.2%; Pred. No. 8.6e-20;
Matches 281; Conservative 0; Mismatches 225; Indels 12; Gaps 3;

547 GGTATGCGGGGAGCTAGGAAGACGACTCTGCCCAATGCTTCAATGATAGAGAGTA 606
76 GGCATGCGGGGAGCTAGGAAGACGACTCTGCCCAATGCTTCAATGATAGAGAGTA 135
607 ATTGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAAAGAAAGAG 666
136 AAGAAACATTTTGTGTTGAACCTTGTTTGTCTCGAAGATTTTAAAGAAAGAG 195
667 TTGATTAAGAAATTTGATGATCTATTGA-----GAAAGTCACTTGCGCATGAGC 720
196 AATAACAAAGGATCTTCAAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTT 255
721 TTGCTCCACTTCAAAAGAGCTTGCGCATGAGATTTGAAATTTGAAATTTGAAATTTG 780
256 CTTATACAGCTTCAAGTCAAAATTTGAAAGAGCTTGAAAGAGAGAGTCTTATTTGTT 315
781 TTGATGATTTTGAATGAAGATCAAGATTAAGAGAGCTTGAAAGAGAGTCTTGAAG 840
316 TTGATGATTTTGAATGAAGATCAAGATTAAGAGAGCTTGAAAGAGAGTCTTGAAG 375
841 GTTGAAGAGAGCTTGCTTCTTCAACCACTACTCTGCTTGAAGAGAGTCTTGAAG 900
376 CAAGAGATTAAGAGATTAAGATTAAGAGATTAAGAGATTAAGAGATTAAGAGATTA 435
901 ATGGGAATTTGCAACCAATGATTAAGATTTGCAATTTGCTCAAGAGAGATTTGCTG 960
436 ATGGGTTTGGGCAATTAAG---TGGGAATTTGCTTCAAGAGAGATTTGCTGCTTGA 492
961 TTCAATGCAAGCTGATTTGGCAACCAAG---AGAAATTAATTTTAAATCTTGTGCTATC 1017
493 TTCAACCAATTTCACTTAAGAAATTAAGAGATTTGCAAGAGATTTGCAAGATTTGA 552
1018 GGAAGAGAGATTTGAAATTAATTTGCTGCTGCTCT 1055
553 GGAAGAGAGATTTGCAAGAGATTTGCAAGAGATTTGCTGCTCT 590

RESULT 8
US-09-004-838-3
Sequence 3-3, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1036
OTHER INFORMATION: /note= "RLGIC"
US-09-004-838-3

Query Match 3.2%; Score 93.6; DB 3; Length 1036;
Best Local Similarity 48.2%; Pred. No. 1.3e-16;
Matches 375; Conservative 0; Mismatches 376; Indels 27; Gaps 3;

308 GTCAACAGATTTGGGAAAGATGAAAGATTTATGAGAACTAGATGATTTGCGCG 367
254 GTATAGAGATGATGCGAGGTTATGATGATTTGCGCGTAAAGTAAAGAACTGTTGAG 313
368 AAGAAATTAATTTGATTTGATGAAAGAGCTATAGAGAGAGAGTGTGCTACGCGCAA 427
314 CGAAATTAATTTGATTTGATGAAAGAGAGCTATAGAGAGAGAGTGTGCTACGCGCAA 373
428 CAGGTTTGTGTTGAATGAAGCAAGATTTATGAGAGAGAGAGAGAGAGAGAGAGAG 487
374 AGCGGTTTGTGATGATGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 433
488 TGAATTCGAT-----AACAATGATGATGATGATGATGATGATGATGATGATGAT 541
434 TTCAAGAGCTTTGGGGAATCTTATGATGATGATGATGATGATGATGATGATGATGAT 493
542 TACTTGATTTGGGGAATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 601
494 TACTTGATTTGGGGAATCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 553
602 GAGTATTAAGAGATTTCCATCCCAAAATTAAGATTTGTCTGCGAAGATTTTAATGAG 661
554 AAGTGAAGATCACTTGAAGATCAAGGATTTGATGATGATGATGATGATGATGATGATG 613
662 AAGGTTGATTAAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 721
614 CCAATTAAGAGAGATTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 673
722 TGGCTCACTTCAAAAGAGCTTGGGAGCTTGTGATGATGATGATGATGATGATGATGAT 781
674 TAAATCTGTTCAAGAGAGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 733
782 TGAATGATTTTGAATGAGATCAAGATTAAGTGGGCTTAAGTAAAGAGAGAGAGAG 841

DB 2612 ATGA 2615

RESULT 10

US-08-947-823-1

Sequence 1, Application US/08947823

Patent No. 6114605

GENERAL INFORMATION:

APPLICANT: Williamson, Valerie M.

APPLICANT: Kalooshian, Jagonhi

APPLICANT: Yaghoobi, Jafar

APPLICANT: Bodeau, John

APPLICANT: Molligan, Stephen

TITLE OF INVENTION: Procedures and Materials for Confering

TITLE OF INVENTION: Pest Resistance in Plants

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/947,823

FILING DATE: 09-OCT-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/18802

FILING DATE: 09-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/028,191

FILING DATE: 10-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 023070-070210US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 51952 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-947-823-1

Query Match 3.0%; Score 88.4; DB 3; length 51952;

Best Local Similarity 46.1%; Pred. No. 4,4e-14;

Matches 444; Conservative 0; Mismatches 511; Indels 9; Gaps 4;

DB 46750 AGAGGAAACAACTTGTATCTTGAAGAGTCAACAGTGGATGGAGATCTAGATGCA 46809

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536 TCCCAATATCTTGTATGAGGAGTCAAGAGTCTTGGCCCAATGCTTCTCATG 595

46810 TTTCGATCAGTGGATGCGGGTTCAGGTAAATCTTGGCATACAAAGTATACATG 46869

596 ATGAGAGATATGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTA 655

46870 ATAAAGTCACTTTCAGCCGTTTCAGCTTGTGATGTCACGTCGACCAAGATGTG 46929

656 ATGAGAGATATGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTA 715

46930 ATGAGAGATATGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTA 46989

DB 716 TGAGCTGGCTCCACTTCAAAAAGCTTGGGCACTTGATGAGAAAAATATTTTC 775

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47050 TTGCTTTTATGATGATGTTGGAT--ACTATCACTGAGATGATTAACAGACCTTTTCC 47107

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47108 TGAATCTTAAG--AAGAAATGAGATTAATTTTGAACACTCGGAAAAGAGTGGCTTGC 47166

896 CAATTATGAGCACTTGCACCAATGAATATGTCATTAATTTGTCAGAAATTTGCTGT 955

47167 ATGAAAAGCTGACATGATCTCTTGAACCTTGATGTCAGACCAAGTAAAGTTGGG 47226

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47227 AACTATTAGAAAGGCAATTTGG--AATGAGATTCCTGATGAACTATGATG 47283

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47284 TCGGTAAAGAAATAGCCGAAATTTGTAAGGCTTCTTGTGGCTGATCTGATTTGCTG 47343

1073 GAGGTATTTTGGCTTAAAGAGAAAGAACAGTGGGAAACATGAGAGATAGTGA 1132

47344 GAGCATTTGCTGGAGGAAAGAAAGAGTGTGCTTGAAGTTCACAAAGTATTTGA 47403

1133 TTGGAAATTCCTCAAGAAAGATTTCTATTTCTGCTGCTTGAAGCTTAATTAACATC 1192

47404 GTTCTTTTATTTGAACAGTGAAGTGAAGTGAATTAATTAAGTATTAAGTATGAC 47463

1193 AACTTCACTTGAATTTGAACATATGCTTATCAATTTGTGAGATTTCCCAAGATACCG 1252

47464 ATTTACCAATCACTTCAACCAATGCTTGTGATTTTGAAGTTCGAAAGCACTT 47523

1253 AAATGAAAGGAAATCTATCTCTCTGAGTGCATGTTTATTTATTCGAAAG 1312

47524 CATTGACATCTATGATTTGAATGTTATTTTCGCTGAGAGATTTGGGAAACCG 47583

1313 GAAACTTGAAGTGAAGATGATGATTAATGATGATGATTAATTAATTAACAGTCT 1372

47584 AGATGAACAGTATGAAGAAAGTGTGAAGTATTAATTAATTAACAGTCT 47643

1373 TCTTCAAGAGATTAAGTATTAATGCTCAACTTATTCAGAGATGATGATCTATTC 1432

47644 TGGTAAATTTGTTCAATGAGATGATTAATGACTGAATTTCCAAATTCATGATCTGTGC 47703

1433 ATGA 1436

47704 ATGA 47707

RESULT 11

US-09-004-838-4

Sequence 4, Application US/09004838

Patent No. 6350933

GENERAL INFORMATION:

APPLICANT: Michelmore, Richard W.

APPLICANT: Shen, Kathy

APPLICANT: Meyers, Blake

TITLE OF INVENTION: Procedures and Materials for

TITLE OF INVENTION: Confering Pest Resistance in Plants

NUMBER OF SEQUENCES: 140

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..946
OTHER INFORMATION: /note= "RLGID"
US-09-004-838-4

Query Match 3.0%; Score 88; DB 3; Length 946;
Best Local Similarity 48.1%; Pred. No. 5.1e-15;
Matches 277; Conservative 0; Mismatches 294; Indels 5; Gaps 1;

308 GTCAACAGATTGGGAAAAGATGAAAAAGATTATGAGAAACTAGATTAATTGACGGG 367
245 GTTAGAGATGATCCAGTCAAGTAGATGATATGCGACAGGTTACAAGACTGATGAGG 304
368 AACGAATTAAGTTTATTTGATGAAAAGCATATGAGAGACAGTCTCTACAGCCAA 427
305 CAAAAAATATCTTGGTTAAGTGATTAACATATGAAAAGCCCAAAATTAAAGTTTG 364
428 CAGTTTGTGTTGAATGACACAAAGTTTATGAGAGACAAAAGAAAGGACGATAG 487
365 AGGATCTTTGGTAGACAAAGTGATTTTGGCGTTAGATGATGAAAAAATTGA 424
488 TGAATTCCTGATTAACATATTTAGCAATGCC-----CAACACTTCCAGTCTCCCAAT 542
425 TGGAGAGCTGTGAGAGATTAAGATGAAATCGGAGTCMAAATTCACAGATCTGCGCAT 484
543 ACTTGATGAGGGGAGCTAGAGAAAGACATCTTCCCAATTTGCTTCAATGATCAGAG 602
485 AATTGGTATGGGTGAGGTGGCMAAACACTTACCTGACTCTTGTGTTGATGAAAAGAC 544
603 AGTATTTAGAGATTTCCATCCCAAAATATGATTTGTGCTCGAAGATTTTAATGAGAA 662
545 AGTGAAGATCACTTGAATCTAGGCGCTTGAGTTGTGTTCTGATGATTCAGATTTCT 604
663 GAGGTGTAAGAGAAATTTGATGATCTATTTGAAGAAAGTCACTTGTGCGATGAGATT 722
605 CAACATAGCAAAAGTTATCTATCAATCTGTGACCGGGGAAAAAGAGTTGAAGACTT 664
723 GGTCTCACTTCAAAAGAGCTTGGGACTTGTGATGAGAAAAAATATTTGCTGCTCTT 782
665 AAATCTGCTTCAAGAGCTTTAGAGGAAACTACAAAACAATTTCTTAATTAAGTTT 724
783 AGATGATGTTGGAATGAAGATCAAGATAGGGGCTAAGTTAAGCAAGTCTTGAAGGT 842
725 GATATGATTAATGTTGAGAAAGCTATGATGATTTGGAGAAATTTAGTGGCCCAATTCATGC 784
843 TGGAGCAAGTGGCGCTTCTGTCTTAACCACTACTCG 878

Db 785 TGGAGCTTGGAAAGTAGAATATCATGACTACTCG 820

RESULT 12

US-09-004-838-10
Sequence 10, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..544
OTHER INFORMATION: /note= "RLGID"
US-09-004-838-10

Query Match 2.9%; Score 87.4; DB 3; Length 544;
Best Local Similarity 49.5%; Pred. No. 5.5e-15;
Matches 251; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

556 GGACTAGAAAAGACGATCTTGGCCAAATGCTCTTCAATGATCAGAGATTAATGAGCAT 615
18 GGTGTGTGTAAGACGACTTAGCTAGACTTTTGTATGAGAAATGCAAGGAGAGATCAC 77
616 TTCATCCCAAAATATGATTTGTGCTCGGAAAGATTTTAATGAGAAAGGTGATAAG 675
78 TTCAACTTAAGGGGTGATGTGTTTCTGATGATTTGATATCTTCAATATTAAGCAA 137
676 GAAATTTGATATCTATTTGAAGAAAGTCACTTGTGCGATGAGACTTGGCTCCACTCAA 735
138 ATATCTTACATGATGATAGGAGGTGGAACCAAGAAATTTACGACTTAACCTGCTTGA 197
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198 GTACCTTAAAGAGAGATCTCAAGAAAAAGATTTCTTGTCTTGAATGATGATTTGG 257

QY	AATGAAGATCAAGATAAGGGGCTAAGTAAACAAGCTTGAAAGGTGACAACTGGC	855
Db		
QY	796 AATGAAGATCAAGATAAGGGGCTAAGTAAACAAGCTTGAAAGGTGACAACTGGC	855
Db	258 AGTGAAGACTATCCGATTGGGAAATTNGAACGCCCATTTCTTCAGGGGCACCTTGA	317
QY	856 GCTTCTGTCTPAACCACTACTGCTTGAAAAGTTGATCAATTATGGAACTTTGCAA	915
Db	318 AGTAGATATTAATATCACCAACCGGAAGCTGATATTGTAAACAACTCGTTACATTCAA	377
QY	916 CCATATGAATTTGTCAAATTTGTCTCAAGAAGATTTGTTGTTTGTTCATGCAACGTGCA	975
Db	378 CCTTACAACCTTTCGTTTGTGCACATGGAANGCTTGTCTTTATTTGTGCACATGCA	437
QY	976 TTGGGCAACAAGA--AGAAATAATCTTAATCTTTGGCTATCGGAAGAGATTTGTG	1033
Db	438 TTGGGTGAAGATACTTCAATTCACATCCAACACTTAAACCACATGGCGMAGTATTTGT	497
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Db	498 GAAAAATGTGATGTGCATTTGGCA	524

RESULT 13

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US-09-004-838-137
Sequence 137, Application US/09004638
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Micheltore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance i
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..544
OTHER INFORMATION: /note="RtGlb - Diana"
US-09-004-838-137

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Query Match	2.9%;	Score 87.4;	DB 3;	Length 544;
Best Local Similarity	49.5%;	Pred. No. 5.5e-15;		

Matches	251; Conservative	0; Mismatches	253; Indels	3; Gaps	1
QY	556	GCACTAGAGAAAGAGCACTTGGCCCAATGGCTCTTCAATGATCAGAGAGTAATTAAGCAT	615		
Db	18	GGTGTGGTGAAGACGACTCTAGCTAGACTTCTTGTGATGAGAAATCCAGAGGAGGATGATAC	77		
QY	616	TTCCATCCCAAAATATGGAATTTGTGTCTCGAGAGATTTTAATGAGAAAGGTGATTAAG	675		
Db	78	TTCCGAACTTAAGGGGTGGGTATGTGTTCTGATAGTTTGATATCTTCAATATTAAGCAA	137		
QY	676	GAAATTTGAGATCTATTGAAAGAAAGTCACTTGGTGCATGSACTTGGCTCCACTTCAA	735		
Db	138	ATTATCTTTCATCGATAGTGGTGGAAACCAAGAAATTTACGACTTAAACCTGTGTTGA	197		
QY	736	AAGAAGCTTGGGAGCTTGGCTGAATGSAAAAAAATATTGTCTCGTCTTATGATGATGTTTGG	795		
Db	198	GTACCTTTAAAGAGAGAGATCTCAAGAAAGATTTCTCTTGTCTTGATGATGTTTGG	257		
QY	796	AATGAGATCAAGATTAAGTGGGCTTAAGTTAAGACAAGTCTTGAAGGTTGAGACAGTGGC	855		
Db	258	AGTAAAGCTTAAACCGATTTGGAAATTTTGAAGGCCCATTTCTTGCAGGGGCACTTGA	317		
QY	856	GCTTCTGTCTTAACCACTACTCGTCTTGAAAGGTGGATCAATTATGGAACATTGCA	915		
Db	318	AGTAAAGATTAATTAACCAACCCGAGAGCTGTCATTTGTTAAACAAACTGGTTACATGCA	377		
QY	916	CCATATGAATTTGCAAAATTTGTCTCAAGAGATTTGGTGTGTTGTCATGCACAGTGA	975		
Db	378	CCTTTAAACCTTTGGGTGTTGTGCACATGAGATCTTTGTTCTTATTTCTGACAGATGCA	437		
QY	976	TTTGGGACACCAAG--AGAAATTAATCTTTATCTTGGGCTATGCGAAAGAGATTTG	1032		
Db	438	TTGGGTGAAGATTAATCTTCAATTTCAATCCACACTTAAACCAATGGCGAAGATTTGTT	497		
QY	1033	AAAAAATGTGGTGTGGCTCTAGCA	1059		
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RESULT 14

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US-09-245-928A-15
Sequence 15, Application US/09245928A
Patent No. 6613962
GENERAL INFORMATION:
APPLICANT: KEYGENE N. V.
TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
FILE REFERENCE: 960-35
CURRENT APPLICATION NUMBER: US/09/245,928A
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: PCT/EP97/04340
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: EP96401764.4
PRIOR FILING DATE: 1996-08-09
PRIOR APPLICATION NUMBER: EP97401101.7
PRIOR FILING DATE: 1997-05-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 9870
TYPE: DNA
ORGANISM: Mi resistance gene
US-09-245-928A-15

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Query Match 2.8%; Score 82.4; DB 4; Length 9870;
Best Local Similarity 45.0%; Pred. No. 9e-13;
Matches 434; Conservative 0; Mismatches 521; Indels 9; Gaps 3;

QY 476 AGACGAGATAGTGAATAATCTGATTAACATGTTACCAATGCCCAAACTTCCATCC 535

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QY 536 TCCCATATCTTGGTATGAGGGGACTAGAAGACGACTTTGCCCAATGCTTCAATG 595

Db 4974 TTTGATCAACCGGATGCGGGTTCAGGTAAACCTATTGGCATACAAAGTATACAAATG 5033
Qy 596 ATCAGAGATATATGAGCATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTA 655
Db 5034 ATAGTCAGTTTCTAGACATTTTGGACCTTCGCGATGTCACGCTCATCAGATATG 5093
Qy 656 ATGAGAGAGGTTGATTAAGAAATATGATATCTATTGAAAGAAAGTCACTTGTGCGCA 715
Db 5094 ACGACAGAGAGTTGTTGGATACAAATTTTCAAGTATAGTGGCTCAGATTCAAATTTGA 5153
Qy 716 TGGACTTGGCTCCACTTCAAAAGAGCTTCGGAGCTTGTGTAATGAAAAAATTTTGC 775
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Qy 776 TCGTCTTATGATGATTTTGAATGAAATCAAGATTAAGGCGCTAAGTTAAGACAGTCT 835
Db 5214 TTGCTTATGATGATGTTGGATGTTCTACTAC--TTGATGATGTTGCAAGACCTTTTC 5270
Qy 836 TGAAGTTGAGAGCAAGTGGCGCTTCTGTTCTAACCACTACTGTTGAAAGGTTGGAT 895
Db 5271 CTGAAGCTAAGAAAGAGATGAGATATTTTGAACAACCTCGAAGAAAGAGTGGCTTGC 5330
Qy 896 CAATTATGGAACATTCGACACCAATGATGTAATGTCAAATTTGTCAGAGAAATGTTGCT 955
Db 5331 ATGGAAGCTGAACATGATCTCTTGAACCTTCGATTCGATGAAGACGATGAAGTTGG 5390
Qy 956 TGTGTTATGCAACGTGATTTGGGCAACCAAGAAATTAATTTATCTTGTGGCTA 1015
Db 5391 AACTTTTGAAGAAAGACATTTG--TAATGAGATGGCCCTGATGAACATTAATGATG 5447
Qy 1016 TCGGAAAGAGATTTGTAAGAAATGTTGTTGTTGCTCTTACAGACTAA--AACTTTG 1072
Db 5448 TCGGAAAGAAATGCGGAAATTTGTAAGGCTTCTTGTGTCGATCTGATTTGCTG 5507
Qy 1073 GAGGATTTTGGCTTTAAGAGAGAAAGACAGTGGAAACATGAGATTAAGTGA 1132
Db 5508 GAGTCATTTGCTGGAGGAGAAAGAAAGAGATGTTGCTGAAGTTCAAGTATGTTGA 5567
Qy 1133 TTTGGAATTTGCTCAAGAAAGATTTCTATTTCTGCTGCTGAGCTTATGATACATC 1192
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Qy 1313 GAACTTGGAGCTAGAGATGATGATATGAGATATGAAATGATTAATCTTGAAGTCTT 1372
Db 5748 AGATGAAAGGTAATGAAAGATGGAAGATTTATATGATTAATTTTCCAGTACT 5807
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Qy 1433 ATGA 1436
Db 5868 ATGA 5871

RESULT 15
US-08-947-823-4
; Sequence 4, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:

; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kailashan, Irgouhi
; APPLICANT: Yaghobbi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen

; TITLE OF INVENTION: Procedures and Materials for Confering
; TITLE OF INVENTION: Pest Resistance in Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baslian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..3860
; OTHER INFORMATION: /note="Copy 2 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
US-08-947-823-4
Query Match 2.7%; Score 80.8; DB 3; Length 3982;
Best Local Similarity 44.9%; Pred. No. 1.5e-12;
Matches 433; Conservative 0; Mismatches 522; Indels 9; Gaps 3;
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Db 1843 ACGACAGAGAGTTGATTAATTAATTTTCAAGTATGCTCAGATTCAAATTTGA 1902
Qy 716 TGGACTTGGCTCCACTTCAAAAGAGCTTCGGAGCTTGTGTAATGAAAAAATTTTGC 775
Db 1903 GTGAGATATTTGATGTTGCTGATTAATTTGGGAAACAACATGTTTGAAGAGTATCTTA 1962
Qy 776 TCGTCTTATGATGATTTTGAATGAAATCAAGATTAAGTGGCTAAGTTAAGACAGTCT 835
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QY	836	TGAAGGTGGAGCAAGTGGCCGCTTCGTTCTTACACACTGCTGTGTAAGAAAGTTGGAT	895
Dp	2020	CTGAAGCTTAAGAAAGAGTAGATTAATTTTGAACACTCGAAGAAAGAAAGAGGCTTTCG	20797
QY	896	CAATTATGGAACAATTGCACCACTATGTAATGTCAAATTTGTCCTCAGAAGATTTGGGT	955
Dp	2080	ATGGAACCTGAACACTGATCCTCTTGACCTTCGATTGCTGAAGACCAATGAAAGTTGGG	21399
QY	956	TGTTGTCATGCACGTCGATTTGGGACCAAGAAGAAATTAATCTTATCTTGCGCTA	10151
Dp	2140	AACCTTTTAGATTAAGAAAGCAATTTGG---TAATGAGATGGCCGTGATCACTATTAAGATG	21966
QY	1016	TCGGAAGAGAAATTGTGAAGAAATGTGGTGGTGCTCTTAGCACTAA---AACTCTTG	10722
Dp	2197	TCGGTAAAGAAATAGCCGAAAATGTAAAGGCTTCTTTGGTGGCTGATCTGAATGGCTG	22566
QY	1073	GAGGTATTTTGGCTTTTAAGAGAGAAAGAAACAAGTGGAAACATGTGAGAGATATGTGAGA	11323
Dp	2257	GAGTCATTGTGGGAGGAGAAAGAAAGAGAGTGCTGGCTTGAAGTTCAAGATGTTTGA	2316
QY	1133	TTTGGAAATTCGCTCCAGAAAGAAAGTTCTATTTCCCTGCGCCCTAGACTTATGTTACATC	1192
Dp	2317	GTTCTTTATTTTGAACGTAAGGTGGAAGATGAAGAAATTAATGAATTAAGTTATGAC	2376
QY	1193	ACCTTCCACTTGATTTTGAACAATGCTTTACATATTGTGCAGATATTCCTCAAGAGTACCG	1252
Dp	2377	ATTTACCCACATACCTCAAGCCATGCTTGCTTCACTTGGCAAGTTGGCCGAAGACACTC	2436
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Dp	2437	CTTTGACATCTATTTTGTTACTGTTTATTTGGGTCTGAAAGGAAATTTGTGAAAAGACGG	2496
QY	1313	GAAACTTGACCTAGAGAGATGTAGGTATGAAGTATGAGATGAATTTATCTTGAAGTCTT	1372
Dp	2497	AGATGAAGGGGTATGAGAAAGTGTGTAAGATTTATATGATGAATTTATTTCCAGTACCT	2556
QY	1373	TCTTCCAAGAAATTTGAAGTTAAATCTGGTCAAACTTTATTTTCAAGATGATGATCTCATTC	1432
Dp	2557	TGTGTAATTTTGTTCATATGAGATAGGTGATATATCTGAATTTCCAAATTCATGATCTTGTC	2616
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%

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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

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3	2541.8	85.7	US-10-647-268-9	Sequence 9, Appl1
4	2309	77.8	US-10-647-268-5	Sequence 5, Appl1
5	2077.2	70.0	US-10-360-522-48	Sequence 48, Appl1
6	1880.8	63.4	US-10-360-522-52	Sequence 52, Appl1
7	1805.8	60.9	US-10-360-522-49	Sequence 49, Appl1
8	1805.8	60.9	US-10-360-522-50	Sequence 50, Appl1
9	1771.6	58.5	US-10-360-522-51	Sequence 51, Appl1
10	1736.2	53.9	US-10-360-522-53	Sequence 53, Appl1
11	1599.2	32.22	US-10-647-268-7	Sequence 7, Appl1

12	274.4	9.2	2409	18	US-10-437-963-67879	Sequence 67879, A
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15	268.6	9.1	3852	18	US-10-437-963-33659	Sequence 33659, A
16	268.6	9.0	2565	18	US-10-437-963-56879	Sequence 56879, A
17	257.8	8.7	2597	18	US-10-437-963-50413	Sequence 50413, A
18	255.2	8.6	3366	18	US-10-437-963-57476	Sequence 57476, A
19	242.4	8.2	6779	18	US-10-437-963-29812	Sequence 29812, A
20	236.6	8.0	3669	18	US-10-437-963-51007	Sequence 51007, A
21	236.2	8.0	2883	18	US-10-437-963-65758	Sequence 26579, A
22	234.2	7.9	4206	18	US-10-437-963-96687	Sequence 96697, A
23	232.4	7.8	5498	18	US-10-437-963-29817	Sequence 29817, A
24	217.6	7.3	2415	18	US-10-437-963-24753	Sequence 24753, A
25	212.2	7.2	3858	18	US-10-437-963-52795	Sequence 57795, A
26	211.4	7.1	3759	17	US-10-425-114-29667	Sequence 29667, A
27	201.8	6.8	2603	18	US-10-437-963-40346	Sequence 40346, A
28	201.8	6.8	3369	18	US-10-437-963-40347	Sequence 40347, A
29	192.6	6.5	2949	18	US-10-437-963-79939	Sequence 79939, A
30	192.6	6.5	4372	18	US-10-437-963-87934	Sequence 87934, A
31	184	6.2	2481	18	US-10-437-963-92298	Sequence 92298, A
32	183.6	6.2	2982	18	US-10-437-963-94718	Sequence 94718, A
33	182.6	6.2	3172	18	US-10-437-963-10860	Sequence 10860, A
34	181.4	6.1	3497	17	US-10-424-599-24653	Sequence 24653, A
35	181	6.1	2709	18	US-10-437-963-15352	Sequence 15352, A
36	180.8	6.1	3633	18	US-10-437-963-29281	Sequence 29281, A
37	180.4	6.1	3276	18	US-10-437-963-92169	Sequence 92169, A
38	177.6	6.0	2985	18	US-10-437-963-26581	Sequence 26581, A
39	177	6.0	1226	18	US-10-437-963-57477	Sequence 57477, A
40	174.6	5.9	708	17	US-10-424-599-25254	Sequence 25254, A
41	174.2	5.9	2229	18	US-10-437-963-6807	Sequence 6807, Ap
42	173	5.8	1158	17	US-10-424-599-97562	Sequence 97562, A
43	170	5.7	3822	18	US-10-437-963-100477	Sequence 100477, A
44	169	5.7	2067	18	US-10-437-963-100511	Sequence 100511, A
45	168.8	5.7	3447	18	US-10-437-963-17974	Sequence 17974, A

ALIGNMENTS

RESULT 1
US-10-647-268-1 Application US/10647268
; Sequence 1, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647, 268
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 3193
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52) ..(3018)
US-10-647-268-1

Query Match 100.0%; Score 2967; DB 18; Length 3193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2967; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCTGAAGCTTCTTCAAGTCTGTAGACATCTGTTTCATCCAAAGGGA 60
DB	52	ATGCTGAAGCTTCTTCAAGTCTGTAGACATCTGTTTCATCCAAAGGGA 111
QY	61	CTTGATGATTTCTTGGTTTAAAGATGATGAAAAAGCTTCAAGCAGCTTACTACA 120
DB	112	CTTGATGATTTCTTGGTTTAAAGATGATGAAAAAGCTTCAAGCAGCTTACTACA 171

QY 121 ATCCAGCTGTGTAGAGATGCTCAGAGAACCAATTGAGACCAAGCAATAGAAAT 180
DB 172 ATCCAGAGCTGTGTAGAGATGCTCAGAGAACCAATTGAGAGCAAGCAATAGAAAT 231
QY 181 TGGTTCAGAGAACTCATGTGCTGTGATATGAGGCTGATGACATCTTGGACGAATGAA 240
DB 232 TGGTTCAGAGAACTCATGTGCTGTGATATGAGGCTGATGACATCTTGGACGAATGAA 291
QY 241 ACTGAGGACCAATTGACAGAGAGAGAAACAATATGAGGCTGATGACATCTTGGAC 300
DB 292 ACTGAGGACCAATTGACAGAGAGAGAAACAATATGAGGCTGATGACATCTTGGAC 351
QY 301 ACTTTCGTCAACAAGTTGGGAAAAGAGTGAATAATATGAGGAAATATGATGAT 360
DB 352 ACTTTCGTCAACAAGTTGGGAAAAGAGTGAATAATATGAGGAAATATGATGAT 411
QY 361 GCAGCGGAAAGATTAAGTTCAATTTGATGAAAGAGCTATAGAGACAAAGTTGCTACA 420
DB 412 GCAGCGGAAAGATTAAGTTCAATTTGATGAAAGAGCTATAGAGACAAAGTTGCTACA 471
QY 421 CCCCAACAGCTTTTGTGTAATGAAACAAGTTTATGAGAGACAAAGAGAGAC 480
DB 472 CCCCAACAGCTTTTGTGTAATGAAACAAGTTTATGAGAGACAAAGAGAGAC 531
QY 481 GAGATAGTGAATAATCCTGATTAACAATGTTAGCAATGCCCAACACTTCCAGTCTCCCA 540
DB 532 GAGATAGTGAATAATCCTGATTAACAATGTTAGCAATGCCCAACACTTCCAGTCTCCCA 591
QY 541 ATACTTGTGATGGGGGACCTAGAGAGAGACACTTGTGCCAATGCTTCAATGATCAG 600
DB 592 ATACTTGTGATGGGGGACCTAGAGAGAGACACTTGTGCCAATGCTTCAATGATCAG 651
QY 601 AGAGTATTTGAGCATTTCCATCCAAAATATGAGATTTGCTGGAGATTTTAAATAG 660
DB 652 AGAGTATTTGAGCATTTCCATCCAAAATATGAGATTTGCTGGAGATTTTAAATAG 711
QY 661 AAGAGTTGATTAAGAGAAATGTAGAACTATTTGAAGAGAAAGTCACTTGTGAGAC 720
DB 712 AAGAGTTGATTAAGAGAAATGTAGAACTATTTGAAGAGAAAGTCACTTGTGAGAC 771
QY 721 TTGGTCCACCTTCAAAAAGAGCTTGGGACTTGGCAATGAGAAAAATATTTGCTGCTC 780
DB 772 TTGGTCCACCTTCAAAAAGAGCTTGGGACTTGGCAATGAGAAAAATATTTGCTGCTC 831
QY 781 TTAGATGATTTTGGATGAGATCAAGATTAAGTGGCTAAGTTAAGCAAGTCTTGAAG 840
DB 832 TTAGATGATTTTGGATGAGATCAAGATTAAGTGGCTAAGTTAAGCAAGTCTTGAAG 891
QY 841 GTTGGAGCAAGTGGGCTTCTGTTCTAACTAAGTCTTGGAGAAAGTTGATCAATT 900
DB 892 GTTGGAGCAAGTGGGCTTCTGTTCTAACTAAGTCTTGGAGAAAGTTGATCAATT 951
QY 901 ATGGGAACATTTGCAACCAATATGTCAAATTTGCTCAAGAGAGTGTGTTG 960
DB 952 ATGGGAACATTTGCAACCAATATGTCAAATTTGCTCAAGAGAGTGTGTTG 1011
QY 961 TTCAATGCAACGTGATTTGGGCAACAAGAGAAATTAATCTTATCTTGGCTATCGGA 1020
DB 1012 TTCAATGCAACGTGATTTGGGCAACAAGAGAAATTAATCTTATCTTGGCTATCGGA 1071
QY 1021 AAGAGATTTGGAATAATGTGTGTGTGCTCTAGACGCTAATACTCTTGGAGGATTT 1080
DB 1072 AAGAGATTTGGAATAATGTGTGTGTGCTCTAGACGCTAATACTCTTGGAGGATTT 1131
QY 1081 TTGGGCTTTTGAAG 1140
DB 1132 TTGGGCTTTTGAAG 1191
QY 1141 TTGGCTCAAG 1200
DB 1192 TTGGCTCAAG 1251

QY 1201 CTTGATTTGAGCAATGCTTTACATATTTGTCAGATTTCCAAAAGATACGAAATGGA 1260
DB 1252 CTTGATTTGAGCAATGCTTTACATATTTGTCAGATTTCCAAAAGATACGAAATGGA 1311
QY 1261 AAGGAAATCTAATCTCTCTGTGATGAGACATGCTTTATTTTATGAGAGAACTTG 1320
DB 1312 AAGGAAATCTAATCTCTCTGTGATGAGACATGCTTTATTTTATGAGAGAACTTG 1371
QY 1321 GAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1372 GAGCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
QY 1381 GAGATGAGATTAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGAT 1440
DB 1432 GAGATGAGATTAATCTGCTCAAACTTATTTCAAGATGATGATGATGATGATGATGAT 1491
QY 1441 GCAACATCTTAATTTTGGGCAAGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1492 GCAACATCTTAATTTTGGGCAAGACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
QY 1501 AATTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1552 AATTACATACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1611
QY 1561 CACTTGAAGAGATTTGCTGCTGAGAGGCTTATTTAAGTGAATTAAGAGAGAGAGAG 1620
DB 1612 CACTTGAAGAGATTTGCTGCTGAGAGGCTTATTTAAGTGAATTAAGAGAGAGAGAGAG 1671
QY 1621 TTACCGTCTTCAATGAGAGATCTAGATCAATTTAAGATACCTTAACTTGTGCAATACT 1680
DB 1672 TTACCGTCTTCAATGAGAGATCTAGATCAATTTAAGATACCTTAACTTGTGCAATACT 1731
QY 1681 AGATTTGTGATGCTTCCAAACCACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1732 AGATTTGTGATGCTTCCAAACCACTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1791
QY 1741 CATGCGTCAATCACTTGTGTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1792 CATGCGTCAATCACTTGTGTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1851
QY 1801 AATCTTTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1852 AATCTTTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1911
QY 1861 ACATGCGTTAAGCTTAACTAAGTATGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1912 ACATGCGTTAAGCTTAACTAAGTATGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1971
QY 1921 GGTGAATTAAG 1980
DB 1972 GGTGAATTAAG 2031
QY 1981 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
DB 2032 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2091
QY 2041 AGCATGAAATGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2100
DB 2092 AGCATGAAATGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2151
QY 2101 CTTGAAGCTCTCAAAACCACTCAATCTGATCTTTTAAACAATGAGGAGCTTCAAGAGA 2160
DB 2152 CTTGAAGCTCTCAAAACCACTCAATCTGATCTTTTAAACAATGAGGAGCTTCAAGAGA 2211
QY 2161 ATCCGCTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
DB 2212 ATCCGCTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2271
QY 2221 ATCACTTGAAG 2280
DB 2272 ATCACTTGAAG 2331
QY 2281 CTAAGATTTGAG 2340

Db 2332 CTGAGGTTGTGAGAGGGGCTGCGAGAGTGAATGATGTTGATTCGAGATTCCTACAGAGA 2391
Qy 2341 AGAAGTTTCCATCTCGAGAAAACCTTAATATAGCCAAATTTGGTAATCGAAGAGATG 2400
Db 2392 AGAAGGTTTCCATCTCGAGAAAACCTTAATATAGCCAAATTTGGTAATCGAAGAGATG 2451
Qy 2401 CTGAAAAAGAGAGAGAGAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTTGC 2460
Db 2452 CTGAAAAAGAGAGAGAGAGCAATGCCCTGTGCTTGAAGATAGAGATTAATGTTGC 2511
Qy 2461 CTAATGTTTGTATTCGAACCCCTTTCTTCTGCAAGAAATTTGATGATGAGGAGACAG 2520
Db 2512 CTAATGTTTGTATTCGAACCCCTTTCTTCTGCAAGAAATTTGATGATGAGGAGACAG 2571
Qy 2521 TCAATGCAATAGGTTTCAGTTCCATCTAATCTAATCTAGGCTCTTACTCTCCCTCAAAAT 2580
Db 2572 TCAATGCAATAGGTTTCAGTTCCATCTAATCTAATCTAGGCTCTTACTCTCCCTCAAAAT 2631
Qy 2581 CGCTAATAAGAGAGAGAGTCTTCACTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTC 2640
Db 2632 CGCTAATAAGAGAGAGAGTCTTCACTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTC 2691
Qy 2641 AAATACTGCAATATCTCTTTTAACTTCAATCTTAAAGAGCTGCTACAGCCTGAGT 2700
Db 2692 AAATACTGCAATATCTCTTTTAACTTCAATCTTAAAGAGCTGCTACAGCCTGAGT 2751
Qy 2701 CTCAATGCTTGAAGCATCTGGAATATCATAGTTTATGCACTAGAGAGTCTCCCGAG 2760
Db 2752 CTCAATGCTTGAAGCATCTGGAATATCATAGTTTATGCACTAGAGAGTCTCCCGAG 2811
Qy 2761 GAAGGTGGAAGGTTTAATTTCACTCACTCAAGTTATCATACATCTGGAAGTGA 2820
Db 2812 GAAGGTGGAAGGTTTAATTTCACTCACTCAAGTTATCATACATCTGGAAGTGA 2871
Qy 2821 CAATGTTTACCGAGAGATGACAGACCTTAACAGCCCTCACAAATTTATCAGTTGAGTT 2880
Db 2872 CAATGTTTACCGAGAGATGACAGACCTTAACAGCCCTCACAAATTTATCAGTTGAGTT 2931
Qy 2881 TGTCCAAACCTGCGCAAGCGGTGTGAGAGAGGATAGAGAGATCTGTACAAATTTGCT 2940
Db 2932 TGTCCAAACCTGCGCAAGCGGTGTGAGAGAGGATAGAGAGATCTGTACAAATTTGCT 2991
Qy 2941 CACATTCCTGCTGTTTATTTATTTAG 2967
Db 2992 CACATTCCTGCTGTTTATTTATTTAG 3018

RESULT 2
US-10-647-268-3
Sequence 3, Application US/10647268
Publication No. US20040237137A1
GENERAL INFORMATION:
APPLICANT: Oosumi et al., Teruko
TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
FILE REFERENCE: 0155 02
CURRENT APPLICATION NUMBER: US/10/647,268
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 60/407,100
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 3595
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: CDS
LOCATION: (57)..(487)
OTHER INFORMATION: Spull1 protein
FEATURE:
NAME/KEY: Intron
LOCATION: (488)..(899)

FEATURE:
NAME/KEY: CDS
LOCATION: (900)..(13432)
US-10-647-268-3
Query Match 85.7%; Score 2541.8; DB 18; Length 3595;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 428 CAGGTTTGTGTAATGAACCAAGTTTATGGAAGAGCAAAAGAGAGAGAGATG 487
Db 896 CAGGTTTGTGTAATGAACCAAGTTTATGGAAGAGCAAAAGAGAGAGATG 955
Qy 488 TGAATATCTGATTAACAATGTTAGCAATGCCCAACAATCTCAGTCTCCCAATACTG 547
Db 956 TGAATATCTGATTAACAATGTTAGCAATGCCCAACAATCTCAGTCTCCCAATACTG 1015
Qy 548 GTATGAGGAGAGCTAG 607
Db 1016 GTATGAGGAG 1075
Qy 608 TTGAGCAATTCATCCCAAAATATGAGATTTGCTGGAAGATTTTATGAGAGAGT 667
Db 1076 TTGAGCAATTCATCCCAAAATATGAGATTTGCTGGAAGATTTTATGAGAGAGT 1135
Qy 668 TGATTAAG 727
Db 1136 TGATTAAG 1195
Qy 728 CACTTCAAAAG 787
Db 1196 CACTTCAAAAG 1255
Qy 788 ATGTTTGAATGAAGATCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
Db 1256 ATGTTTGAATGAAGATCAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
Qy 848 CAGTGGCGCTTCTGTTCTAACAATCTGCTCTTGAAGAGAGAGAGAGAGAGAGAG 907
Db 1316 CAGTGGCGCTTCTGTTCTAACAATCTGCTCTTGAAGAGAGAGAGAGAGAGAGAG 1375
Qy 908 CATTGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 967
Db 1376 CATTGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
Qy 968 AACGTGATTTGGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
Db 1436 AACGTGATTTGGGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1495
Qy 1028 TTGTAAG 1087
Db 1496 TTGTAAG 1555
Qy 1088 TTAAG 1147
Db 1556 TTAAG 1615
Qy 1148 AAG 1207
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Qy 1208 TGAG 1267
Db 1676 TGAG 1735
Qy 1268 ATCTAATCTCTCTGAG 1327
Db 1736 ATCTAATCTCTCTGAG 1795
Qy 1328 AGATGAG 1387
Db 1796 AGATGAG 1855

1388 AAGTTAAATCTGTCGAACCTATTATTCAGATGATGATCTCATGATGATGCAAGAT 1447
1856 AAGTTAAATCTGTCGAACCTATTATTCAGATGATGATCTCATGATGATGCAAGAT 1915
1448 CTGATATTTGGGCAAGACATCAAGCAGCAATATCCGAGAAATATTTAGAAAATTA 1507
1916 CTGATATTTGGGCAAGACATCAAGCAGCAATATCCGAGAAATATTTAGAAAATTA 1975
1508 TACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1567
1976 TACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2035
1568 AGAATTTGTCCTGTCGAGGTCCTTAATCTAAGCATATAAATTTAGCAGTTACCGT 1627
2036 AGAATTTGTCCTGTCGAGGTCCTTAATCTAAGCATATAAATTTAGCAGTTACCGT 2095
1628 CTTCATTTGAGATCTAGTATGATTAAGATATCTAAGCTTCTGTCGCAATATGAT 1687
2096 CTTCATTTGAGATCTAGTATGATTAAGATATCTAAGCTTCTGTCGCAATATGAT 2155
1688 GTACTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTATCTACATG 1747
2156 GTACTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTATCTACATG 2215
1748 GTACTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTATCTACATG 1807
2216 GTACTCTTCCAAACAGTATGCAAGCTTCAAAATCTGCAAGCTTGTATCTACATG 2275
1808 TACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1867
2276 TACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2335
1868 TTAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1927
2336 TTAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2395
1928 TACGAAACCTGATCTCTATGATGATGATGATGATGATGATGATGATGATGAT 1987
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2456 ATATGATGCAAAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 2515
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2516 ATATGATGCAAAAGCAATGATGATGATGATGATGATGATGATGATGATGAT 2575
2108 CTCTCAAAACCACTCAATCTGATGATGATGATGATGATGATGATGATGATGAT 2167
2576 CTCTCAAAACCACTCAATCTGATGATGATGATGATGATGATGATGATGATGAT 2635
2168 TCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2227
2636 TCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2695
2228 GCAAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2287
2696 GCAAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2755
2288 TGTGAGGAGGAGTCTGCGAAGTGAATGATGATGATGATGATGATGATGATGAT 2347
2756 TATGAGGAGGAGTCTGCGAAGTGAATGATGATGATGATGATGATGATGATGAT 2815
2348 TTCCATCTCTGAGAAAATTATATACGCAATTTGATGATGATGATGATGATGAT 2407
2816 TTCCATCTCTGAGAAAATTATATACGCAATTTGATGATGATGATGATGATGAT 2875
2408 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2467
2876 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2935
-QY 2468 TTGTTATTCACACCTTTCTTCTGTCAGAAATTTGATGATGATGATGATGATG 2527

2396 TTGTTATTCACACCTTTCTTCTGTCAGAAATTTGATGATGATGATGATGATG 2995
2528 CAATAGGTTTCAGTTCCATATCTATATCTCATGCTCTTACTTCCCTCAAAATTC 2587
2396 CAATAGGTTTCAGTTCCATATCTATATCTCATGCTCTTACTTCCCTCAAAATTC 3055
2588 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2647
3056 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3115
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3116 TGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3175
2708 CTTTGAAGCATCTGGAATTCATATGTTGATGATGATGATGATGATGATGATG 2767
3176 CTTTGAAGCATCTGGAATTCATATGTTGATGATGATGATGATGATGATGATG 3235
2768 TGAAGGTTTAAATTTCACTACACAGTTATCCATACATCTGGAATGCTACATG 2827
3236 TGAAGGTTTAAATTTCACTACACAGTTATCCATACATCTGGAATGCTACATG 3295
2828 TACCGAGGAGGATGCAACCTTACACAGCTTCAACAAATTTATCAGTTTGTCCA 2887
3296 TACCGAGGAGGATGCAACCTTACACAGCTTCAACAAATTTATCAGTTTGTCCA 3355
2888 CACTGCGCAAGCGGTGGAAGAGGAGGATGAGAGAGGAGGAGGAGGAGGAGGAG 2947
3356 CACTGCGCAAGCGGTGGAAGAGGAGGATGAGAGAGGAGGAGGAGGAGGAGGAG 3415
2948 CTGCTGTTTAAATTTATGATGATGATGATGATGATGATGATGATGATGATG 2967
3416 CTGCTGTTTAAATTTATGATGATGATGATGATGATGATGATGATGATGATG 3435

RESULT 3
US-10-647-268-9
Sequence 9, Application US/10647268
Publication No. US20040237137A1
GENERAL INFORMATION:
APPLICANT: Oosumi et al., Teruko
TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
FILE REFERENCE: 0155.02
CURRENT APPLICATION NUMBER: US/10/647,268
PRIOR APPLICATION NUMBER: 60/407,100
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 5028
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURES:
NAME/KEY: Promoter
LOCATION: (1) ..(953)
OTHER INFORMATION: Potato Ub13 promoter
FEATURE:
NAME/KEY: gene
LOCATION: (973) ..(4566)
OTHER INFORMATION: Solanum bulbocastanum genomic Shu11
FEATURE:
NAME/KEY: CDS
LOCATION: (1029) ..(1459)
FEATURE:
NAME/KEY: Intron
LOCATION: (1460) ..(1871)
FEATURE:
NAME/KEY: CDS
LOCATION: (1872) ..(4404)
US-10-647-268-9

Query Match 85.7%; Score 2541.8; DB 18; Length 5028;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 2538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 428 CAGGTTTGTGTTGATGATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 487
Db 1868 CAGGTTTGTGTTGATGATGACCAAGTTTATGGAAGACAAAGAAAGACGAGATG 1927
Qy 488 TGAATATCTGATTAACATGATGATGATGATGATGATGATGATGATGATGATG 547
Db 1928 TGAATATCTGATTAACATGATGATGATGATGATGATGATGATGATGATGATG 1987
Qy 548 GTATGGGGGAGCTAGAAAGAGAGACTCTGGCCCAATAGTCTTCAATGATGAGAGTAA 607
Db 1988 GTATGGGGGAGCTAGAAAGAGAGACTCTGGCCCAATAGTCTTCAATGATGAGAGTAA 2047
Qy 608 TTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAAGATTTTATGAGAGAGT 667
Db 2048 TTGAGCATTTCCATCCCAAAATATGATTTGTGTCTCGAAAGATTTTATGAGAGAGT 2107
Qy 668 TGATTAAGGAATTTGATGATCTATGTAAGAAAGTCACTTGGGAGATGATGATGATG 727
Db 2108 TGATTAAGGAATTTGATGATCTATGTAAGAAAGTCACTTGGGAGATGATGATGATG 2167
Qy 728 CACTTCAAAAGAGCTTGGGAGCTTGTGTAATGGAAGAAATATTTGCTGCTTATGATG 787
Db 2168 CACTTCAAAAGAGCTTGGGAGCTTGTGTAATGGAAGAAATATTTGCTGCTTATGATG 2227
Qy 788 ATGTTGGATGAAAGATCAAGATTAAGTGGCTAAGTAAAGACAGCTTGAAGGTTGAG 847
Db 2228 ATGTTGGATGAAAGATCAAGATTAAGTGGCTAAGTAAAGACAGCTTGAAGGTTGAG 2287
Qy 848 CAAAGGGGCTTCTGTTCTAACTACTGCTTGAAGAGTGGATCAATTAATGGAAG 907
Db 2288 CAAAGGGGCTTCTGTTCTAACTACTGCTTGAAGAGTGGATCAATTAATGGAAG 2347
Qy 908 CATTGCAACATATGATTTGTCAATTTGTCTCAAGAGATTTGTGTTGTTCAATGC 967
Db 2348 CATTGCAACATATGATTTGTCAATTTGTCTCAAGAGATTTGTGTTGTTCAATGC 2407
Qy 968 AACGTGATTTGGGACCAAGAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGAGA 1027
Db 2408 AACGTGATTTGGGACCAAGAGAAATTAATCTTAATCTTGTGGCTATCGGAAAGGAGA 2467
Qy 1028 TTGTGAAATTAATGAGTGTGCTGCTCTAGAGAGTAAATCTTGAAGATTTTGGCT 1087
Db 2468 TTGTGAAATTAATGAGTGTGCTGCTCTAGAGAGTAAATCTTGAAGATTTTGGCT 2527
Qy 1088 TTAAGAGAGAGAGAGACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGCTC 1147
Db 2528 TTAAGAGAGAGAGAGACAGTGGGAACTGTGAGAGATGAGATTTGAAATTTGCTC 2587
Qy 1148 AAGAGAAAGTTCTAATCTGCTGCTGCTGAGACTTAATCAATCACTTGCATGAT 1207
Db 2588 AAGAGAAAGTTCTAATCTGCTGCTGCTGAGACTTAATCAATCACTTGCATGAT 2647
Qy 1208 TGAGACATGCTTAACTATGATGATGATGATGATGATGATGATGATGATGATG 1267
Db 2648 TGAGACATGCTTAACTATGATGATGATGATGATGATGATGATGATGATGATG 2707
Qy 1268 ATCTAATCTCTCTGATGAGCACTGATTTTATTTTATCGAAGAGAACTTGAAGCTAG 1327
Db 2708 ATCTAATCTCTCTGATGAGCACTGATTTTATTTTATCGAAGAGAACTTGAAGCTAG 2767
Qy 1328 AGAATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1387
Db 2768 AGAATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2827
Qy 1388 AAGTTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1447
Db 2828 AAGTTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2887
Qy 1448 CTCTAATTTTGGGAGACATCAAGCAGCATATCCGAGAAATATGTAAGAAATTTACA 1507

Db 2888 CTCTAATTTTGGGAGACATCAAGCAGCATATCCGAGAAATATGTAAGAAATTTACA 2947
Qy 1508 TACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1567
Db 2948 TACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3007
Qy 1568 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1627
Db 3008 AGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3067
Qy 1628 CTTCATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1687
Db 3068 CTTCATTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3127
Qy 1688 GTAGTCTTCCAAACAGTTATGAGAGCTTCAAAATCTGAGAGATGATGATGATGATG 1747
Db 3128 GTAGTCTTCCAAACAGTTATGAGAGCTTCAAAATCTGAGAGATGATGATGATGATG 3187
Qy 1748 GTCATTCATCTTGTGTTGGCAAAAGCAACAACTTGTATGATGATGATGATGATG 1807
Db 3188 GTCATTCATCTTGTGTTGGCAAAAGCAACAACTTGTATGATGATGATGATGATG 3247
Qy 1808 TACTTGAATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1867
Db 3248 TACTTGAATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 3307
Qy 1868 TTAAGATCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1927
Db 3308 TTAAGATCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3367
Qy 1928 TACGAAACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1987
Db 3368 TACGAAACCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 3427
Qy 1988 ATATGATGCAAAAGAGAGCAATTTATCTGCAAAAGAAATCTGATCTTTAAGATGA 2047
Db 3428 ATATGATGCAAAAGAGAGCAATTTATCTGCAAAAGAAATCTGATCTTTAAGATGA 3487
Qy 2048 AATGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2107
Db 3488 AATGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3547
Qy 2108 CTCTCAACACCACTGCAATCTGATGATGATGATGATGATGATGATGATGATGATG 2167
Db 3548 CTCTCAACACCACTGCAATCTGATGATGATGATGATGATGATGATGATGATGATG 3607
Qy 2168 TCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2227
Db 3608 TCCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3667
Qy 2228 GCAAAAACCTGCTACATCTTACACCTTGTGATGATGATGATGATGATGATGATG 2287
Db 3668 GCAAAAACCTGCTACATCTTACACCTTGTGATGATGATGATGATGATGATGATG 3727
Qy 2288 TGTGAGAGGGGCTGCGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATG 2347
Db 3728 TGTGAGAGGGGCTGCGGAGAGTGAATGATGATGATGATGATGATGATGATGATGATG 3787
Qy 2348 TTCCATCTGAGAGAACTTAATATACGCGAATTTGATGATGATGATGATGATGATG 2407
Db 3788 TTCCATCTGAGAGAACTTAATATACGCGAATTTGATGATGATGATGATGATGATG 3847
Qy 2408 AGAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2467
Db 3848 AGAAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 3907
Qy 2468 TTGTTATTCACACCTTCTTCTGTCAAGAAATGATGATGATGATGATGATGATGATG 2527
Db 3908 TTGTTATTCACACCTTCTTCTGTCAAGAAATGATGATGATGATGATGATGATGATG 3967
Qy 2528 CAATAGGTTTCAGTTCCATATCTAATCTCAATGATGATGATGATGATGATGATGATG 2587

Dh 3968 CAATAGTTTCAGTTCATATCTAATCTCATGCTCTTACTTCCCTCCAAATTCGTATA 4027
Oy 2588 ACAAAGAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGCAAAATCTCAAAATCT 2647
Dh 4028 ACAAAGAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGCAAAATCTCAAAATCT 4087
Oy 2648 TGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2707
Dh 4088 TGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4147
Oy 2708 CTCTGAGCATCTGGAATATCTGATGTTGATGCTGATGCTGATGCTGATGCTGATG 2767
Dh 4148 CTCTGAGCATCTGGAATATCTGATGTTGATGCTGATGCTGATGCTGATGCTGATG 4207
Oy 2768 TGAAGGTTTAAATTCATCTCACAGTATCATCAATCAATCAATCAATCAATCAATCA 2827
Dh 4208 TGAAGGTTTAAATTCATCTCACAGTATCATCAATCAATCAATCAATCAATCAATCA 4267
Oy 2828 TACCGAGGATTCAGACACCTTAACAGCCCTCACAAATTTACAGTTGATTTGCTCAA 2887
Dh 4268 TACCGAGGATTCAGACACCTTAACAGCCCTCACAAATTTACAGTTGATTTGCTCAA 4327
Oy 2888 CACTGCGCCACAGCGGTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATG 2947
Dh 4328 CACTGCGCCACAGCGGTGAGAGAGAGATGAGAGAGATGAGAGAGATGAGAGAGATG 4387
Oy 2948 CTGCGTGTATTTATTTATTTAG 2967
Dh 4388 CTGCGTGTATTTATTTATTTAG 4407

RESULT 4

US-10-647-268-5
; Sequence 5, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(509)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (510)..(788)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (789)..(3344)
US-10-647-268-5

Query Match 77.8%; Score 2309; DB 18; Length 3347;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2773; Conservative 0; Mismatches 190; Indels 330; Gaps 2;

Oy 1 ATGGCTGAGCTTCTTCAAGTCTGTGAGCAATCTGACTGTTCATCCAAAGGGAA 60
Dh 57 ATGGCTGAGCTTCTTCAAGTCTGTGAGCAATCTGACTGTTCATCCAAAGGGAA 116
Oy 61 CTGTGATGATCTTGTGTTTAAAGATGATTCGAAAAGCTTCAAGCAGTTTACTACA 120
Dh 117 GTTGATGATGATCTTGTGTTTAAAGATGATTCGAAAAGCTTCAAGCAGTTTACTACA 176
Oy 121 ATCCAGCTGTGCTGAAGATGCTCAGAGAGCAATTGAAGGACAAAGCAATTGAAAT 180

Dh 177 ATCCAGCTGTGCTGAAGATGCTCAGAGAGCAATTGAAGGACAAAGCAATTGAAAT 236
Oy 181 TGTGTGAGAAACCTCAATGCTGCTGCAATGAGGCTGATGACATCTTGAGCAATGTA 240
Dh 237 TGTGTGAGAAACCTCAATGCTGCTGCTGATGAGCTGATGACATCTTGAGCAATGTA 296
Oy 241 ACTGAGGACCAATTTAGACAGAGAGAGAAACAAATATGAGTGTATCATCCAAAGTTATC 300
Dh 297 ACTGAGGACCAATTTAGACAGAGAGAGAAACAAATATGAGTGTATCATCCAAAGTTATC 356
Oy 301 ACTTTGTGTCACAAAGATTTGGAAAAAGATGAAAAATTTAGAGAACTAGATGTAAT 360
Dh 357 GCTTCCGTCACAAAGTTGGAAAAAGATGAAAAATTTAGAGAACTAGATGTAAT 416
Oy 361 GCAGCGGAGAAATTAATGTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Dh 417 GCAGCGGAGAAATTAATGTTTCAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Oy 421 CGCCAAA----- 427
Dh 477 CGCCAAACAGTGTCTATCTTATATTTTCTTAAAAAAACAGTTTATATCATGAAT 536
Oy 428 ----- 427
Dh 537 CATGTGTGTTGGATTTTCTTATCTAATGATGTTCTCAAGTCTAAGATGATGATGAG 596
Oy 428 ----- 427
Dh 597 ATCCAGATTGATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 656
Oy 428 ----- 427
Dh 657 AAAGCTGAGTGTGTTTAGACATTATTAATTAATTAATTAATTAATTAATTAATTAAT 716
Oy 428 ----- 427
Dh 717 GTGATATATGTCGTGCTTCTCAAGCTTATCATGTCCTTTATTTGCAAAATTCCT 776
Oy 428 ----- 427
Dh 777 TTGCTTTTTCGCTGACTCTTCACTGAGCTTGACACAGGTTTGTTTTAAATGACCA 836
Oy 454 GTTATGAGAGAGACAAAG 513
Dh 837 GTTATGAGAGAGACAAAG 896
Oy 514 AATGCCAAACACTTCAGTCTCCCAATATCTTGATGAGAGAGAGAGAGAGAGAGAGAG 573
Dh 897 GATGCCCAACACTTCAGTCTCCCAATATCTTGATGAGAGAGAGAGAGAGAGAGAGAG 956
Oy 574 CTGCGCCAAATGCTTCAATGATCAGAGAGATGAGATGAGATGAGATGAGATGAGATG 633
Dh 957 CTGCGCCAAATGCTTCAATGATCAGAGAGATGAGATGAGATGAGATGAGATGAGATG 1016
Oy 634 ATTTGTGCTCGAAGATTTTAATGAGAGAGGTTGATTAAGAGAAATTTGATGATCT 693
Dh 1017 ATTTGTGCTCGAAGATTTTAATGAGAGAGGTTGATTAAGAGAAATTTGATGATCT 1076
Oy 694 GAAGAAAAGTCACTTGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
Dh 1077 GAAGAAAAGTCACTTGTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
Oy 754 CTGAATGAGAAAATATTTGCTGCTTATGATGATGTTGATGATGATGATGATGATGAT 813
Dh 1137 CTGAATGAGAAAATATTTGCTGCTTATGATGATGTTGATGATGATGATGATGATGAT 1196
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Dh 1197 TGGGCTTAAGTTAAGACAGCTTGAAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256
Oy 874 ACTGCTTGAAGAGGTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 933

Db 1257 ACTGCTTTGAAAAGGTTGGATCAATTATGCAACTTTGGCAACATATGATTTGTCAAC 1316
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Db 1317 TTGTGTCAAGAAAGATTGCTGGTTGTTGTTTCATGCAACGTCATTTGGGCAACCAAGAA 1376
Qy 994 ATAAATCTTAATCTTTGTGGCTATTCGAAAAGAGATTTGGAAAAATTTGGTGTGCT 1053
Db 1377 ATAAATCAATATCTTTGTGGCTATTCGAAAAGAGATTTGGAAAAATTTGGTGTGCT 1436
Qy 1054 CTAGAGCTTAAACCTTTGGAGATTTTGGCCCTTTAGAGAGAAAGAAAGACATGGGAA 1113
Db 1437 CTAGAGCTTAAACCTTTGGAGATTTTGGCCATTCAGAGCAAGAAAGACATGGGAA 1496
Qy 1114 CATGAGAGATAGTAGATTGGAATTTGCTCAAGAAAGAAAGTTCTATTGCTGCTG 1173
Db 1497 CATGAGAGATAGTAGATTGGAATTTGCTCAAGAAAGAAAGTTCTATTGCTGCTG 1556
Qy 1174 CTGAGACTTATGTTACATCACTTCCACTTGAATTTGAGACAAATGCTTTACATATTG 1233
Db 1557 CTGAAACTTATGTTACATCACTTCCACTTGAATTTGAGACAAATGCTTTACATATTG 1616
Qy 1234 GTATTTCCAAAGGATACCGAAATGGAAGAAATCTATCTCTCTGATGTCACAT 1293
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Qy 1354 GAATTAATCTTGAGGCTCTTCTTCCAGAGATTTGAAGTTAAATCTGCTCAACTTATTC 1413
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Qy 1414 AAGATGATGATCTATTCATGATGATGATGATGATGATGATGATGATGATGAT 1473
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Qy 1534 AAAGGTATCTTCTTACTCTCTTCCACTTGCAGAAATTTGCTGTTGAGGCTGCT 1593
Db 1917 AAAGGTATCTTCTTACTCTCTTCCACTTGCAGAAATTTGCTGTTGAGGCTGCT 1976
Qy 1594 AATCTAAGTACATATAAATTAAGAGATTAACGCTTCCATTTGAGATCTAGTACATTTA 1653
Db 1977 AATCTAAGTACATATAAATTAAGAGATTAACGCTTCCATTTGAGATCTAGTACATTTA 2036
Qy 1654 AGATTAATCTTAATCTTGTGCGCAATCTAGTATTTGATGATGATGATGATGATGAT 1713
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Qy 1714 CTTCAAAATCTGCAGACTCTTATCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1773
Db 2097 CTTCAAAATCTGCAGACTCTTATCTAGCTTGTGCTAGAGACTTCTGTTTGGCAAAA 2156
Qy 1774 GAACCAAGCAAACTTGTAGTCTTGAATCTTTTACTGATGATGATGATGATGATGAT 1833
Db 2157 GAACCAAGCAAACTTGTAGTCTTGAATCTTTTACTGATGATGATGATGATGATGAT 2216
Qy 1834 TGTATGCAACCAAGATAGATCTTTGATGATGATGATGATGATGATGATGATGATG 1893
Db 2217 TGTATGCAACCAAGATAGATCTTTGATGATGATGATGATGATGATGATGATGATG 2276
Qy 1894 GGAATTTCAAGAAAGTTGTCAACTTGTGATGATTAAGAAACCTGATCTGATGCTCA 1953
Db 2277 GGAATTTCAAGAAAGTTGTCAACTTGTGATGATTAAGAAACCTGATCTGATGCTCA 2333
Qy 1954 ATTGAATCAACGATCTTGTAGAGATGAAATGATGATGATGATGATGATGATGATGAT 2013
Db 2334 ATTGAATCAACGATCTTGTAGAGATGAAATGATGATGATGATGATGATGATGATGAT 2393

Qy 2014 TCTGCAAAAGAAATCTGCATCTTTAAGATGAATGAGATGACGATGAACGTCACCT 2073
Db 2394 TCTTCAAAAGAAATCTGCATCTTTAAGATGAATGAGATGAGATGAGATGAGATGAGAT 2453
Qy 2074 ATATATGATCAAGAAAGTTGAAGTCTTGAAGCTCTCAACCACTCCATCTGACT 2133
Db 2454 AGATATGATCAAGAAAGTTGAAGTCTTGAAGCTCTCAACCACTCCATCTGACT 2513
Qy 2134 TGTATTAATCAAGAGGCTTCAAGAGAAATCCGCTCCAGACTGATGATGATGATGATGAT 2193
Db 2514 TGTATTAATCAAGAGGCTTCAAGAGAAATCCGCTCCAGACTGATGATGATGATGATGAT 2573
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Qy 2254 TTTGGTGAAGCTGCTGCTTGTCTTAAAGTCTAGATTTGAGAGGAGCTTGGCAAGTGAG 2313
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Qy 2314 TATGTTGATCTGATCTGATCTCCATCAAGAAAGTTTCATCTGAGAAACTTAATTA 2373
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Qy 2434 CTGGAAGATAGAGATTAATTTGCTGCTATGTTGTTATTCACCACTTTCTTCTGTC 2493
Db 2814 CTGGAAGATAGAGATTAATTTGCTGCTATGTTGTTATTCGACCTTTCTTCTGTC 2873
Qy 2494 AAAGAAATGATAGTAAAGTGGGAGCAAGTCAGATGCAATAGTTCATCTAAT 2553
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Qy 2554 CTGATGCTCTTACTTCCCTCCAAATTCGCTATAAACAAGATGCTTCACTCCAGAA 2613
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Qy 2614 GAGATGTTCAAAAGCTTGCAGAAATCTCAATATCTGAAATATCTTACTTCAATCTT 2673
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Db 3114 TGTATGCACTAGAGAGTCTCCCGAGAGAGTGTGAAGGTTTAAATTTCACTCACAG 3173
Qy 2794 TTATTCATTAATATCTGTAATGCTTCAATGTTTACCGAGAGATTCAGACCTTAACA 2853
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Db 3294 ATAGAGAAAGCTGCTTACCAAAATGCTCAATTCCTGCTGTTTAAATTAATTA 3346

RESULT 5
US-10-360-522-48
; Sequence 48, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Ailefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360,522
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02075565.8
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 2913
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(2913)
OTHER INFORMATION: /note="Rpi-d1b"
US-10-360-522-48

Query Match 70.0%; Score 2077.2; DB 17; Length 2913;
Best Local Similarity 83.5%; Pred. No. 0;
Matches 2495; Conservative 0; Mismatches 388; Indels 105; Gaps 8;

1 ATGGCTGAAGCTTCTTCAAGTCTGTAGACAATCTGATGTTTCATCCAGGGGAA 60
1 ATGGCTGAAGCTTCTTCAAGTCTGTAGACAATCTGATGTTTCATCCAGGGGAA 60
61 CTGGATGATCTTCTGTTTAAAGATGATGATGATGATGATGATGATGATGATGAT 120
61 CTGGATGATCTTCTGTTTAAAGATGATGATGATGATGATGATGATGATGATGAT 120
121 ATCCAGCTGCTGTAAGATGCTCAAGAAAGCAATGAAAGCAAGCAATGAAAT 180
121 ATCCAGCTGCTGTAAGATGCTCAAGAAAGCAATGAAAGCAAGCAATGAAAT 180
121 ATTCAGCCGCTCTGTAAGATGCTCAAGAAAGCAATGAAAGCAAGCAATGAAAT 180
181 TGGTTGCAAGAACTCAATGCTGCTGATGATGATGATGATGATGATGATGATGAT 240
181 TGGTTGCAAGAACTCAATGCTGCTGATGATGATGATGATGATGATGATGATGAT 240
181 TGGTTGCAAGAACTCAATGCTGCTGATGATGATGATGATGATGATGATGATGAT 240
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241 ACTGAGCAACCAATTAAGACAGAAAGCAATATGGGTTTATCATCCAAAGTTATC 300
241 ACCAAGGCAACA--AGATCTCCAGTCTGATATGAGCGTTATCATCCAAAGTTATC 297
301 ACTTTTGTCAACAAGTTGGGAAAAAGATGAAAAAGATTATGGAAACTGATTAAT 360
301 ACTTTTGTCAACAAGTTGGGAAAAAGATGAAAAAGATTATGGAAACTGATTAAT 360
298 CTTTTCGTCAACAAGTTGGGAAAAAGATGAAAAAGATTATGGAAACTGATTAAT 357
361 GCAGCGAAGCAATTAAGTTGATTTGATGATGATGATGATGATGATGATGATGAT 420
361 GCAGCGAAGCAATTAAGTTGATTTGATGATGATGATGATGATGATGATGATGAT 420
358 GCTGAGAAAGAAAGAAATTTTCTTTCATGCAAGAAAAATTTGAGAGCAAGCTTTGA 417
421 CGCCAAACAGGTTTGTGTTTGAATGAACCAACAAGTTATGGAAGAGCAAAAGAAAGAC 480
421 CGCCAAACAGGTTTGTGTTTGAATGAACCAACAAGTTATGGAAGAGCAAAAGAAAGAC 480
418 CGGAAACAGGTTTGTGTTTGAATGAACCAACAAGTTATGGAAGAGCAAAAGAAAGAT 477
481 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTTCCA 540
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478 GAGTATGTAAGAAATCTGATTAACAATGTTGCAATGCCCAACACTTCCAGTCTTCCA 537
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541 ATACTTGTATGGGGGAGCTAGAAAGACAGCTCTTGCCCAATGATCTTCAATGATCAG 600
538 ATACTTGTATGGGGGAGCTAGAAAGACAGCTCTTGCCCAATGATCTTCAATGATCAG 597
601 AGAGTAATTTAGCAATTTCCATCCCAAAATATGATTTGTCTCTGGAAGATTTTATGAG 660
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598 AGAGTAATTTAGCAATTTCCATCCCAAAATATGATTTGTCTCTGGAAGATTTTATGAG 657
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778 GTCTTAAGATGATTTGGAATGAAGATCAAGATTAAGGCTTAAGCAAGCTTGG 837
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1258 GAAAGAGAAATCTATCTCTCTGATGAGCAATGTTTATTTATGAAAGAAAC 1317
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1258 GAAAGAGAAATCTATCTCTCTGATGAGCAATGTTTATTTATGAAAGAAAC 1317
1318 TTGAGCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
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1378 CAAGAGATTAAGTAAATCTGCTGCAACTTATTTCAAGATGATGATGATGATGAT 1437
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1558 TCCCACTTGAAGAGTTGATCTGCTGAGGAGGTTTATCTAAGTGAATTAACCTTAA 1617
1618 CAGTTACGCTTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGGCAAT 1677
1618 CAGTTACGCTTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGGCAAT 1677
1618 CAGTTACGCTTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGGCAAT 1677
1618 CAGTTACGCTTCCATTTGAGATCTAGTACATTTAAGATACCTTAACTTGGCAAT 1677
1678 ACTAGATTTGATGATCTTCAAAACAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1737
1678 ACTAGATTTGATGATCTTCAAAACAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1737
1678 ACTAGATTTGATGATCTTCAAAACAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1737
1678 ACTAGATTTGATGATCTTCAAAACAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1737
1675 AGTGGCATGCTGATCTTCAAAAGCAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1734
1675 AGTGGCATGCTGATCTTCAAAAGCAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1734
1675 AGTGGCATGCTGATCTTCAAAAGCAGTTATGCAAGCTTCAAAATCTGCAAGCTTGGAT 1734
1738 CTACATGCTGATCACTTGTGTTTGGCAAAAGAAACAGCAAACTTGGAGCTT 1797
1738 CTACATGCTGATCACTTGTGTTTGGCAAAAGAAACAGCAAACTTGGAGCTT 1797
1738 CTACATGCTGATCACTTGTGTTTGGCAAAAGAAACAGCAAACTTGGAGCTT 1797
1735 CTACATGCTGATCACTTGTGTTTGGCAAAAGAAACAGCAAACTTGGAGCTT 1794
1735 CTACATGCTGATCACTTGTGTTTGGCAAAAGAAACAGCAAACTTGGAGCTT 1794
1798 GAAATCTTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1857

Db	1795	CGAATCTTTTACTGTAGTAGTAGCCAGTCATTTGACTTGTATGCAACCAAGATAGATCA	1854
Qy	1858	TTGACATGCCCTTAAAGACTCTAAGTAGATTTGTGTGGAAATTCAGAGAAAGTTGTCAA	1917
Db	1855	TTGACATGCCCTTAAAGACTCTAAGTAGATTTGTGTGGAA---GGAAGAAAGTTATCAA	1911
Qy	1918	CTTGTGTAAATTAAGAAACCTTGAAATCTCTATGTGTCATTTGAAATACAGCATCTTGAGAGA	1977
Db	1912	CTTGTGTAACTTAAAGAAACCTTAAATCTCTATGTGTCATTTAAATCTGTCAATCTTGAGAGA	1971
Qy	1978	GTGAAGAAATGATATGAGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCATCTC	2037
Db	1972	GTGAAGAAATGATATGAGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCATCTC	2031
Qy	2038	TTAAGCATGAATGGATGACATGAATGAAAGTTCACGTATATATGATACAGAAAAAGTTGAA	2097
Db	2032	TTAAGCATGAATGGATGAATTAATCTTTGGAC---CAATATATATGATACAGAAAGTTTAA	2088
Qy	2098	GTGCTTGAAGCTCTTCAAACCACTCCATCTGTACTGTTTAAACATCAGGGCTTGACA	2157
Db	2089	GTGCTTGAAGCTCTTCAAACCACTCCATCTGTACTTCTTTAAAAATCTATGTGCTTGACA	2148
Qy	2158	GGAAATCCGCTCCCGAGCTGGAATATCACTCACTTTTGAAGAAATGTGTCTATTTGAA	2217
Db	2149	GGAAATCCATCTCCCGAGCTGGAATATCACTCACTTTTGAAGAAATGTGTCTATTTCTA	2208
Qy	2218	ATCATACAGTTGCCAAAACTGCTCATGCTTACCACTTTGTGTGAGCTGCTTGTCTAAAA	2277
Db	2209	ATTAGCACTTCAGAAATCTGCTCATGCTTACCACTTTGTGTATCTGCTTGTCTAGAA	2268
Qy	2278	AGCTTAAGATTGTGAGAGGGGTCTTCCGAGCTGAGATATGTTG-----	2320
Db	2269	AGCTTAAGATTGTGAGAGGGGTCTTCCGAGATGTGAGATATGTTGAAAGATATTTGAT	2328
Qy	2321	----ATTCTGGAATCCCTTACAAAGAAAGATTCATCTCTGAGAAAACTTAATATGCG	2376
Db	2329	GTTCATCTCTGGAATCCCTTACAAAGAAATGATTCATCTCTGAGAAACTTGATATATGCG	2388
Qy	2377	GAATTTTGGTATCTGAAAGAGATTGCTGTAAGAAAGAAAGAGAGCAATCCCTGTGCTT	2436
Db	2389	GACTTTGGTATCTGAAAGAGATTGCTGTAAGAAAGAAAGAGAGCAATCCCTGTGCTT	2448
Qy	2437	GAAGAGATGAGATTTAAATGTTGCCCTATGTTGTATTTCCAACTCTTCTGTGTCAG	2496
Db	2449	GAAGAGATGATTAATTCAGAGTGC-----TTTCTGACCTTTCT-----	2490
Qy	2497	AAATTTGATGTTAGTGGGAGACAGTCAAGATGCAATAGCTTTCAGTTCCATATCTAATCTC	2556
Db	2491	-----TCATATCTT-----	2499
Qy	2557	ATGAGCTCTTACTTCCCTCCAAATTCGCGATATTAACAAAGAGATGCTTCACTCCGAGAGAG	2616
Db	2500	AGGAGCTCTTACTTCCCTCCAAATTTGCTATATATTAAGTAGACTTCAATCTCCGAGAGAG	2559
Qy	2617	ATGTTCAAAAGCCCTTGCAATCTCAAAATACTTGATATCTCTTTTTCATTCAATCTTAA	2676
Db	2600	ATGTTCAAAAACTTGCAATCTCAAAATACTTGACATCTCTCGGTCAATTAATCTCAA	2619
Qy	2677	GAGCTGCTTACAGCCCTGGCTAAGTCTCAATGCTTTGAAGCATCTGGAATTCATAGTTGT	2736
Db	2620	GAGCTGCTTACAGCCCTGGCTAAGTCTCAATGCTTTGAAAGCTTAAAAATTTCAATGTGTGT	2679
Qy	2737	TATGACATGAGAGATCTCCCGAGAGAAAGGTGTAAAGGTTTAAATTTCACTCAACAGTTA	2796
Db	2680	TGCGCATAGAGATCTCCCTGAGAGAAAGGCTGAGAGGTTTATCTTCACTCAAGAGTTA	2739
Qy	2797	TCCATTAACATATCTGTGAATGCTTCAATGTTTACCGAGAGGATTTGCAGACCTTAACAGCC	2856
Db	2740	TTTGTGTGAACCTGTGAACATGCTTAATATGTTTACAGAGGGATTTGCAGACCTTAACAGCC	2799
Qy	2857	CTCACAAATTTATCACTTGAAGTTTGTTCACAACCTGGCCAAAGCGGTGTGAAGGGGATA	2916

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Db      2800 CTGACAAATTAAAAATTCGGGGAGTGCACAACACTGAATCAAGCGGTGAGAAAGGAATA 2855
Qy      2917 GGAGAAGACTGTGTCAAATAATTCCTCACATTTCTCGTGTTTTATTAT 2964
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Db      2860 GGAGAAAGACTGGCAGAAAATTTCTCACATTTCTTAATGTGAATATATAT 2907
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RESULT 6
US-10-360-522-52
; Sequence 52, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.,
; APPLICANT: Voessen v.d., Edwin A.G.,
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 3971
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3971)
; OTHER INFORMATION: /note="RGC3-blb"
US-10-360-522-52

Query Match           63.4%; Score 1880.8; DB 17; Length 3971;
Beet Local Similarity 85.5%; Pred. No. 0;
Matches 2173; Conservative 0; Mismatches 342; Indels 27; Gaps 6;

Qy      426 AACAGTTTTGTTTGAATGAACCACAAAGTTTATGAAAGAGACAAAGAAAAGACGAGAT 485
Db      1454 ACCAGATTCTGTGTTAAGTAACTAACCCAAAGTTTATGAAAGGAGCAABAAAAAGATGAGAT 1513
          ||||||
Qy      486 AGTGAATAATCTGTATTAACAATGTTAGCAATGCCCAACACTTCAGTCTCCCAATACT 545
Db      1514 AGTGAATAATCTTAATAACAATGTATGATGCCCAAAACTCTCAGTCTCCCAATACT 1573
          ||||||
Qy      546 TGTATATGGGGGACTAGGAAGAAGCATCTTTGGCCCAATGCTCTCAATGATCAGAACT 605
Db      1574 TGATATGGGGGACTAGGAAGAAGCAACTCTTTCCCAATGCTCTCAATGATCAGAACT 1633
          ||||||
Qy      606 AATTGAGCATTTCCATCCC AAAATATGAGATTTGTGCTCGGAAGATTTTATGAGAAGAG 665
Db      1634 AACTGAGCGTTTCTATCCAAAATATGAGATTTGTGCTCGGATGATTTTATGAGAAGAG 1693
          ||||||
Qy      666 GTTGATTAAGAAATTTAGAAATCTATTTGAAGAAAAGTCACTTGTTGGCATGAGCTTGGC 725
Db      1694 GTTGATTAAGCAATAGTAGAATCTATTTGAAGGGAAGTCCCTCAGTGACATGAGCTTGGC 1753
          ||||||
Qy      726 TTCACTTCAAAAAGAGCTTGGGACTTGTGGAATGGAAGAAAATATTTGTGCTCGTCTTAGA 785
Db      1754 TTCACITCAAAAAGAGCTTCAAGGTGTCGAATGGAAGAAAAGATCACTTGTGCTTAGA 1813
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Qy      786 TGAATGTTGAATGAAGATCAAGATTAAGTGGGGCTAAGTTAAGCAAACTCTTGAAGGTTGG 845
Db      1814 TGAATGTTGAATGAAGATCAAACTAAGTGGGGCTAATTTAAGAGCACTCTTGAAGGTTGG 1873
          ||||||
Qy      846 AGCAAGTGGGCTTCTGTTCTAACCATACTCGTCTTGAAGGTTGGATCAATTATGGG 905
Db      1874 AGCAAGTGGGCTTCTGTTCTAACCATACTCGTCTTGAAGGTTGGATCAATTATGGG 1933
          ||||||
Qy      906 AAATTGCAACCATATGAAATTTGTCAATTTGTCTCAAGAAAGATTTGTGTTGTTCAT 965
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.Db 1934 AACATGCAACCATATGAAATTGTCAATCTGTCTCAGAGGATTGTTGTTTTCAT 1993
QY 966 GCAACGTGCAATTTGGGCAACCAAGAAATAATCTTATCTTTGGCTATCGGAAAG 1025
Db 1994 GCACCGTGCAATTTGGCAACCAAGAAATAATCTTATCTTTGGCAATCGGAAAG 2053
QY 1026 GATTGTGAAAAATGTGGTGTGTGCTCTAGCAGCTAAAATCTGTGGAGGATTTTGG 1085
Db 2054 GATTGTGAAAAATGTGGTGTGTGCTCTAGCAGCTAAAATCTTTGGAGGATTTTGG 2113
QY 1086 CTTTAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1145
Db 2114 CTTCAAG 2173
QY 1146 TCAAG 1205
Db 2174 TCAAG 2233
QY 1206 TTTGAGACAAATGCTTTACATATTTGAGATTTCCCAAGAGATCCGAAATGGAAGAG 1265
Db 2234 TTTGAGACAAATGCTTTGATTTGTGCGATTTCCCAAGAGACCAAAATGGAAGAG 2293
QY 1266 AAATCTAATCTCTCTGAGATGAGACATGTTTTATTTATGGAAGAGAACTTGAAGCT 1325
Db 2294 AAATCTAATCTCTCTGAGATGAGACATGTTTTATTTATGGAAGAAATTTGAGCT 2353
QY 1326 AGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1385
Db 2354 AGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2413
QY 1386 TGAAGTTAAATCTGTGCAAACTTATTTCAAGATGATCTCATTCATGATCTGCAAC 1445
Db 2414 TGAAGTTAAATCTGTGCAAACTTATTTCAAGATGATCTCATTCATGATTTGGCTAC 2473
QY 1446 ATCTCTAATTTTGGCAAGACATCAAGAGACATTCGAGAGAAATTTGAGAAATTA 1505
Db 2474 ATCTCTGTTTTGCAAGCAACATCAAGAGACATTCGAGAGAAATTTGAGAAATTA 2533
QY 1506 CATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
Db 2534 TGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2593
QY 1566 GCAGAGATTTGTCTGATGAGGATCTTAATCTAATGACATTAATTAAGCAGTTACC 1625
Db 2594 GCAGAGATTTGTCTGATGAGGATCTTAATCTAATGACATTAATTAAGCAGTTACC 2653
QY 1626 GTCTTCATGAGAGATCTAATGATTTAAGATCTTAATCTTGTCTGCAATCTAGTAT 1685
Db 2654 ATCTTCATGAGAGATCTAATGATTTAAGATCTTAATCTTGTCTGCAATTTTGAAT 2713
QY 1686 TCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGAGACTCTGATCTACATGG 1745
Db 2714 TCGATGCTTCCAAACAGTTATGCAAGCTTCAAAATCTGAGACTCTGATCTACATTA 2773
QY 1746 CTGTCAATCTTGTGTTGTTGCCAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1805
Db 2774 TTGGGACATCTCTTCTTGTGTTGCCAAAGAAAGAAAGAAAGAAAGAAAGAAAGCT 2833
QY 1806 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
Db 2834 TTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2890
QY 1866 CCTTAAGACTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1925
Db 2891 CCTTAAGCTCTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2947
QY 1926 ATTACGAAGCTGATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1985
Db 2948 ACTTAAAGAACTTAAATCTATGCTCAATTTCAATCAAAAGCTTGAAGAGAGAGAA 3007
QY 1986 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
Db 3008 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3067

QY 2046 GAAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
Db 3068 GAGTTGGACCTTATGAGAA--ACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3115
QY 2106 AGCTCTGAAACCAACATCTCAATCTGATTTTAAATCAAGAGAGAGAGAGAGAGAGAGAGAG 2165
Db 3116 AGCCCTTAAACCAACATCTCAATCTGATTTTAAATCAAGAGAGAGAGAGAGAGAGAGAGAG 3175
QY 2166 TCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2225
Db 3176 TCTCCAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3235
QY 2226 TTGCAAAACCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2285
Db 3236 TTGCAAAACCTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3295
QY 2286 GTTGTGAG 2345
Db 3296 GTTACACACCGGGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3352
QY 2346 GTTTCATCTCTGAGAAACTTAATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2405
Db 3353 GTTTCATCTCTGAGAAACTTGTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3412
QY 2406 AAAG 2465
Db 3413 AAAG 3472
QY 2466 GTTGTATTTCAACCTCTTCTCTGCAAGAAATGATGATGATGATGATGATGATGATGATGAT 2525
Db 3473 GTTGTATTTCAACCTCTTCTCTGCAAGAAATGATGATGATGATGATGATGATGATGATGATGAT 3586
QY 2526 TGCATATGATTTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT 2585
Db 3527 TGCATATGATTTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT 3586
QY 2586 TTAACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2645
Db 3587 TTAACAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3646
QY 2646 CTGGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2705
Db 3647 CTGGAATATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3706
QY 2706 TGCCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2765
Db 3707 TGCCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3766
QY 2766 TGTGAAAGGTTTAAATTTCACTCAACAGTTATCTAATCTAATCTAATCTAATCTAATCTAAT 2825
Db 3767 TGTGAAAGGTTTAAATTTCACTCAACAGTTATCTAATCTAATCTAATCTAATCTAATCTAAT 3826
QY 2826 TTTTACCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2885
Db 3827 TTTTACCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3886
QY 2886 AAGACATGAG 2945
Db 3887 AAGACATGAG 3946
QY 2946 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2967
Db 3947 TCCATATTTGACTCTAATGAG 3968

RESULT 7
US-10-360-522-49
; Sequence 49, Application US/10360522
; Publication No. US2003022125A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360,522
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02075565.8
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 49
LENGTH: 3592
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(3591)
OTHER INFORMATION: /note="Rpi-b1b including intron sequence (position
US-10-360-522-49

Query Match 60.9%; Score 1805.8; DB 17; Length 3592;
Best Local Similarity 84.2%; Pred. No. 0;
Matches 2159; Conservative 0; Mismatches 302; Indels 102; Gaps 7;
426 AACGCTTTTGGTGAATGAACCAAGTTATGGAAGACCAAGAAAGAGAGAGAT 485
1102 ACCAGGTTCTGTATTAACCGAACCGAGGTTATGGAAGACCAAGAAAGAGAT 1161
486 AGTGAATTCCTGATTAACATGTAGCAATGCCCAACCTTCAGTCTCCCAACT 545
1162 AGTGAATTCCTGATTAACATGTAGCAATGCCCAACCTTCAGTCTCCCAACT 1221
546 TGTATGAGGGGAGCTAGGAAGACGCTCTGCCCCAAATGTCTTCAATGATCAGAGT 605
1222 TGTATGAGGGGAGCTAGGAAGACGCTCTGCCCCAAATGTCTTCAATGATCAGAGT 1281
606 AATTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAAAGAAAG 665
1282 TACTGAGATTTCCATCCCAAAATATGATTTGTCTCGAAGATTTTAAAGAAAG 1341
666 GTTGATAAAGAAATTTAGATCTATTGAAGAAAGTCT--ACTTGGTCATGAGCTT 722
1342 GTTATAAAGCAATTTGATGATCTATTGAAGAAAGCACTTCTGATGATGAGCTT 1401
723 GGTCTCCACTTCAAAAGAAAGCTTCGGGACTTGTGATGAGAAATTTTGTCTGCTT 782
1402 GGTCTCCACTTCAAAAGAAAGCTTCAGAGTGTGATGAGAAATTTTGTCTGCTT 1461
783 AGATGATTTTGGATGAAGATCAAGATTAAGTGGCTTAAGTTAAGCAAGTCTGAAGT 842
1462 AGATGATTTTGGATGAAGATCAAGATTAAGTGGCTTAAGTTAAGCAAGTCTGAAGT 1521
843 TGGAGCAAGTGGCGCTTCTGTTCTTAACCACTACTGCTTGAAGAAAGTGTGAATTA 902
1522 TGGAGCAAGTGGCGCTTCTGTTCTTAACCACTACTGCTTGAAGAAAGTGTGAATTA 1581
903 GGAACATTTGCAACCATATGATTTGCTCAAGAGATTTGTTGTTGTT 962
1582 GGAACATTTGCAACCATATGATTTGCTCAAGAGATTTGTTGTTGTT 1641
963 CATGCAAGTGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGCTATGGA 1022
1642 CATGCAAGTGTGATTTGGGCAACCAAGAAATTAATCTTAATCTTGTGCTATGGA 1701
1023 GGAATTTGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1082
1702 GGAATTTGGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1761
1083 GCGCTTTAAGAGAGAAAGCAAGTGGAAATGATGAGATGATGATGATGATGAT 1142
1762 GCGCTTTAAGAGAGAAAGCAAGTGGAAATGATGAGATGATGATGATGATGAT 1821

1143 GCTTCAAGAAAGATTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1202
1822 GCTTCAAGAAAGATTTCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1881
1203 TGAATTTGAGCAATGCTTTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1262
1882 TGAATTTGAGCAATGCTTTTACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1941
1263 GGAATTTCTATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1322
1942 GGAATTTCTATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2001
1323 GCTGAGATTTAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1382
2002 GCTGAGATTTAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2061
1383 GATTGAAGTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1442
2062 GATTGAAGTTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2121
1443 AACATCTTATTTTCCGCAACGATCAAGCAATTCGCAAGAAATTAATGTAAGAA 1502
2122 AACATCTTATTTTCCGCAACGATCAAGCAATTCGCAAGAAATTAATGTAAGAA 2181
1503 TTACATCATATGATGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1562
2182 TTACATCATATGATGCTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2241
1563 CTTCAGAAAGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1622
2242 CTTCAGAAAGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2301
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2539 ATGCTTTAAGCTCTTGAATGCTTATGATTAAGATTAAGATTAAGATTAAGATTA 2595
1923 TGAATTTAAGAACTGATCTTATGCTCAATTAAGATTAAGATTAAGATTAAGATTA 1982
2596 TGAATTTAAGAACTGATCTTATGCTCAATTAAGATTAAGATTAAGATTAAGATTA 2655
1983 GAATGATTTGAGATGCAAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAG 2042
2656 GAATGATTTGAGATGCAAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAG 2715
2043 CATGAATTTGAGATGCAAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAG 2102
2716 CATGAATTTGAGATGCAAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAG 2772
2103 TGAAGCTTCAAAACGATCTTATGCTCAATTAAGATTAAGATTAAGATTAAGATTA 2162
2773 TGAAGCTTCAAAACGATCTTATGCTCAATTAAGATTAAGATTAAGATTAAGATTA 2832
2163 CCGTCTCCGAGCTGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2222
2833 CCGTCTCCGAGCTGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2892

Qy	2223	CAGTTTGAAAAACGCTGCATGCTTACACACCCCTTTGGAGCGCTGCTTAAAGAGCT	2282
Db	2893	CACTTCAGAAACTGCTCATGCTTACACACCTTTGGATCTGCTTGTCTAGAAAGCT	2952
Qy	2283	AGAAGTTGTGGAGGGGCTCTGCGGAGAGTGAATGTTG-----A	2321
Db	2953	AGAGTTACACTGGGGGCTCTGCGATGTGGAATAGTTCAAGAGTGAATATGATTTCA	3012
Qy	2222	TTCTGGAATCCCTTACAAAGAGAGTTTCCATCTCTGAGAAAACCTTAATATACCGAAT	2381
Db	3013	TTCTGGAATCCCTTACAAAGAGAGTTTCCATCTCTGAGAAAACCTTAATATGGAAT	3072
Qy	2382	TGGAATCTGAAAGAGATGCTGAAAAAGAGAGAGAGAGAGATGCCCTGTCTGGAAGA	2441
Db	3073	TGGAATCTGAAAGAGATGCTGAAAAAGAGAGAGAGAGAGATGCCCTGTCTGGAAGA	3122
Qy	2442	GATAGAGATTAAATGTTGCCCCCTATGTTTATTTTCAACCCCTTCTCTGTCAAAGAAAT	2501
Db	3133	GATGATATATTCAAGAGTGGCC-----TTTCTGACCCCTTCT-----	3169
Qy	2502	GGTAGTTATGTGGGAGCAAGTCAGATGCATATAGTTTCAGTTCCATATTTATCTCATGCG	2561
Db	3170	-----TCTAATCTTAAAGGCG	3183
Qy	2562	TCTTACTTCCCTCCCAAAATTCGCTATTAACAAGAGAGATGCTTCACTCCAGAGAGATGT	2621
Db	3184	TCTTACTTCCCTCCCAAAATTCGCTATTAACAAGAGAGATGCTTCACTCCAGAGAGATGT	3243
Qy	2622	CAAAAGCCTTGCAAAATCTCAAAATCTTGAAATATCTTTTAACTTCAATCTTAAAGAGCT	2681
Db	3244	CAAAAGCCTTGCAAAATCTCAAAATCTTGAAATATCTTTTAACTTCAATCTTAAAGAGCT	3303
Qy	2682	GCTTACCAAGCCTGGCTAGTCTCAATGCTTTGAGAGATCTGGAATTCATAGTTGTATGC	2741
Db	3304	GCTTACCAAGCCTGGCTAGTCTCAATGCTTTGAGAGATCTGGAATTCATAGTTGTATGC	3363
Qy	2742	ACTAGAGAGTCTCCCCGAGAGAGGTGAAGGTTAATTTCACTCAACAGATTATCCAT	2801
Db	3364	ACTAGAGAGTCTCCCCGAGAGAGGTGAAGGTTAATTTCACTCAACAGATTATTTGT	3422
Qy	2802	AACATCTCGTGAATGCTACATGTTTATCCGAGAGGATTGAGCACTTAAGCCCTCAC	2861
Db	3424	TGAACACTGTAACTGCTAATATGTTTACAGAGAGGATTGAGCACTTAAGCCCTCAC	3483
Qy	2862	AAATTTATCACTGATGATTGTTGTCCAACACTGCGCAAGCGGTGTGAGAGGAAATGAGAGA	2921
Db	3484	AAATTTAAAAATTCGGGAGATGCCCAACTGATCAAGCGGTGTGAGAGGAAATGAGAGA	3543
Qy	2922	AGACTGTGTACAAATTTGCTCATCTTCCCTCGTGTGTTATTTAT	2964
Db	3544	AGACTGTGTACAAATTTGCTCATCTTCCCTCGTGTGTTATTTAT	3586
RESULT 8			
US-10-360-522-50			
Sequence 50, Application US/10360522			
Publication No. US20030221215A1			
GENERAL INFORMATION:			
APPLICANT: Alliefs, Josephus J.H.M.			
APPLICANT: Vossen v.d. Edwin A.G.			
TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH			
FUNGAL RESISTANCE AND RELATED METHODS			
FILE REFERENCE: U 014413-9			
CURRENT APPLICATION NUMBER: US/10/360,522			
CURRENT FILING DATE: 2003-02-07			
PRIOR APPLICATION NUMBER: EP 02075555.8			
PRIOR FILING DATE: 2002-02-08			
PRIOR APPLICATION NUMBER: PCT/NL03/00091			
PRIOR FILING DATE: 2003-02-07			
NUMBER OF SEQ ID NOS: 63			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 50			
LENGTH: 5191			

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? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: sequence of
? OTHER INFORMATION: 5.2 kb Sca I genomic DNA fragment of S.
? OTHER INFORMATION: bulbocastaneum BAC SPB 4 present in pRSC2-blb
? US-10-360-522-50

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Query Match	60.9%;	Score 1805.8;	DB 17;	Length 5191;
Best Local Similarity	84.2%;	Pred. No. 0;		
Matches 2159;	Conservative	0;	Mismatches 302;	Indels 102;
				Gaps 7.

QY	426	AACAGGTTTTGTTTGAATTAACACCAAGTTTATGGAAGACAAAGAAAAGCAGCAT	485
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QY	486	AGTGAATATCTCGATTAACAATGTTAGCAATGCCCCAACCTTCCAGTCTCCCAATATCT	545
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Db	3012	GCCTCAAGATTAAGTCTATCTTTCGCTGCCTGAGACTTATGTTACCATCACTTTCACAT	3071
QY	1203	TGATTTGAGACAATGCTTTACATATTTGTGACATTTCCCAAGATACCGAATGGAATA	1262
Db	3072	TGATTTGAAACAATGCTTTGTGTGTGTGCGGTGTTCCCAAGATGCAAAAATGGAATA	3131
QY	1263	GGGAATCTAATCTCTCTGTGATGGAACATGTTTTATTATTAACGAAGAAACTTGA	1322
Db	3132	AGAAAGCTAATCTCTCTGTGATGGAACATGTTTTATTATTAACGAAGAAACTTGA	3191
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Qy 2283 AGAGTTTGGAGGGGCTGCGGGAAGTGAATGTTG-----A 2321
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Qy 2322 TTCTGAGATTTCCCTACAGAGAAAGTTTCCATCTGAGAGAAATTAATATACGGAAAT 2381
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RESULT 9
US-10-360-522-51
; Sequence 51, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J H M.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: PCT/ML03/00091
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 3260
; TYPE: DNA
; ORGANISM: Solanum bulbocastaneum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3260)
; OTHER INFORMATION: /note="RGCl-blp"
US-10-360-522-51
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Query Match 59.7%; Score 1771.6; DB 17; Length 3260;
Best Local Similarity 82.8%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 389; Indels 54; Gaps 7;
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Db 2198 ---CGAAGAGAAAGTATACACTTGTGTAAGCTTGAATTTAACTCCGTGTGCAAT 2254
Qy 1956 TGAATCAACGATCTTGAAGAGTGAAGAAATGATATGATGCAAAAGAACCAATTTATC 2015
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Db 2383 AACTGAAATCAGTAAAGCTATGAGCTTCAAGAGTTTCAATTTCCAAATTTGATGAT 2442
Qy 2185 CACTCAGTTTGAAGAAATGTTGTCTCTATGAAATCATCACTGTCAAAAATGCTCAT 2244
Db 2443 GCTTCGTTTGAAGAAATGTTGTCTCTATGAAATGAA---TGTGAAGATGCTGAGCT 2499
Qy 2245 TTACACCCCTTGTGAGAGCTGCTGTCTAATAAGCTCAGAGTTGTGAGAGGAGCTG 2304
Db 2500 TTACACCCCTTGTGAGAGCTGCTGTCTAATAAGCTCAGAGTTGTGAGAGGAGCTG 2559
Qy 2305 GAGTGTGATGTT---GATTTGATTTCCCTCAAGAGAGATTTCCATCTGTGA 2361
Db 2560 GAGTGTGATGTT---GATTTGATTTCCCTCAAGAGAGATTTCCATCTGTGA 2619
Qy 2362 AAATTAATATACCGCAATTTGTATCTGAAGAGATTTGTAAGAGAGAGAGAG 2421
Db 2620 GACTTGTCTATGAAAGATTTCCAAATCTGAAAGAGATGCTGAGAGAGAGAGAG 2679
```

Oy	2422	CAATGCCCTGCTCTTAAGAGATAGATTAATTAAGTTGCCCAATGTTGTAATTCACACC	2481
Db	2680	AAATTCCTCATGCTTTAAGAAATGAGAAATTTGGCATTTGCCATATGTTGTTTTCAGCA	2739
Oy	2482	CTTCTTCTCTGTACAGAAATTTGATGTTAGTGAGGAGCAAGTCAGATGCAATAGATTTCCAGT	2541
Db	2740	TTCTCTTCTGTCAACGAAATTTGATGTCCTGGGGGGAA--TAAATGACAGCAAGCTTACG	2796
Oy	2542	TCCATATCTAATCTCATGCGCTCTTACTTCCCTCCAAATTTGGCTATTAACAAAGAAAGTCT	2601
Db	2797	TCCAATATCTAAGCTTACCACTCTTACGTCCTCTCATTTGATCATTAACCTTTGAAGCAACA	2856
Oy	2602	TCACTCCCAAGAGATGTTCAAAAGCCTTGCAAATCTCAAAATCTTGAATATCTCTTT	2661
Db	2857	ACTCTCCCAAGAGATGTTCAAAAGCCTTGTAAATCTTGAGTCTTGAAGCATTTATATAC	2916
Oy	2662	TACTTCAATCTTAAAGAGCTGCTTACACAGCCTGAGTCTCATATGCTTTGAAGCATCTG	2721
Db	2917	TTCAAAAAAATCTCAGAGAGTTGCCACAGCCTGAGTCTCATATGCTTTGAAGCATCTA	2976
Oy	2722	GAAATTCATAGTTGTTATATGACATAGAGAGTCTCCCGAGAGAGTGTGAAGAGTTTAAAT	2781
Db	2977	AAAAATTCATTAATTTGTTACCACTAGAGAGTCTCCCGAAGAGAGATGGAAGGCTTAACT	3036
Oy	2782	TCACTCACACAGTTATCCATTAACATCTGTGAATGTCAACATGTTTACCGAGAGATTG	2841
Db	3037	TCACTCACCGACTTATATGTTCAAAATGTGAGATGCTTAATATGTTTACCTGAGGAGATTG	3096
Oy	2842	CAGCACTTAACAGCCTCTCAAAATTTATCATGTTGATGTTTGTCCACACATGGCCAGCGG	2901
Db	3097	CAGCACTTAAGAGCCTCTCACTAGTTTACAAATTTATGCTGTCCAGATTTGAAAAAGCGG	3156
Oy	2902	TGTGGAAGGGAATGAGGAAGAAGCTGTACAAATTTGCTCAATCTCTCGTGTGTTATT	2961
Db	3157	TGTGGAAGGGAATGAGGAAGAAGCTGTCAAAATTTGCTCAATCTCTCAATGATATATT	3216
Oy	2962	TATTAG 2967	
Db	3217	TGTTAG 3222	
RESULT 12			
US-10-437-963-67879			
Sequence 67879, Application US/10437963			
Publication No. US2004012343A1			
GENERAL INFORMATION:			
APPLICANT: La Rosa, Thomas J.			
APPLICANT: Kovalic, David K.			
APPLICANT: Zhou, Yihua			
APPLICANT: Cao, Yongwei			
APPLICANT: Wu, Wei			
APPLICANT: Boukharov, Andrey A.			
APPLICANT: Bardazuk, Brad			
APPLICANT: Li, Ping			
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with			
FILE REFERENCE: 38-21(53221)B			
CURRENT FILING DATE: 2003-05-14			
NUMBER OF SEQ ID NOS: 204966			
SEQ ID NO 67879			
LENGTH: 2409			
TYPE: DNA			
ORGANISM: Oryza sativa			
FEATURE:			
OTHER INFORMATION: Clone ID: PAT_MRT4530_68697C.1			
US-10-437-963-67879			

QY	58	GAAC	TGGATTTGA	TTCTCG	TTTTAAGA	TAGAGTTCG	AAAGAGCTTCA	AAGACGTTTACT	117	
Db	76	GACATTA	AAATTTTCTTG	GAATG	TTAAGGTG	AGCTGCG	AAAGAGCTTCA	AAGACGTTTACT	117	
QY	118	ACAA	TCCAAAGCTG	TGCTGA	GAATGCTC	GAAAGCAATTTGA	AGACAAAGGCAATTA	GA	177	
Db	136	GCTATTTT	GTGCTTCTGA	AAAGATG	CAAAAAGAAAGCAATCTA	CAACAAGTTTCA	CAACAAGTTTCA	195		
QY	178	AAT	TGTTGCA	GAATCTCA	ATGCTGCTGCATATAG	AGCTGATGATCTTG	GAAGCA---A	234		
Db	196	CATTG	GGCTTGA	AAATCTCA	AAAGATGTTGTCTATG	CATAGATGATGTTCTG	GAATGATGTT	255		
QY	235	TGTA	AAACTGAG	CGACCAATTA	TGACAGAAAGCAATATG	GGTGTATCATCTCA	AAAC	294		
Db	256	GGGAC	ACAGAGTGTG	CAGACAGAAAGTTA	GAAAGGTGAATCTG	TACTTAATTTTG	CCCCA	315		
QY	295	GTTAT	CACCTTTT	CGTCAACA	GAATTTGGG	AAAAAGATGA	AAAAAGATTA	TGA	354	
Db	316	CTAAC	CCATCTTCTT	CTTTTGA	CTGGGAAAGAAAAATTA	AAAAAGGTGCTG	GA	375		
QY	355	GTA	ATTGCA	GGCGGACGAATTA	AGTTTCATTTG	TGATGAAGCACTAT	TAGAGA	408		
Db	376	GAA	TAGCTGCGCTT	AAAAAGATTTTGA	ATTTGAAGAAAGCAATG	ACACACCTTCA	435			
QY	409	---	CAAGTGT	CACGCGCAACAG	TTTTGTGTAATG	AACCAAGTTATG	GAAGA	465		
Db	436	GAT	CAAAATTTGCC	AGAGAAACA	CACTCCCTTATAG	CGCGCAAAATATTTT	TGGAAGA	495		
QY	466	GACAA	AGAAAGGACG	AGATGTG	TAATAA	TCTGATTAACATG	TT---AGCA	TGCCCCA	522	
Db	496	GAT	AAAGGTAA	AAATGATATGTG	CAAGATGATTTCA	GAACTGCTGAATCT	TAATTTCTAAT	555		
QY	523	ACAC	TTCCAGTCTCC	CAATACTTG	TATG	GGGGGACCTAG	GAAGAACGACCTTTG	CCCCA	582	
Db	556	AAC	CTGTCAGTCTT	CCACTAATTTG	AATGGAATGG	AGGTGATAGCAAGCTG	CCCTAGCAAA	615		
QY	583	ATG	CTTTCATGAT	CAAGAGTATTA	GAGATTTTCC	ATCCCAATATATG	ATTTG	TGCTC	642	
Db	616	CTG	GATTTTAATG	ATTAATCA	CAAGAGTATGTTG	ATTAAGATGCTAT	TGGCAATCTG	TA	675	
QY	643	TGCG	AGATTTTAATG	AGAGAGGTG	TATTAAGAAATTTG	ATGATCTATTTGA	AGAAAG	702		
Db	676	TCT	ATATGCGTTT	GACCTTA	AAACATATTTG	TAATATATCAATACAT	ATAGAGGTG	AA	735	
QY	703	TCA	CTGTGTGC	ATGACATTTG	GCTTCACTTA	AAAGAAAGCTT	CGGACCTTG	CTGAT	762	
Db	736	AGCA	ATAACCAATTA	ACCCTTA	GGAAGCATTTA	CAAGAAAGCTTCA	TGACCTTTTA	AGGAC	795	
QY	763	AAAA	AAATTTTGT	CGTCTTAG	ATGATGATGTTG	GAATGAAGTCAAGTCA	ATAGTGG	CGCTAAG	822	
Db	796	AAG	AGATATCTTG	CTAGTGTG	ATGATGACATATCA	AAAT---GAT	ATATGTC	ATCTGGGA	852	
QY	823	TTA	GACAAAGTCTT	GAAAGTTG	AGCAAGTGG	CGCCTTCTG	TTCAACCACTA	CTGCTT	882	
Db	853	TTG	ATAAACCTG	TACCGAGTGG	TAGAAAGTGCATG	ATTTTAATCATCTAC	ACGCTT	912		
QY	883	GAAA	AGTTGGA	TCAATTA	TGGAACATTTG	GAACATATG	TAATTTG	CTCA	942	
Db	913	ACAA	AAATTTGAT	ATGAATTA	GAACATTTAG	ACCCTATG	CAAGAGTCC	CAAACTTCA	972	
QY	943	GAA	ATTTGTTG	TGTTGTTG	TATCATCAACG	TGTCATTTTG	GGCCCAAGAA	GAATTAATCTT	1002	
Db	973	GAA	BAATGCA	GGAAAAATTT	TGTTGATATCTT	TCAGAGGA	AAAAAGG	CGAAGAT	1032	
QY	1003	AAT	CTTGTG	CTATCG	AAAGGAATTTG	TGA	AAAAATG	TGTGTG	CTCTAG	1062
Db	1033	GAG	TTAATCA	AAAAATTTG	GAGATTCATATG	TACAGAAATG	TATGATG	CTCTT	TAGAC	1092
QY	1063	AAA	ACTCTG	GAGGTA	TTTTGCG	CTTTAAGG	AGAAAGCA	CTGGG	ACATG	1122
Db	1093	AGAA	CAATTTGG	ATCCCT	TAATG---TTCA	GAA	AAAGCATTTCTA	TATGTG	CAAGAA	1149
QY	1123	GAT	GATGAT	TTTGA	AAATG	CTCAAGAAAGAAATTC	TATTTCTG	CTG	CCCTG	1182

Db 1150 GAAATATATTTGCTGAGTACTGCGAAGTAAGATGATATCTGTCAGTATTAACCTC 1209
Qy 1183 AGTTACCATCACTCCCTGCACTTTGAGACAATGCTTTACATATTTGAGATTTCCCA 1242
Db 1210 AGTTATGATGACCTTCATCTGATTTAAACCTTTTCTCTGTTATTCACCTTTTCCA 1269
Qy 1243 AAGATACCGAATATGAAAGGAATCTMACTCTCTGATGAGCATGCT---TTT 1299
Db 1270 AAGGCTATGATATTTTTCAGAACTTATTAATGATATGATGAGCAATGGCTTATTTG 1329
Qy 1300 ATTTTATGAAAGGAACCTTGAGCTAGAGAAATGATGATTAAGATGAATGAATTA 1359
Db 1330 AATCCAGCTAGTCGAACCTAGAGGCAATTAAGATGGAGAAATATCTTAATAGCTT 1389
Qy 1360 TACTGAGCTCTTTCTTCCAGAGATGATGATTAATGTCGCA-----CTTATTTG 1413
Db 1390 GCTGGAAGATCTTTTCCAGACTATGTTTAAATCAATGATGGAGCATCTCACATTGC 1449
Qy 1414 AAGATGATGATCTCATTCATGATCTGCAACATCTATTT 1455
Db 1450 AAAATGATAGCTTGTTCATGATCTAGCAATATCTGTCT 1491

RESULT 13

US-10-437-963-79971
; Sequence 79971, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79971
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1
US-10-437-963-79971

Query Match 9.1%; Score 269; DB 18; Length 3333;

Best Local Similarity 52.1%; Pred. No. 1e-59;
Matches 748; Conservative 0; Mismatches 645; Indels 42; Gaps 5;

Qy 7 GAAGTTTCCCTCAAGTCTGTTAGACAATCGAATCTTTTCATCCAGGGGAAGCTTGA 66
Db 22 GAGGCTTCATGCAACCCCTCTCCAGAAATTTGACAGCAACCTTGATCATTTCA 81
Qy 67 TTGATTCCTGTTTAAAGATGATTCGAAAAGCTTCAAGCAGTTTACTACATCCAA 126
Db 82 TCTTGAGAGGCAATCATGAGCAAGCTAGAGCCTCTTCCACATCTCTCAAGTAAAG 141
Qy 127 GCTGTCTAGAAAGCTCTCAAGAGCAATTTGAAGACAAAGGCAATTAATTTGGTTG 186
Db 142 GCTTCTCTGAGAGCTGAGAGAGCAATTTGACAGATGATCTGTAGAGGAGATGGCTA 201
Qy 187 CAGAACTCATATGCTGCTGATGATGAGGCTGATGATCTTGAAGATGATTAAGCTGAG 246
Db 202 GCGAAGCTCAAGATATGCGTACGACCTTATGATCTGCTGAGAGCTATTCAGCCAA 261
Qy 247 GCACCAATTAGACAGAGAGAAACAATATGAGGTGTTATCATCCAAAGTTATCATCTTT 306

Db 262 AGTATGCGCATGAAGACAGAGGAGGTATATTTCCCAACAAAGCAAGTTTCTTTCTTC 321
Qy 307 -----CGTCAACAAGTTGGGAAAGATGAAAGATTAATG 342
Db 322 TCTTTCTGATGAGAAATCTGTACAGATAGATTAAGCATTAAGATTAACATCATATG 381
Qy 343 GAGAACTGATGATTAATTCAGCGGAAACGAATTAAGTTTCAATTTGATGAAGACATATA 402
Db 382 GAGAGATTAATGATATGATGCGCAAGAACGACACCATTTGGGCTCCAGATGATATGTA 441
Qy 403 GAGGACAAAGTTGCTAC-----ACGCCAAACAGTTTGTGTTGAATGAACACAA 453
Db 442 ATGAGACGGTATGATCTCAGACCGTCCGAAATCAAGTTCTCTGTATGATATGCTGGCT 501
Qy 454 GTTATGAGAAAGACAAAGAAAGACAGAGATGAGAAATCTGAT---AAACAAATGT 510
Db 502 GTATTTGATGAGGAGAGGAGACAGAAAGAAATGATGAGCTGTGTCTCTGATATGGA 561
Qy 511 AGCAATGCCAAACACTTCCAGTCTCCCAATCTGATGAGGAGGACTAGAAAGACG 570
Db 562 CATATATCTGCACTTATGATGATTCAGATGTTGGCATGGGTGGCTTGTAAACT 621
Qy 571 ACTTTGCCCCAATGCTTCAATGATCAGAGATTAATGAGCATTTCCATCCCAATA 630
Db 622 ACTCTTATGAGATGGTGTACCATGATGACAGATGAAGAAACATTTGACTTGAGATC 681
Qy 631 TGATTTGTCTGGAAGATTTTAATGAGAAAGGTTGATTAAGAAATGTGAAATCT 690
Db 682 TGATCTATGATGTTGAAGTTTGAATGAGAAAGCTTAACAAAGAAACCTTTGAGCT 741
Qy 691 ATTTG---AAGAAAGTCACTTGTGAGATGAGTCTGCTCCACTTCAAAAGACCTTGG 747
Db 742 TCTGACTATGACCAATCTGTTGATGATCTAATCAATGATATGATCAAGAAACCTGCC 801
Qy 748 GACTTCTGAAATGGAATAAATATTGCTGCTCTTAATGATGATTTGGAATGAAGATCA 807
Db 802 AGAGTATTTGCGGGCAAGAGGTACTCTGCTGTGATGATGATGATGATGAAGACCTT 861
Qy 808 GATAAGTGGCTAAGTAAAGCAAGTCTGGAAGTTGAGAGCAAGTGGCGCTTCTGTTCTA 867
Db 862 GATTAATGACACACTATGAGCAGCTTAAATTTCCAGAGGCTTTGAGAGCAAGTATGCT 921
Qy 868 ACCACTCTGCTTGTGAAGAGTTGATCAATTAATGGAACATTCGAACCATGAAATG 927
Db 922 GTGACATCAGAAATGAAATGTTGGCAGATCATGAGAGAAATAGAGCCCTCAAGATTA 981
Qy 928 TCAATTTGTCTCAAGAGATTTGTTGTTTTCATGCAAGCTGATTTGGGCAACCA 987
Db 982 CAGAACTATCAGATGATGACAGCTGTGTATTTCAAGACCATGCAATTTAGGATGCT 1041
Qy 988 GAAAGAA---TAAATCTTAATCTGTGCTATGGAAGAAAGATTTGAAATAATGTGCT 1044
Db 1042 GACTGACGCGCAGATCCGAGTTGAGGCGATGAAATGAAATGGAAGAACTGAG 1101
Qy 1045 GGTGTGCTCTAGAGCTTAAACTTTGAGATTTTTCGCTTTAAGAGAAAGAAAGA 1104
Db 1102 GGATTTGCTCTGATCAAGAGCATTTAGAGAGCTCTGTTTTCAGAAACAGATGAAGAG 1161
Qy 1105 CAGTGGAAACATGTGAGAGATGATGAAATTTGGAATTTGCTCAAGAAAGAAAGTTCTATT 1164
Db 1162 GAGTGAAGAGCAATACGAAATGACATATGAGAGTTACCGGCAAGATTAACATCTC 1221
Qy 1165 CTGCTGCGCTGAGACATTAATGATCACTTCCACTTGAATTTGAGCAATGCTTTACA 1224
Db 1222 CTGCAACCTCTAGCTTAAGTTACCACTTTTACACACATCTTAAGACAGTCTTGCA 1281
Qy 1225 TATGTGCAATATCCCAAGATACCGAAATGGAAGAAAGGAAATCTAATCTCTCTG 1284
Db 1282 TTCTGTTCTGATATCTTAAGATTAATGTTTCAGAGAGAGAAACGTTTAATATCTCG 1341
Qy 1285 ATGGCAATGTTTATTTATTTATGAAAGAAACTTGAAGCTAGAGAAATGATGATGA 1344
Db 1342 CTAGCACTGTGTTTATCATCAGCAGTCTAGAAAGAAAGAAATGAAAGATTAATGGAATGCA 1401

OY 1345 GTATGATGAATTAATTAAGCTTTCTTCCAGAGATTGAATTAAATCG 1399
DB 1402 TACTTTAATGAGTTAATTAAGAGCTTTCTTCCAGCATATGAGAAATTAATG 1456

RESULT 14

US-10-437-963-33626
; Sequence 33626, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33626
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3771C.1
US-10-437-963-33626

Query Match 9.1%, Score 268.6; DB 18; Length 3615;
Best Local Similarity 57.0%; Pred. No. 1,4e-59;
Matches 553; Conservative 0; Mismatches 409; Indels 9; Gaps 3;

OY 421 CGCCAAACAGTTTGTGTTGAATGAACACAGATTATGAAGAGCAAAAGAGAC 480
DB 814 CCCAAGACCAATGTTATTAATGACATCGAGTGTATGTAGAGAAAGATTAAGAG 873
OY 481 GAGATAGTGAATAATCCATGATTAAGCAATGTAGCAATGCCCA---AACACTTCCAGTCTCT 537
DB 874 GTATTTGAACATGTTACTACACACGATTAATCAACATGTCACCTTTTATCTT 933
OY 538 CCAATTAATGTTAGGGGGAATGAGAAAGCACTCTTCCCAATGCTTTCAATGAT 597
DB 934 CCCATAGGGGTATGAGAGAGTAGAGGAAACACTTAAACAGCTCTACAAATGAT 993
OY 598 CAGAGAGTAATGAGCAATTCATCCCAAAATATGATTTGTCTGAGAAATTTTAT 657
DB 994 GTGAGATTAAGAAAGCAATTCATGTTAAGATGTGGCTGTGTCTTGAAGAACTTGAT 1053
OY 658 GAGAAAGGTTGATTAAGAAATTTGAAATCTATTG---AAGAAAGTCACTTGTGGC 714
DB 1054 GAGCCCAACTTACCAAGAAACGATAGATCAAGTTGAGCGGATTTATATCGCCACA 1113
OY 715 ATGCACTTGGCTCCACTTCAAAAGAGTTGGGACTTGTCTGAATGAGAAAAATATTGG 774
DB 1114 ACAAACATGAACCTGCTTCAAGAAAGCTCTCAACAGCTGAAAGGCAAAAGGTTCTT 1173
OY 775 CTGCTTTAATGATGTTTGAATGAAGATCAAGATTAAGGGGCTAATGAAGCAAGTC 834
DB 1174 CTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1233
OY 835 TTGAAGTTGAGAGAGTGGCGCTTCTGTTAACTACTCTGCTTGAAGAGTTGGA 894
DB 1234 CTAGTTGCTGGTGAAGAAAGAGTAAATATATGATGATGATGATGATGATGATGATGAT 1293
OY 895 TCAATTTAGGCAATGCAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 954
DB 1294 AAATTTAGGGCGGGTGAATCTTACTATCAAAACAGTTATCATCAATGATGATGATGAT 1353

OY 955 TTGTTTTCATGCAACGCTGATTTGGGACCAAGAGAAA---TAAATCTTAATCTTGTG 1011
DB 1354 CATTTATTCAGACATGATGATTTTGCAGATGTGATCTCCAGTGACACCCAAATTTGGA 1413
OY 1012 GCTATGGAAGAGAGATTTGAAAAATGTGTGTGTGCTCTAGAGCTTAAATCTTT 1071
DB 1414 ATGATCGCAAGAAATTTGCTCATATGATGATGATGATGATGATGATGATGATGATGAT 1473
OY 1072 GAGATTTTGTGCTTTAAGAGAGAAAGACAGTGGGAACATGTGAGATGATGATGAT 1131
DB 1474 GGTGCTTATTTATTTGTGTAAGACACAGAGATGATGAAAAATATCTTAAGATGAA 1533
OY 1132 ATTGGAATTTGCTTCAAGAAAGATTTCTATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
DB 1534 ATATGGAATTTGCTTCAAGAAAGATTTCTATTCTTACAGCTGATGATGATGATGATGAT 1593
OY 1192 CACCTTCACTGATTTGAGCAATGCTTTAATATTTGATGATGATTTCCAAAGATACC 1251
DB 1594 CATCTTCACTGATTTGAGCAATGCTTTGATGATGATGATGATGATGATGATGATGATGAT 1653
OY 1252 GAATGGAAGAAAGAAATCTAATCTCTCTGATGATGATGATGATGATGATGATGATGATGAT 1311
DB 1654 GTGTTTGAAGAAAGCAATTTGCTCAGATCTGATGATGATGATGATGATGATGATGATGAT 1713
OY 1312 GGAATCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1371
DB 1714 CGCGGAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
OY 1372 TTCTTCCAGA 1382
DB 1774 TTCTTCCAAA 1784

RESULT 15

US-10-437-963-33659
; Sequence 33659, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33659
; LENGTH: 3852
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3774C.1
US-10-437-963-33659

Query Match 9.1%, Score 268.6; DB 18; Length 3852;
Best Local Similarity 57.0%; Pred. No. 1,4e-59;
Matches 553; Conservative 0; Mismatches 409; Indels 9; Gaps 3;

OY 421 CGCCAAACAGTTTGTGTTGAATGAACACAGATTATGAAGAGCAAAAGAGAC 480
DB 827 CCCAAGACCAATGTTTATTAATGACACTCGAGTGTATGTAGAGAAAGATTAAGAG 886
OY 481 GAGATAGTGAATAATCCGATTAACATGTTAGCAATGCCCA---AACCTTCCAGTCTCT 537
DB 887 GTATTTGAACATGTTACTACACACGATTAATCAACATGTCACCTTTTATCTT 946
OY 538 CCAATTAATGTTAGGGGGAATGAGAAAGCACTCTTCCCAATGATGATGATGATGATGATGAT 597

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2005, 14:12:11 : Search time 8497 Seconds
(without alignments)
13291.360 Million cell updates/sec

Title: US-10-647-268-1_COPY_52_3018

Perfect score: 2967

Sequence: 1 atggctgaagcttccttca.....ctcgctgcttattattag 2967

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hcc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_g881:
9: gb_g882:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	610.8	20.6	670	7	CR61977 33106 In
2	540.4	18.2	594	4	BG96938 EST161457
3	510	17.2	729	4	BG890602 EST16453
4	483	16.3	617	5	BQ111670 EST597246
5	473.6	16.0	732	7	CV499954 64358.1 M
6	472	15.9	664	4	BG097566 EST462085
7	462.8	15.6	808	4	CN214760 28498 Sub
8	449.8	15.2	618	4	B1919903 EST139826
9	421.2	14.2	935	7	CV434731 58221.1 S
10	415	14.0	668	4	BG593905 EST492583
11	414	14.0	577	5	BQ117360 EST602936
12	402	13.5	631	2	AM035144 EST76112
13	399.8	13.5	598	5	BQ511700 EST619115
14	385	12.9	592	2	AM907068 EST143100
15	383.2	12.9	668	7	CV496683 60822.1 M
16	369.6	12.5	575	2	AM032553 EST176112
17	346.2	11.7	855	2	CG944135 MBEN024TF
18	325.8	11.0	882	9	CG939127 MBERT46TF
19	325.4	11.0	571	7	CM644273 7934.1 Af
20	315.4	10.6	424	2	AM928868 EST137656
21	308.2	10.4	418	2	BE342109 EST194950
22	304.8	10.3	787	9	CG956037 MBEC53TF
23	291.6	9.8	504	2	BE920178 EST423947
24	289	9.7	686	8	AZ773501 T221249b

C 25	288.8	9.7	819	9	CG972611 MBEN43TF
C 26	285.8	9.6	886	2	CG965962 MBEP65TR
C 27	282	9.5	407	2	AM032184 EST75638
C 28	280.8	9.5	716	7	CV469963 42731.1 C
C 29	276	9.3	2409	9	CL979800 OBIFCC04
C 30	275.4	9.3	875	9	CG960374 MBEGK4TF
C 31	270.6	9.1	3333	9	CL960744 OBIFCC037
C 32	266.4	9.0	712	9	CR494610 Medicago
C 33	262.2	8.8	375	4	BG096371 EST460890
C 34	258.6	8.7	872	9	CG927653 MBEP90TR
C 35	253.8	8.6	680	9	AZ773502 T221250b
C 36	253.2	8.5	1902	9	CL979799 OBIFCC044
C 37	251.4	8.5	454	2	AM979927 EST34581
C 38	251	8.5	863	9	CG931272 MBEG87TF
C 39	246.8	8.3	932	9	CG944419 MBEG67TF
C 40	246.4	8.3	1714	9	CL955053 OBIFCC000
C 41	240.4	8.1	2499	9	CL944015 OBIFCC001
C 42	240.4	8.1	2499	9	CL965216 OBIFCC011
C 43	238.8	8.0	804	9	CG919643 MBEGH93TR
C 44	237.6	8.0	432	5	BQ505531 EST612946
C 45	236.8	8.0	368	2	AM979626 EST341225

ALIGNMENTS

RESULT 1
CR61977
LOCUS 33106 In vitro Root Solanum tuberosum cDNA, mRNA sequence.
DEFINITION CR61977
ACCESSION CR61977.1 GI:45291634
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 670)
Flinn, B., Kitchell, C., Sardana, R., Griffiths, R., Laque, M., De
Koeber, D., Audy, P., Goyer, C., Li, X.-Q., Wang-prucki, G. and Regan, S.
Generation of ESTs from in vitro root tissues of potato
Unpublished (2004)
COMMENT
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.

FEATURES

FEATURES
SOURCE
1..670
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/tissue_type="Root"
/lab_host="XL10-Gold"
/clone_lib="In vitro Root"
/note="Vector: pBluescript II SK(+) XR, Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Sterile stem
sections from pathogen-free Solanum tuberosum var.
Shepody, clone 1756, nuclear stock were cultured in
Magenta boxes containing 1/10 strength MS medium,
solidified with 0.8% (w/v) Phytagar. Roots of all sizes,
originating from the stem bottoms were collected from
these cultures, washed to remove residual Phytagar, and
used in RNA isolations and library construction."

ORIGIN

Query Match 20.6%; Score 610.8; DB 7; Length 670;
Best Local Similarity 94.5%; Pred. No. 2.1e-149;
Matches 633; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

CY 889 GTTGACATCAATTGGACATTCGACATGATGATGCAATTTGTCTCAAGAGAT 948

Db 1 GTTGATTCATATGGAAGCTTGCACCATATGTAATGTCAAATTTGTCTGCAAGAAAT 60
Oy 949 TGTGATGTTGTTTCATGCAACGTGATTTGGGACCAAGAAATTAATCTTAATCTT 1008
Db 61 TGTGATGTTGTTTCATGCAACGTGATTTGGGACCAAGAAATTAATCTTAATCTT 120
Oy 1009 GTGGCTATCGGAAGAGATTTGAAAAATGTTGTGTGTGCTTACAGCTAAACT 1068
Db 121 ATGGCTATCGGAAGAGATTTGAAAAATGTTGTGTGTGCTTACAGCTAAACT 180
Oy 1069 CTGGAGGATTTTGGGCTTTTAAGAGAAAGACAGTGGACATGTGAGAGATCT 1128
Db 181 CTGGAGGATTTTGGGCTTTTAAGAGAAAGACAGTGGACATGTGAGAGATCT 240
Oy 1129 GAGATTTGGAATTTGGCTCAAGAGAAAGTTCTATTCTGCTGCGCTGAGCTTGTAC 1188
Db 241 GAGATTTGGAATTTGGCTCAAGAGAAAGTTCTATTCTGCTGCGCTGAGCTTGTAC 300
Oy 1189 CATCACTTTCACTTGATTTGAGACAATGCTTTACATATTTGCAATTTCCCAAGAT 1248
Db 301 CATCACTTTCACTTGATTTGAGACAATGCTTTGCAATTTGCAATTTCCCAAGAT 360
Oy 1249 ACCGAAATGGAAGGAAATCTTAATCTCTCTGATGAGCAATGCTTTTATTTATCG 1308
Db 361 ACCGAAATGGAAGGAAATCTTAATCTCTCTGATGAGCAATGCTTTTATTTATCG 420
Oy 1309 AAAGAACTTTGAGCTAGAGATTTAGGTAATGAGTAATGAGTAATTAATTAATCTT 1368
Db 421 AAAGAACTTTGAGCTAGAGATTTAGGTAATGAGTAATGAGTAATTAATTAATCTT 480
Oy 1369 TCTTTCTTCAAGAGATTTAGGTAATGAGTAATGAGTAATTAATTAATCTT 1428
Db 481 TCTTTCTTCAAGAGATTTAGGTAATGAGTAATGAGTAATTAATTAATCTT 540
Oy 1429 ATTCAATGCTGGAACAATCTTATTTGCGCAACACATCAAGAGAAATTCGAGAA 1488
Db 541 ATTCAATGCTGGAACAATCTTATTTGCGCAACACATCAAGAGAAATTCGAGAA 600
Oy 1489 ATAAATTTAGAAATTTACATATGATGATGATGATGATGATGATGATGATGATG 1548
Db 601 ATAAATTTAGAAATTTACATATGATGATGATGATGATGATGATGATGATGATG 660
Oy 1549 TACTCTCTT 1558
Db 661 TACTCTCTT 670

RESULT 2
BG096938 594 bp mRNA linear EST 07-MAR-2003
LOCUS EST161457 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION CSTRB4514 5' sequence, mRNA sequence.
ACCESSION BG096938
VERSION BG096938.1 GI:12586973
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 594)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utechtack, T., Hansen, C.L., Doan, B., Bought, O., Buell, C.R.,
Rouming, C.M., Fry, W.E., Tankley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL.

FEATURES
source
http://genome.arizona.edu/orders/
Location/Qualifiers

1. 594
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CSTRB4514"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/clone_id="potato leaves and petioles"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN

Query Match 18.2%; Score 540.4; DB 4; Length 594;
Best Local Similarity 94.7%; Pred. No. 7.5e-131;
Matches 559; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Oy 1924 GAATTAAGAAACCTGATCTCTATGCTCAATGAAATACGATCTTGAGAGAGAG 1983
Db 2 GAATTAAGAAACCTGATCTCTATGCTCAATGAAATACGATCTTGAGAGAGAG 61
Oy 1984 AATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAGC 2043
Db 62 AATGATATGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGCAATCTTTAGC 121
Oy 2044 ATGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2103
Db 122 ATGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 181
Oy 2104 GAAGCTCTCAACCACTGCAATCTGATCTGTTTAAATCAATGAGGCTTCAAGAGATC 2163
Db 182 GAAGCTCTCAACCACTGCAATCTGATCTGTTTAAATCAATGAGGCTTCAAGAGATC 241
Oy 2164 CGTCTCCAGACGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2223
Db 242 CGTCTCCAGACGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 301
Oy 2224 AGTTGCAAAACCTGCAATCTTACCACTTTGAGAGCTGCTGTAAAGATCTA 2283
Db 302 AGTTGCAAAACCTGCAATCTTACCACTTTGAGAGCTGCTGTAAAGATCTA 361
Oy 2284 GAGTTGTGAGAGGAGGCTCTGCGAGATGAGATGAGATGAGATGAGATGAGATG 2343
Db 362 GAGTTGTGAGAGGAGGCTCTGCGAGATGAGATGAGATGAGATGAGATGAGATG 421
Oy 2344 AGGTTTCCATCTCTGAGAAACCTTAATATAGCGAATTTGTAATCTGAAAGATGCTG 2403
Db 422 AGGTTTCCATCTCTGAGAAACCTTTTATAGCGAATTTGTAATCTGAAAGATGCTG 481
Oy 2404 AAAAAGAGAGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 2463
Db 482 AAAAAGAGAGAGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 541
Oy 2464 AGTTTGTATTTCAACCTTTCTTCTGCAAGAAATGATGATGATGATGATG 2513
Db 542 AGTTTGTATTTCAACCTTTCTTCTGCAAGAAATGATGATGATGATGATGATG 591

RESULT 3
BG890602 729 bp mRNA linear EST 07-MAR-2003
LOCUS BG890602
DEFINITION EST16453 cSTD Solanum tuberosum cDNA clone cSTD18P22 5' sequence,
mRNA sequence.
ACCESSION BG890602
VERSION BG890602.1 GI:14267723
KEYWORDS EST.

SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE 1 (bases 1 to 729)
AUTHORS van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chienlingo, A., Bougri, O., Buell, C.R., Roming, C., Tankley, S. and Baker, B.
TITLE Generations of ESTs from dormant potato tubers
JOURNAL Unpublished (2001)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES
source
Location/Qualifiers
1..729
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="CST18P22"
/tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
/clone_lib="CST18"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tankley lab notebooks."

ORIGIN
Query Match 17.2%; Score 510; DB 4; Length 729;
Best Local Similarity 82.9%; Pred. No. 8.3e-123;
Matches 607; Conservative 0; Mismatches 120; Indels 5; Gaps 2;

1 GGTTTTAAAGATGAGTTCGAAAAGCTTCAAACACAGTTACTACATCCAGCTGCTGCTA 135
|||||
1 GGTTTTCAAAATGAGTTCGAAAAGCTTCAAACACAGTTACTACATCCAGCTGCTGCTT 60
|||||
136 GAAGATGCTCAGAGAAGCAATTTGAAGACAGCAAGCAATGAAAATTGTTGAGAACTC 195
|||||
61 GAAGATGCTCAGAGAAGCAATTTGAAGACAGCAAGCAATGAAAATTGTTGAGAACTC 120
|||||
196 AATGCTGCTCATATGAGGCTGATGACATCTTGAGCAAGATGAAAATGAGGACCAATT 255
|||||
121 AAGCTGCTCAGATATGAGGCTGATGACATCTTGAGCAAGATGAAAATGAGGACCA 177
|||||
256 AGACGAGAGAAACAAATATGAGGCTGATGACATCTTGAGCAAGATGAAAATGAGG 313
|||||
178 GAATTCCTCCAGTCTGACATATGAGGCTGATGACATCTTGAGCAAGATGAAAATG 237
|||||
314 AGATTGGGAAAAGATGAAAAGATTTATGAGAAAATGAGATGTAATGCGAGCAAGAA 373
|||||
238 AGGTGGGAAAAGATGAGCAAGATGAGCAAGATGTAATGCAATTCGTGAGAAAAGAA 297
|||||
374 TTAAGTTTCATTTGAGTGAAGAGCACTATGAGAGCAAGATTCCTCAAGCAAGAGTT 433
|||||
238 AGAATTTTCATTTGAGTGAAGAGCACTATGAGAGCAAGATTCCTCAAGCAAGAGTT 357
|||||
434 TTGTTTGAATGAACCAAGTTTATGAGAGAGCAAGAAAAGAGAGAGATGAGTGA 493
|||||
338 CTGTTTATTAATTAACCAAGATGATGAGAGAGCAAGAGAGAGATGAGTGA 417
|||||
494 TCCTGATTAACCAATGTTGAGATGAGCAAGTTCCTCAAGTTCCTCAATTAAGTATG 553
|||||

Db 418 TCCTGATTAACCAATGTTGAGATTCCTCAAGAAAATGTCAGTCCCGAATCTTGATG 477
Qy 554 GGGGACTGAGAAAAGCACTCTTGCCCAATGATCTTCAATGATCAGAGTAATTGAC 613
Db 478 GGGGACTGAGAAAAGCACTCTTGCCCAATGATCTTCAATGATCAGAGTAATTGAC 537
Qy 614 ATTTCCATCCCAAAATATGATTTTGCTGCGAAGATTTTATGAGAAAGTTGATPA 673
Db 538 ATTTCTATCCCAAAATATGATTTTGCTGCGAAGATTTTATGAGAAAGTTGATPA 597
Qy 674 AGAATTTGATGATCTTATGAGAAAAGTCACTTTGCGAGATGAGACTTGCTCACTTC 733
Db 598 AGCAATTTGATGATCTTATGAGAAAAGTCACTTGAGATGAGACTTGCTCACTTC 657
Qy 734 AAAAGAGCTTCGGGACTTGCTGATGAGAAAATATTTGCTGCTTATGATGATTT 793
Db 658 AAAAGAGCTTCAGAGCTGCTGATGAGAAAAGTCACTTGATGAGATGATTT 717
Qy 794 GGAATGAGATC 805
Db 718 GGAATGATGATC 729

RESULT 4
B0111670
LOCUS
DEFINITION B0111670 mixed potato tissues Solanum tuberosum cDNA clone STWC32
5' end, mRNA sequence.
ACCESSION B0111670
VERSION B0111670.2 GI:21915068
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum.
AUTHORS 1 (bases 1 to 617)
Buell, C.R., Hart, A., Baker, B., Tankley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and Karameycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20163632.
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..617
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binje"
/db_xref="taxon:4113"
/clone="STWC32"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: combination of untreated and phytoptoxora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."

ORIGIN
Query Match 16.3%; Score 483; DB 5; Length 617;
Best Local Similarity 87.4%; Pred. No. 1e-115;
Matches 541; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

1329 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1388

Db 2 GGATGAGGTAATGAGATGGAACAAATATATCTGAGGTCTTTTTCAGAGATTGA 61
QY 1389 AGTTAAATCTGGCAACCTTATTTCAAGATGCAATCTCATTCATGATCTGGCAATC 1448
Db 62 AGTTAAATCTGGCAACCTTATTTCAAGATGCAATCTCATTCATGATCTGGCAATC 121
QY 1449 TCTATTTTGGGCAAGCAATCAAGCAATATCCGAGAAATATATGTAAGAAATATGAT 1508
Db 122 TCTGTTTGGGCAAGCAATCAAGCAATATCCGAGAAATATGTAAGAAATGAT 181
QY 1509 ACATATGATGCTCATTTGTTTCACTAAAGTGTATCTTTTCTCTTTTCCACTTGA 1568
Db 182 ACATATGATGCTCATTTGTTTCACTAAAGTGTATCTTTTCTCTTTTCCACTTGA 241
QY 1569 GAAGTTGTCTGTTGAGGTTGCTTATATGATGCAATTAACCTTAACCTTACCTG 1628
Db 242 GAACCTTTGCTGTTGAGGTTGCTTATATGATGCAATTAACCTTAACCTTACCTG 301
QY 1629 TTCCATGAGATCTAGTACATTTAAGATACCTTAACCTTGTGCAATATCTAGTATTCG 1688
Db 302 TTCCATGAGATCTAGTACATTTAAGATACCTTGTGCAATATCTAGTATTCG 361
QY 1689 TGTCTTCCAAACCAAGTTATGCAAGTTCAAAATCTGCAACTCTTATCTATGATGCTG 1748
Db 362 TGTCTTCCAAACCAAGTTATGCAAGTTCAAAATCTGCAACTCTTATCTATGATGCTG 421
QY 1749 TCATTCACCTTGTGTTTCCAAAGAAACCAAGCAACCTTGTATCTTCCAAATCTTT 1808
Db 422 CACCTCACCTTGTGTTTCCAAAGAAACCAAGCAACCTTGTATCTTCCAAATCTTT 481
QY 1809 ACTTATGATGTTCTATGATGATCTTATGTCACCAAGATATGATCTTATGCAATGCT 1868
Db 482 ACTTATGATGTTCTATGATGATCTTATGTCACCAAGATATGATCTTATGCAATGCT 541
QY 1869 TAAGACTCTAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1928
Db 542 TAAAGCTCTAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 598
QY 1929 AGCAAACTGATCTCTAT 1947
Db 599 AGCAAACTGATCTCTAT 617

RESULT 5
CV499954/c 732 bp mRNA linear EST 04-OCT-2004
LOCUS 64358.1 Mixed Leaf Solanum tuberosum cDNA clone 64358 5', mRNA
DEFINITION
ACCESSION CV499954 GI:53782311
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanales; Solanum.
1 (bases 1 to 732)
Flinn, B., Rochwell, C., Sardana, R., Griffiths, R., Jagu, M., De
Koeijer, D., Rudy, P., Goyer, C., Li, X.-O., Wang-Punski, G. and Regan, S.
Generation of ESTs from a normalized developing leaf library
Unpublished (2004)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
1..732
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultiivar="Shepody"
/db_xref="taxon:4113"

/clone="64358"
/tissue_type="Leaves"
/lab_host="XL10-Gold"
/clone_id="Mixed Leaf"
/note="Vector: pBluescript II SK(+); XR; Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Plants from
pathogen-free Solanum tuberosum var. Shepody, clone 1756,
nuclear stock were grown in a greenhouse under natural
conditions. Emerging, expanding and mature leaves were
harvested along the length of the plant and pooled. RNA
was isolated and used for library construction. A
normalized library was constructed following a modified
protocol of Bonaldo et al. (1996). Genome Research 6:
791-806."

ORIGIN

Query Match 16.0%; Score 473.6; DB 7; Length 732;
Best Local Similarity 88.9%; Pred. No. 3.3e-113;
Matches 523; Conservative 0; Mismatches 64; Indels 1; Gaps 1;

QY 2379 ATTGTTATTTGAAAGATTTGCTGAAAAGAAAGAAAGAAAGATCCCTGCTTGA 2438
Db 732 ATTGTTATTTGAAAGATTTGCTGAAAAGAAAGAAAGAAAGATCCCTGCTTGA 674
QY 2439 AGAGATGAGATTAATGTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2498
Db 673 AGAGATGAGATTAATGTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 614
QY 2499 ATTGTTATTTGAAAGATTTGCTGAAAAGAAAGAAAGAAAGATCCCTGCTTGA 2558
Db 613 ATTGTTATTTGAAAGATTTGCTGAAAAGAAAGAAAGAAAGATCCCTGCTTGA 554
QY 2559 GGCTTTACTTCCCTCCCAATTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2618
Db 553 GGCTTTACTTCCCTCCCAATTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 494
QY 2619 GTTCAAAAGCTTGCAAATTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2678
Db 493 GTTCAAAAGCTTGCAAATTTGCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 434
QY 2679 GCTGCTTACCAAGCTTGCCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2738
Db 433 ATTGCTTACCAAGCTTGCCTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 374
QY 2739 TGCACTAGAGAGCTCCCGAGAGAGTGTGAAAGTTTATTTGCTACACAGTTATC 2798
Db 373 TGCACTAGAGAGCTCCCGAGAGAGTGTGAAAGTTTATTTGCTACACAGTTATC 314
QY 2799 CATTAACAATCTGTAATGCTACATGTTTACCGAGAGATTTGCAACACCTTACAGCCCT 2858
Db 313 CATTAACAATCTGTAATGCTACATGTTTACCGAGAGATTTGCAACACCTTACAGCCCT 254
QY 2859 CACAATTTATCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2918
Db 253 CACAATTTATCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 194
QY 2919 AGAAGCTGTTCAAAATTTGCTACATGTTTACCGAGAGATTTGCAACACCTTACAGCCCT 2966
Db 193 AGAAGCTGTTCAAAATTTGCTACATGTTTACCGAGAGATTTGCAACACCTTACAGCCCT 146

RESULT 6
BG097566 664 bp mRNA linear EST 07-MAR-2003
LOCUS EST462085 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION
ACCESSION BG097566
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;


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Db      195 TTGGTTGCAAAAACCTCAAGTTGCTACATATGAGTTGACATCTTGGATGATATATA 254
Qy      240 AACTGAGGACCAATTTAGACAGAGAAGAACAAATATGGGTGTTATCATCAACGTTAT 299
Db      255 AACTAAGGCGCACAC---CGTTTCTCCAGCTGCTCATATGCGCTTATCATCAAGGTTAT 311
Qy      300 GACTTTTGTGTCACAGATTTGGGAAAAAGATGAAAAAGATTATGAGGAACTGAGTAT 359
Db      312 CCTTTTCCGTCAACAGGTGCGGAAAAAGATGACCTAGTATGAGAAACATAAATGCAT 371
Qy      360 TGCAGGAGGACCAATTTAGTTTCAATTTGGATGAAAAAGACTATAGAGAGACAAAGTTTAC 419
Db      372 TGCAGGAGGAAAAAGATTTTCAATTTGAGACAAAAAGATTATAGAGAGCAAGTTGTTAG 431
Qy      420 AGGCCAANAGGTTTTTTTGTATGAAATGACCAACATTTATGAGAGAGACAAAGAAAGGA 479
Db      432 ATGTAAAAAGAGTTCTGTATTTACCGAACACAAAGTTTATGAGAGGAGCAAAAGAGAGGA 491
Qy      480 CGAGATAGTAAATCTCTGATTAACATGTTAGCAATGCCCAACACTTCCAGTCTGCC 539
Db      492 TAAAGTATGTAAGAAATCTTGATTAATGATGTTAGTATGCCCAACACTTTCATCTTCCC 551
Qy      540 AATACTTGTATGGGAGGAGCTAGAGAAAGACGACTCTT-GCCCAATGCTCTTCATGATC 598
Db      552 AATACTTGTATGGGAGGAGCTAGAGAAAGACGACTCTTGGCCGGAATGATCTTCATGATC 611
Qy      599 AGAGAGTATGAGATTTCCATCCCAAAATPAGATTTGCTCTCGGAAGATTTATG 658
Db      612 AGAAAGTACTAAGCAATTTCTATCCCAAAATPAGGTTTGTGCTCGGATGATTTTGTAG 671
Qy      659 AGAAGAGGTTGAT-AAAGGAAATTTAGATCTATTTGAAGAAAGTCACTTGTGTG--- 713
Db      672 AGAAGAGGTTGATTAAGGCAATTTGATATCTATTTGAAGAGGCCACTTACTTGGGGA 731
Qy      714 --CATGACTTGGCTCCACTTCAAAAGAAAGCTTGGGAGCTTGTGATGAGAAAAATAT 771
Db      732 CATGGAGCTTGGGATCCCACTTCAAAAGAAAGTTCAGAGACTTGTGATGAGGAAAAAGAT 791

```

RESULT 8
BI919903

LOCUS BI919903 618 bp mRNA linear EST 10-MAR-2003

DEFINITION EST539826 potato microtubers, in vitro-grown Solanum tuberosum cDNA clone CST23018 5' end, mRNA sequence.

ACCESSION BI919903

VERSION BI919903.1 GI:16215919

KEYWORDS EST.

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

AUTHORS van der Hoeven,R., Bezzerides,J., Bachem,C., Visser,R., Karamcheva,S.A., Tsai,J., Van Aken,S., Uteckpack,T., Chiemiungo,A., Bougri,O., Buell,C.R., Romning,C., Tanksley,S. and Baker,B.

TITLE Generation of ESTs from in vitro grown microtubers (2001b)

JOURNAL Unpublished (2001)

COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

FEATURES

source

1. .618
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultiyar="Bintje"
/db_xref="taxon:4113"

```

/clone="CST23018"
/tissue_type="axillary buds of stem explants; growing
sink-tubers"
/dev stage="7, 8 and 10 days"
/lab host="SOLR"
/clone_lib="potato microtubers, in vitro-grown"
/note="Vector: pluscript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue supplied by Christian Bachem and Richard
Visser (Department of Plant Breeding, Wageningen
University, The Netherlands); sequencing by The Institute
for Genomic Research. The cDNA libraries will attempt to
capture the induction and initiation/initial growth of the
tuber in an in vitro system as described in Bachem et al.
(Plant Journal, 1996). Small microtubers develop from
axillary buds attached to stem explants when placed on a
high sucrose medium (10%). Visible morphological changes
occur synchronously at day five in the axillary buds. The
first library, cDNA (1-20) consists of axillary buds
harvested on days 1-3. This targets those genes involved
in induction of the microtubers. The following libraries,
cDNA (21-40) and cDNA (41-60), capture genes involved in
tuber initiation and outgrowth. This library is noted as
p3 in Tanksley lab notebooks."

```

ORIGIN

Query Match 15.2%; Score 449.8; DB 4; Length 618;
Best Local Similarity 83.9%; Pred. No. 5.9e-107;
Matches 521; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

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Qy      39 GACTTGTTCATCCAGGAGGAACTTGATGATCTTGTGTTTAAAGATGATGCGAAAA 98
Db      1 GACTTCTTTCATCCAAAGGAACTTGATGATCTTGTGTTTAAAGATGATGCGAAAA 60
Qy      99 GCTTCAAGACGTTTACTACATCCAGCTGTGCTAGAAAGATGCTCAGAAAGCAATT 158
Db      61 TATTTGAGAGAGGTTTCTCAATTCAGGCGCTTGAAGATGCTCAGAGAAAGCAACT 120
Qy      159 GAAGACAGAGCAATAGAAATTTGTTGAGAAATCAATGCTGCTGATATGAGGCTGA 218
Db      121 AAAGACAGAGCAATTTAAATCTGTTACAGAAATCTGATGCTGATATGAAAGTTGA 180
Qy      219 TGACATCTTGAAGCAATGTAAATCTGAGGCCAATTTAGACAGAAAGAAACAAATATGG 278
Db      181 TGACATTTATGAGCAATGTAAATCTGATGCTGATGCTGATGCTGATGCTGATGCTG 237
Qy      279 GTGTTATCATCCAAAGCTTATCATCTTGTGCTCAGATTTGGGAAAGATGAAAGAT 338
Db      238 GCGTTATCATCCAAAGCTTATCATCTTGTGCTCAGATTTGGGAAAGATGAAAGAT 297
Qy      339 TATGAGAAATAGATGATATTGACAGGAAACGAATTAATTTGATTTGATGAAAGAGC 398
Db      298 GATGAGAAATAGATGATATTGCTAGAGAAAGAAAGATTTTCAATTTGACAGAAAGAT 357
Qy      399 TATAGAGACAAAGTTGCTACACGCAACAGGTTTGTGTTGAATGAACCAAGTTTA 458
Db      358 TATAGAGACAAAGTTGCTAGACCGGAAACAGGTTTGTGTTTAACTGAACCAAGTTTA 417
Qy      459 TGAAGAGACAAAGAGAGAGAGATGAGAAATCCGATTAACAAAGTTAGCAATGC 518
Db      418 TGAAGAGAGCAAGAGAGAGATGAGAAATCCGATTAACAAAGTTAGCAATGC 477
Qy      519 CCAAACTTCCAGTCTCCCAATATCTTGATTTGGGAGGACTAGAGAAAGCACTTTGC 578
Db      478 CCAAGAGCTTTTGTGCTCCCAATATTTGATTTGGGAGGCTAGAGAAAGCACTTTGC 537
Qy      579 CCAATGCTTTCATAGATCAGAGATTAATTGAGACTTTCCATCCCAATATGATTTG 638
Db      538 CCAAGATGCTTTCATAGATCAGAGATTAATTGAGACTTTCCATCCCAATATGATTTG 597
Qy      639 TGTCTCGAAGATTTTAATGA 659
Db      598 TGTCTCGAAGATTTTAATGA 618

```


RESULT 9
LOCUS CV434731
DEFINITION 58221.1 Suspension culture Solanum tuberosum cDNA clone 58221 5',
mRNA sequence.
ACCESSION CV434731
VERSION CV434731.1 GI:52844021
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 935)
AUTHORS Plim, B., Rothwell, C., Sardana, R., Griffiths, R., Lagre, M., De
Koeyer, D., Audy, P., Goyer, C., Li, X.-O., Wang-Puski, G., and Regan, S.
Generation of ESTs from potato suspension cultures
Unpublished (2004)
TITLE JOURNAL
COMMENT The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
Email: bflim@bioatlantech.nb.ca
Seq primer: 73.
FEATURES
Source
1..935
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
/db_xref="taxon:4113"
/clone="58221"
/tissue_type="Callus-derived suspension culture"
/lab_host="X110-Gold"
/clone_id="Suspension culture"
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; supplier: Developmental series. Callus was
induced from Shepody, Clone 1756, sterile stem sections by
culture on Callus Induction Medium (CIM), comprised of MS
medium (pH 5.6) containing 10 mg/L thiamine-HCl, 0.1 mg/L
kinetin and 3 mg/L 2,4-D solidified with .8% (w/v)
phytagar. Suspensions were induced by placing callus from
the plates into 125 ml Erlenmeyer flasks with liquid CIM
(no phytagar) at a density of 10% (w/v) in volumes of
approximately 30-35 ml. Cells were subcultured weekly by
transfer to fresh media, with the density remaining at 10%
(w/v) and the volume remaining around 30 ml. Cells were
collected for RNA isolations and library construction 5
days after subculture."

ORIGIN
Query Match 14.2%; Score 421.2; DB 7; Length 935;
Best Local Similarity 85.5%; Pred. No. 2.3e-99;
Matches 518; Conservative 0; Mismatches 78; Indels 10; Gaps 4;
QY 1355 AATTATCTGAGGCTTTCTTCCAGAGATGAATGAATGCTCAACTTATTTCA 1414
DB 1 AATTATCTGAGGCTTTCTTCCAGAGATGAATGAATGCTCAACTTATTTCA 60
QY 1415 AGATGATGATCTCATTCATGATCTGGCAACATCTCTATTTTGGCAAGCAATCAACA 1474
DB 61 AGATGATGATCTCATTCATGATTTGGCTACATCTCTTTTGGCAAGCAATCAACA 120
QY 1475 GCATATCCGGAATATTTGAGAAATTTACATCATATGATGCTGCTTGGTTCACCTA 1534
DB 121 GCATATCCGGAATATTTGAGAAATTTACATCATATGATGCTGCTTGGTTCACCTA 180
QY 1535 AAGTGGATCTTCTACTCTCTTTTCCACTTGCAGAGTTTGTCTGTTGAGGGTGC 1591
DB 181 AAGTGGATCTTCTACTCTCTTTTCCACTTGCAGAGTTTGTCTGTTGAGGGTGC 240
QY 1592 TTAATCTAAGTGACATTAAGAGTTACCGCTTCTTCATTTGAGATCTTAAGTACATT 1651
DB 241 TTAATCTAAGTGACATTAAGAGTTAAGTTCATTTGAGATCTTAAGTACATT 300

QY 1652 TAAGATACCTAACTTGTCTGGCAATAGTATCTTGAGTCTTCCAAACCGATTATGCA 1711
DB 301 TAAGATACCTAACTTGTCTGGCAATC---AATTATAGACTTCCAAAGATTATGCA 357
QY 1712 AGCTTCAAAATCTGACACTTGTATCTACATGAGCTGTCACTTGTGTTGCCAA 1771
DB 358 AGCTTCAAAATCTGACACTTGTATCTACAAATATGACACCTTGTGTTGCCCTA 417
QY 1772 AAGAAACAGAACTGTGATGCTTGAATCTTTACTTGAATGTTGCATGATTTGA 1831
DB 418 AAAAAACAGAACTGTGATGCTTCCAAATCTTTACTTGAATGCTTATATTTGA 477
QY 1832 CTTGTATGCCACCAAGATAGATCTTGTGACATGCTTAAGACTTAAGTATTTGTGG 1891
DB 478 TTTGTATGCCACCAAGATAGATCTTGTGACATGCTTAAGACTTATGCTTTGTCA 537
QY 1892 TGGCAATTCAGAGAAAGTTTCACTTGTGTG-AAATTACGAACCTGAATCTTATGCG 1950
DB 538 TTGGCA---AGAGAAAGATGCTCACTTGTGTGAAGTACGAATCTGAATCTTATGCG 594
QY 1951 TCATTT 1956
DB 595 TCAGTT 600

RESULT 10
LOCUS BG593905
DEFINITION EST492583 cSTS Solanum tuberosum cDNA clone STS514 5' sequence,
mRNA sequence.
ACCESSION BG593905
VERSION BG593905.1 GI:13612045
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 668)
AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A.,
Bougri, O., Buell, C.R., Romming, C., Tanksley, S., and Baker, B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
TITLE JOURNAL
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13P-R.
FEATURES
Source
1..668
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="STS514"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/clone_id="cSTS"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."

ORIGIN
Query Match 14.0%; Score 415; DB 4; Length 668;
Best Local Similarity 87.6%; Pred. No. 9e-98;

	Matches	465;	Conservative	0;	Mismatches	65;	Indels	1;	Gaps	1
QY	426	AACAGCTTTTGTTTGAATGAAACCAAGCTTATGAAAGAGCAAAAGAAAAGACGAGAT								485
Db	127	AACATGTTTTTGTTCACTGAACAAAAGTTATGAAAGGCAAAAGAGAAATGAGAT								186
QY	486	AGTGAATACTCGATPAAACAATGTTAGCAATGCCCAACACATCCAGTCCTCCCAACT								545
Db	187	AGTGAATAATTCGATPAAACAACATTAAGATGCCCAAGACCTTTCAGTCCTCCATACT								246
QY	546	TGATATGGGGGGAAGTGAAGAAAGACATCTGGCCCAATATGCTTCATATGATCAAGAGT								605
Db	247	TGATATGGAGAGACTGAGAAAGACATCTGGCCCAATATGCTTCATATGATCGAAGAGT								306
QY	606	AATTGAGCATTTCCATCCCAAAATATGATTTGTGTCGAGAAATTTTAATGAGAAAG								665
Db	307	AATGAGCATTTTCGTCCTCCAGATATGATTTGTGTCGAGTATTTTGAATGAGAAAGA								366
QY	666	GTTGATTAAGAAATTTGTAAGATCTATTGAAAGAAAAGTCATTTGGTGCAATGACTTGGC								725
Db	367	GTTGATTAAGGCAATTTGTAAGATCTATTGAAAGAAAGGCCCTTGGATGCAATGGAATTTGGC								426
QY	726	TCCAATTCMAAAGAAGCTTCGGGACTTGTCTGAATGGAAGAAAATATTTGTCGCTTGA								785
Db	427	TCCAATTCMAAATTAAGCTTCAGGAATTTGTGAATGGAGAAAGATACCTTTCTTGGCTTGG								486
QY	786	TGATGTTTGGAAATGAAGATCAAGATTAATATGGGCTTAAGTAAACAAGCTTTGAAGTTGG								845
Db	487	TGATGTTTGGAAATGAAGATCAAGAAATATGGGATTAATTTAAAGCAAGCTTGAATGGTTGG								546
QY	846	AGCAAGTGGCGCTTCTGTTCTPAACCACTACCTGCTTGAAGAAAGTTGGATCAATTAAGG								905
Db	547	AGCTCGTGGCACTTCTGTTCTPAACCACTACCTGCTTGG - AAAGTTGGATCAATTAAGG								605
QY	906	AACATTCGAACCATATGAATTTGCAAAATTTGCTCAAGAAATTTGTTGTT								956
Db	606	AACCTTGGCAACCATATCAATGTTCAAAATATTTCTCAAGAAATATTTGTTGTT								656

RESULT	11
LOCUS	B0117360
DEFINITION	B0117360 EST662995 mixed potato tissues Solanum tuberosum cDNA clone STWDIST5' end, mRNA sequence.
ACCESSION	B0117360
VERSION	B0117360.2 GI:21918256
KEYWORDS	EST.
SOURCE	Solanum tuberosum (potato)
ORGANISM	Solanum tuberosum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheospermata; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE	1 (bases 1 to 577) Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Reestrepo,S., Griffiths,H., van der Hoeven,R., Tsai,T. and Karatnycheva,S.A. Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)
TITLE	Unpublished (2002)
JOURNAL	On Apr 17, 2002 this sequence version replaced gi:20169322.
COMMENT	

The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: T3.

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FEATURES
    source
        location/Qualifiers
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                /organism="Solanium tuberosum"
                /mol_type="mRNA"
                /cultivar="Kennebec or Binjete"
                /db_xref="taxon:4113"
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/clone="STMDS17"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/clone_id="mixed potato tissues"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and phytophthora
infestans-created libraries of scions, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

```

Query Match	14.0%	Score 414	DB 5	Length 577
Best Local Similarity	84.4%	Pred. No. 1,6e-97		
Matches 491	Conservative	0	Mismatches 85	Indels 6
			Gaps	2
QY	1404	AACATATTTCAAGATGATGATCTCATCTTCAATTCGACATCTCTAATTTTCGGCAAG	1463	
DB	2	AACATATTTCAAGATGATGATCTCATCTTCAATTCGACATCTCTAATTTTCGGCAAG	61	
QY	1464	CACATCAAGCAGCAATTCGAGAAATTTGTAAGAAATTCATACATCATATGATGTCAT	1522	
DB	62	ACCATCAAAACGCAATTCGAGAAATTTGTAAGAAATTCATACATCATATGATGTCAT	121	
QY	1524	TGGTTTTCATTAAGTGTATCTTTCTACTCTCTTCCCACTTGCAGAAATTTGTCTGTT	1583	
DB	122	TGGTTTTCGTCAGTGGAGTCTTCTACTCTCATCTCATTTTGTGTGGAGAACTTTGTCTGTT	181	
QY	1584	GAGGGTGTCTTAATCTTAAGTACATTAACCTTAAGCAGTTTACCGTCTTCCATTTGAGATCT	1643	
DB	182	GAGGGTGTCTTAATCTTGGGTTTACTTAAGAACCAATGTAACCGTCTTCCATTTGAGATCT	241	
QY	1644	AGTACATTTAAGATACCTTAACCTTGTCTGGCAATCTAGTATTTGTAAGTCTTCAAAACA	1703	
DB	242	AGTACATTTAAGATACCTTAACCTTGTCTGGCAATCTAGTATTTGTAAGTCTTCAAAACA	301	
QY	1704	GTTATGCAAGCTTCAAAATCTGACAGCTCTTGATCTTACATGCGCTGTCATTCACCTTTTGG	1763	
DB	302	GTTATGCAAGCTTCAAAATCTGACAGCTCTTGATCTTACATGCGCTGTCATTCACCTTTTGG	361	
QY	1764	TTTGGCAAAAGAAACAAGCAAACTGTGTGTCCTTGGCAATCTTTTAACTGTAAGTGTCTA	1823	
DB	362	TTTGGCAAAAGAAACAAGCAAACTGTGTGTCCTTGGCAATCTTTTAACTGTAAGTGTCTA	418	
QY	1824	TGGAATGACTTGTATGTCACCAAGAGATAGAGATCTTTGACATGCTCTTAAGACTTAAAGTGA	1883	
DB	419	TGGAATGACTTGTATGTCACCAAGAGATAGAGATCTTTGACATGCTCTTAAGACTTAAAGTGA	478	
QY	1884	ATTGTGTGTGGGAATTCAGAAAGAAAGTTGTCACTTGTGTAAATTAAGAAACCTGAATCT	1943	
DB	479	ATTGTGTGTGGGAATTCAGAAAGAAAGTTGTCACTTGTGTAAATTAAGAAACCTGAATCT	535	
QY	1944	CTATGGCTCAATGAAATCAAGCATCTTGAAGAGTGAAGAA	1985	
DB	536	CTATGGCTCAATGAAATCAAGCATCTTGAAGAGTGAAGAA	577	

RESULT 12				
AM035144				
LOCUS				
DEFINITION		631 bp	mRNA	linear EST 18-MAY-2001
	ESTJ80406 tomato callus, TATU Lycopersicon esculentum cDNA clone			
ACCESSION				
VERSION	AM035144			
KEYWORDS	AM035144.1 GI:5893900			
SOURCE	EST.			
ORGANISM	Lycopersicon esculentum (tomato)			
	Lycopersicon esculentum			
	Eumariotae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.			
REFERENCE	1 (bases 1 to 631)			
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,			
	Holt,I.E., Liang,F., Updon,J., Claven,M.B., Bowman,C.L., Ahn,S.,			
	Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and			

TITLE
JOURNAL
COMMENT

Giovannoni, J.
Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES

Source

Location/Qualifiers

1. 631
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEC32D21"
/issue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRP"
/clone_id="tomato callus, TAMU"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni laboratory; cLEC - Copyedoms of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"

ORIGIN

Query Match 13.5%; Score 402; DB 2; Length 611;
Best Local Similarity 80.9%; Pred. No. 2.4e-94;
Matches 520; Conservative 0; Mismatches 111; Indels 12; Gaps 4;

1397 CTGGCAACCTATTATTCAGATGATGATCATTCATGATCTGGCAATCTCTATTT 1456
1 CCGGAAATCTATTATTCAGATGATGATCATTCATGATCTGGCAATCTCTATTT 60

1457 CGGCAAGACATCAAGACGATATCCGAGAAATATTGAGAAATTACATACATATGA 1516
61 TGGCAAGGACATCAAGACGATATCCGAGAAATATTGAGAAATTACATACATATGA 120

1517 TGTCATGCTTCTCTAAGTGTATCTTCTACTCTCTTCCCATCTGGCAAAAGTTTG 1576
121 TGTCATGCTTCTCTAAGTGTATCTTCTACTCTCTTCCCATCTGGCAAAAGTTTG 180

1577 TCTGCTTGAAGGTGCTTAACTAAAGTGAATAACTTAAGCAATTAAGCTTCCATTG 1636
181 TCTGCTTGAAGGTGCTTAACTAAAGTGAATAACTTAAGCAATTAAGCTTCCATTG 240

1637 GAGATCTAGTACATTAAGTAACTTGTCTGGCAATACCTAGTATTCGTAGTCTTC 1696
241 GAGATCTAGTACATTAAGTAACTTGTCTGGCAATACCTAGTATTCGTAGTCTTC 297

1697 CAACCACTATGCAAGCTTCAAAATCTGCAAGCTCTTGAATCTAAGGCTGCTATTC 1756
298 CAGAGAGGTATGCAAGCTTCAAAATCTGCAAGCTCTTGAATCTAAGGCTGCTATTC 357

1757 TTGTGTTTGGCAAAAGCAAACTTGGTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 1816
358 TTGTGTTTGGCAAAAGCAAACTTGGTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 417

1817 GTTGCTATGATGATCTGTATGCAAGCAAGATAGATCTTGTGATGATGATGATG 1876
418 ---GCTGCTATGATCTGTATGCAAGCAAGATAGATCTTGTGATGATGATGATG 474

1877 TAACTAGATTTGTGTGGGAAATCAGAAAGAAAGTTGCACTTGTGATGATGATG 1936
475 TAGGTTTCTTATTTGTGGGAA---GCAAGAAAGGCTCATCACTCGGTGAACGAA 531

1937 TGAATCTCTAAGGCTCAATGAAATCAGCACTTGAAGAGTGAAGAAATATATGATG 1996
532 TAAATCTTTGGGCTCAATTTCAATGCAACCTTTGAGAGTGAAGATATATCGGATG 591

1997 CAAAGAGCAATTTATCTGCAAAAGAAATCTGATCTTT 2039

Db 592 C---CGAAGCAATTTATCTGCAAAAGCAATCTGCAATCTTT 631

RESULT 13
B0511700
LOCUS
DEFINITION
B0511700 598 bp mRNA linear EST 07-MAR-2003
EST019115 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STMHT23
5' end, mRNA sequence.

ACCESSION
B0511700
VERSION
B0511700.2 GI:21927352
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
Buell, C.R., Hart, A., Baker, B., Tankley, S., Fry, W., Smart, C.,
1 (bases 1 to 598)
Reestrop, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.

TITLE
JOURNAL
COMMENT
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Jun 10, 2002 this sequence version replaced gi:21370569.
Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
<http://genome.arizona.edu/orders/>
Seq primer: T3.

FEATURES
Source
Location/Qualifiers

1. 598
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binje"
/db_xref="taxon:4113"
/clone="STMHT23"
/issue_type="mixed tissues"
/lab_host="SOLR"
/clone_id="generation of a set of potato cDNA clones for
microarray analyses mixed potato tissues"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

ORIGIN

Query Match 13.5%; Score 399.8; DB 5; Length 598;
Best Local Similarity 81.4%; Pred. No. 8.8e-94;
Matches 489; Conservative 0; Mismatches 107; Indels 5; Gaps 2;

76 GGTTTAAGATGATGTTGCAAAAGCTTCAAGCAAGTTTCTACATCAAGCTGTGCTA 135
1 GGTTTAAGATGATGTTGCAAAAGCTTCAAGCAAGTTTCTACATCAAGCTGTGCTT 60

136 GAGATCTCAGAGGAAGCAATTTGAGACAGGCAATAGAAATTTGTTGCAAAATC 195
61 GAGATCTCAGAGGAAGCAATTTGAGACAGGCAATTTGAGACAGGCAATTTGTTGCAAAATC 120

196 AATGCTGCTGATTTGAGGCTGATGATCAATCTTGGACGAATGTAATTAAGGCTCA 255
121 AATGCTGCTGATTTGAGGCTGATGATCAATCTTGGATTAATTAAGGCTCAAGGCTCA 177

256 AGACAGAAAGAAACAATATGAGTGTATCATCAAGCT--TATCATTTTGTGACA 313
178 CGATTTCTCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 237

314 AGATTTGGAAGGATGAAAGATTTATGAGAAATCTAGATGATGATGATGATGATGATG 373

Db 238 AGTCGGGAAAAGATGACCAAGTGATGACAAAGCTAAATGCAATTGCTGAGAAAGA 297
 Qy 374 TTAAGTTTCAATTGATGAAAGCATATGAGAGACAACTTCTACGCCCAACAGTT 433
 Db 238 AGAATTTTCAATTGACGAAAATATTTATACAGACCAATCTTTAGATAGAAACAGTT 357
 Qy 434 TTGTTTTGAATGACACCAAGTTTATGAAAGAGCAAAAGAAAGCAGATAGTAA 493
 Db 358 CTGTTTATTTGATACCAAGATATGAGAGGACAAAGAGAAATGATATGTA 417
 Qy 434 TCTGATTAACAAATGTTAGCAATGCCCAACATCTTCACTCTCCCAATCTTGATG 553
 Db 418 TCCATATTAACAAATGTTGATGATCCCAAAATATGCACTCTCCCAATCTTGATG 477
 Qy 554 GGGGACTGGAAGACGACTGTCGCCAAATGCTTTTCAATGATGAGAGATTTGAGC 613
 Db 478 GGGGACTGGAAGACGACTGTCGCCCAATGCTTTCAATGATGAGAGATTTGAGC 537
 Qy 614 ATTTCATCCCAAAATATGATTTGTTCTCGAAGATTTTATGAGAAAGTTGATTA 673
 Db 538 ATTTCATCCCAAAATATGATTTGTTCTCGAAGATTTTATGAGAAAGTTGATTA 597
 Qy 674 A 674
 Db 598 A 598

RESULT 14

LOCUS AM907068 592 bp mRNA linear EST 10-MAR-2003
 DEFINITION EST343100 potato stolon, Cornell University Solanum tuberosum cDNA
 clone cSTASM3, mRNA sequence.
 ACCESSION AM907068
 VERSION AM907068.1 GI:8071187
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 592)
 van der Hoeven, R., Bezzerides, J., Bachem, C., Horvath, B., Visser, R.,
 Holt, I.E., Liang, F., Hansen, T.S., Utechtack, T., Bowman, C.L.,
 Doan, B., Bougri, O., Buehl, C.R., Roming, C.M., Tankley, S.D. and
 Baker, B.
 Generation of ESTs from potato swelling stolons
 Unpublished (1999)
 Contact: Robin Buehl
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 This clone can be obtained from the University of Arizona Genomics
 Institute. Orders can be made through URL:
 http://genome.arizona.edu/orders/
 Location/Qualifiers

FEATURES

source
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /culivar="Bintje"
 /db_xref="taxon:4113"
 /clone="cSTASM3"
 /tissue_type="axillary buds of stem explants, swelling stolons"
 /dev_stage="1 to 3 days"
 /lab_host="SOLR"
 /clone_lib="potato stolon, Cornell University"
 /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; RNA was supplied by Christian Bachem & Beatrix Horvath (Laboratory of Plant Breeding, Dept. of Plant Sciences, Wageningen University, The Netherlands). Total RNA was isolated from developing axillary buds of potato nodal stem cuttings cultured on medium for the introduction of tuber formation as described in Bachem et

ORIGIN

Query Match 13.0%; Score 385; DB 2; Length 592;
 Best Local Similarity 89.2%; Pred. No. 7e-90;
 Matches 415; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

al. (Plant Journal 1996). Tissue samples were taken of stages corresponding to growing stolons and the early stages of tuber formation."

Qy 733 CAAAAGAGCTTGGGAGCTTGCTGAATGAAAAAATATTTGCTGCTTATGATGATGTT 792
 Db 128 CAGAAAGAGCTTGCAGCTTGTTGAATGAAAAAGATTACTTGCTTGTATGATGATGTT 187
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 Qy 853 GGGCCTTCTGTTCTTAACCACTACGCTTGAAAAAGTTGGATCAATTAATGGAACATTTG 912
 Db 248 GGTGCTTCTGTTCTTAACCTACCTGCTTGAAGAGTTGATCAATTAATGGAACATTTG 307
 Qy 913 CAACCATATGAATTTGCAATTTGCTCAAGAAAGATTTGTTGTTTCAATCAAGT 972
 Db 308 CAACCATATGAATTTGCAATTTGCTCAAGAAAGATTTGTTGTTTCAATCAAGT 367
 Qy 973 GCATTTGGGACCAAGAAATTAATCTTAATCTTGCTATCGGAAGAGATTTGTTG 1032
 Db 368 GCATTTGACATCAAGAAATTAATCTTAATCTTGCTATCGGAAGAGATTTGTTG 427
 Qy 1033 AAAAAATGTTGGTGTGTCCTTACAGCTAAACTTTGAGAGTATTTGGCTTTAAG 1092
 Db 428 AAAAAATGTTGGTGTGTCCTTACAGCTAAACTTTGAGAGTATTTGGCTTTAAG 487
 Qy 1093 AGAGAAAGAAACAGTGGGAACATGTAGAGATGTAATTTGGAATTCCTCAAGAA 1152
 Db 488 AGAGAAAGAAAGAAATGGAACATGTAGAGATGTAATTTGGAATTCCTCAAGAT 547
 Qy 1153 GAAAGTTCTAATTCGCTGCGCTGAGACTTAAGTACCATCACTT 1197
 Db 548 GAAATGCTTATTTTGCTGCTGCTTAAGCTTAATATCATCTT 592

RESULT 15

LOCUS CV496683 668 bp mRNA linear EST 04-OCT-2004
 DEFINITION 60822.1 Mixed Leaf Solanum tuberosum cDNA clone 60822 5', mRNA
 sequence.
 ACCESSION CV496683
 VERSION CV496683.1 GI:53779040
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 668)
 Keyser, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Prunki, G. and Regan, S.
 Generation of ESTs from a normalized developing leaf library
 Unpublished (2004)
 Contact: Barry Filim
 The Canadian Potato Genome Project - BioAtlantech
 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
 Email: bfilim@bioatlantech.nb.ca
 Seq primer: T3.
 Location/Qualifiers

FEATURES

source
 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /culivar="Shepody"
 /db_xref="taxon:4113"
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/lab host="Xla0-Gold"
 /clone_lib="Mixed leaf"
 /note="vector: plusacript II SK(+) XR; Site_1: EcoRI;
 Site_2: XhoI; supplier: Developmental series. plants from
 pathogen-free Solanum tuberosum var. Shepody, clone 1756,
 nuclear stock were grown in a greenhouse under natural
 conditions. Emerging, expanding and mature leaves were
 harvested along the length of the plant and pooled. RNA
 was isolated and used for library construction. A
 normalized library was constructed following a modified
 protocol of Bonaldo et al. (1996. Genome Research 6:
 951-806)."

ORIGIN

[illegible]

Search completed: April 16, 2005, 20:33:49
Job time : 8504 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 20:42:26 ; Search time 9229 Seconds
(without alignments)
5187.318 Million cell updates/sec

Title: US-10-647-268-2
5127
1 MAEAFGLVLDNLTCFIQGE.....EKIGEDWYKIAHPRVFIY 988

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=genbml -QMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genbml:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3774	73.6	79178	8	AY303170 Solanum b
2	3766.5	73.5	2913	6	AX814112 Sequence
3	3766.5	73.5	2913	6	AX816331 Sequence
4	3648	71.2	3260	6	AX814115 Sequence

5	3648	71.2	3260	6	AX816334
6	3648	71.2	3260	8	AY426260
7	3642	71.0	163635	8	AY303171
8	3638.5	71.0	3592	6	AX814113
9	3638.5	71.0	3592	6	AX816332
10	3638.5	71.0	5191	6	AX816333
11	3638.5	71.0	6824	6	AX136128
12	3638.5	71.0	7349	6	AX814114
13	3638.5	71.0	7349	6	AX426259
14	3606.5	70.3	3971	6	AX814116
15	3606.5	70.3	3971	6	AX816335
16	3606.5	70.3	3971	8	AY426261
17	3604.5	70.3	3641	8	AY426266
18	3594	70.1	3344	8	AY426263
19	3543	69.1	3196	8	AY426263
20	3518.5	68.6	3689	8	AY426264
21	3420.5	66.7	163635	8	AY303171
22	3400	66.3	3899	6	AX814117
23	3400	66.3	3899	6	AX816336
24	3400	66.3	3899	6	AY426262
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27	2020.5	39.4	118130	2	AC148359
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30	1993.5	38.9	124758	2	AC133864
31	1987.5	38.8	114098	8	AC144459
32	1977.5	38.6	148813	2	AC135162
33	1961	38.2	65807	2	AC146556
34	1951	38.1	122167	2	AC146806
35	1945.5	37.9	120197	2	AC124216
36	1938	37.8	124857	2	AC134049
37	1936	37.8	133198	2	AC137553
38	1916.5	37.4	120576	8	AC136141
39	1903	37.1	114576	8	AP004490
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42	1839.5	35.9	122058	8	AC135312
43	1726.5	33.7	125127	2	AC146971
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ALIGNMENTS

RESULT 1
AY303170/c
LOCUS
DEFINITION Solanum bulbocastanum chromosome 8 clone CB3A14, complete sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS
1 (bases 1 to 79178)
Haberlach,G.T., Liu,J., Kuang,H., Austin-Phillips,S., Buell,C.R.,
Song,J., Bradeen,J.M., Naess,S.K., Raasch,J.A., Wielgus,S.M.,
Heigeson,J.P., and Jiang,J.
Gene RB cloned from Solanum bulbocastanum confers broad spectrum
resistance to potato late blight
Proc. Natl. Acad. Sci. U.S.A. 100 (16), 9128-9133 (2003)
JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 79178)
Song,J., Bradeen,J.M., Naess,S.K., Raasch,J.A., Wielgus,S.M.,
Haberlach,G.T., Kuang,H., Austin-Phillips,S., Heigeson,J.P.,
Liu,J., Tallon,L.J., Zaborosky,J., Buell,C.R., and Jiang,J.
Direct Submission
Submitted (21-MAY-2003) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
COMMENT
Address all correspondence to: rbuell@tigr.org Clone CB3A14 is

mRNA

CDS

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Pred. No.: 1,286-286 Length: 79178
Score: 3774.00 Matches: 778
Percent Similarity: 70.07% Conservative: 79
Best Local Similarity: 63.61% Mismatches: 127
Query Match: 73.61% Indels: 239
DB: 8 Gaps: 7

US-10-647-268-2 (1-988) x AV303170 (1-79178)

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DB 39719 AAAATCTATGGCTTCAGAGAAATCCATCTCCAGATGATGAATCACTAGATTAAGAA 39660
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DEFINITION Sequence 35 from Patent EP1334979.
ACCESSION AX814112

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ORGANISM	Solanum bulbocastanum	
REFERENCE	van der Vossen, E.A. and Allieff, J.J.	
AUTHORS	Gene conferring resistance to phytophthora infestans (late-blight)	
TITLE	In solanaceae	
JOURNAL	Patent: EP 1334979-A 35 13-AUG-2003;	
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 Solanum bulbocastanum
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE
 1 Allefs, J. J. and van der Vossen, E. A.
 AUTHORS
 TITLE Gene conferring resistance to phytophthora infestans (late-blight)
 in solanaceae
 JOURNAL Patent: WO 03066675-A 48 14-AUG-2003;
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LOCUS Sequence 38 from Patent EP1334979.
ACCESSION AX814115
VERSION AX814115.1 GI:39103417
KEYWORDS
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ORGANISM
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Solanum bulbocastanum
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS
TITLE
1 van der Vossen, E.A. and Allefs, J.J.
Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
JOURNAL
Patent: EP 1334979-A 38 13-AUG-2003;
KweeK-en Researchbedrijf Agrico B.V. (NL)
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LOCUS AX816334
DEFINITION Sequence 51 from Patent WO03066675.

ACCESSION AX816334
VERSION AX816334.1 GI:39646825
KEYWORDS
SOURCE
ORGANISM Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS 1 Allefs,J.J. and van der Vossen,E.A.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
JOURNAL Patent: WO 0306675-A 51 14-AUG-2003;
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Pred. No.: 1.47e-278 Length: 3260
Score: 3648.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
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ORIGIN

Alignment Scores:
Pred. No.: 1,47e-278 Length: 3260
Score: 3648.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
Query Match: 71.15% Indels: 114
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similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNA are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arjan Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

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RESULT 8

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AX814113
LOCUS AX814113 3592 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 36 from Patent EP1334979.
ACCESSION AX814113
VERSION AX814113.1 GI:39103415
KEYWORDS
SOURCE
ORGANISM

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Solanium bulbocastanum
Solanium bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanium.

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REFERENCE
1 van der Vossen, E.A. and Allefs, J.J.
Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
Patent: EP 1334979-A 36 13-AUG-2003;
Kwee- en Researchbedrijf Agrico B.V. (NL)
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/db_xref="taxon:147425"
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ALIGNMENT Scores:

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Pred. No.: 9.5e-278 Length: 3592
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: 6 Gaps: 9

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US-10-647-268-2 (1-988) x AX814113 (1-3592)

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QY 21 LeuGlyLeuIleLeuGlyPheLysAspGlnPheGlnIleuLysLeuGlnIleThrPheThr 40
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 QY 61 TTPLeuGlnLysLeuAsnAlaAlaAlaTyrGlnLysAspAlaLeuAspGlnLys 80
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 QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlnLysLeuAspValIle 120
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 DB 1858 GCTTAGTTACCAATCACTTCACTTAATTTGAACAATGCTTGTGCGATTTGGGGTGT 1917
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RESULT 9
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DEFINITION Sequence 49 from Patent WO03066675.
ACCESSION AX816332
VERSION AX816332.1 GI:39646823
KEYWORDS
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ORGANISM Solanum bulbocastanum
Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyle;
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE
1 Allefs,J.J. and van der Vossen,E.A.
AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
in solanaceae
TITLE Patent: WO 03066675-A 49 14-AUG-2003;
JOURNAL Kweek- en Researchbedrijf Agrico B.V. (NL)
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428-1106) #"


ORIGIN



Alignment Scores:



| Pred. No.:             | Length: | Matches: | Score:  |
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| 68.03%                 | 78      | 129      | 61.65%  |
| Best Local Similarity: | 70.97%  | 262      |         |
| Query Match:           | Gaps:   | 9        |         |



US-10-647-268-2 (1-988) x AX816332 (1-3592)



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 |||
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 |||
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Db 2278 AGGTGATTCGACATTTAATAAGATTAACATCTTCAATGAGATTAATTAATTAATTA 2337
Qy 553 rIleuAsnIleuSerIySbIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 573
Db 2338 CTTGAACTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2394

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QY 573 nasnlenglnthleuaspleuhisglycysHisSerleucysCysleuprolysgluTh 593
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QY 593 tSerlyseuGlySerleuArgasnleuLeuaspGlyCysTyrglyLeuThCyme 613
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QY 613 tProProArgllleglySerleuThCysleuTySthleuSerArgpHevalValglyl 633
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QY 633 eGlnlyseSerCysGlnleuGlyGluLeuArgasnleuLeuTyrglySerlllegl 653
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QY 693 rGlnSerGlyuArgVallyGluAlleuGluAlaenlySproHisSerAsnleuThrCysle 713
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QY 713 uThrllleArgglyPheArgglylleArgleuProAspTrpMetAsnHisSerValleuLy 733
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QY 733 sasValValSerlllegluilleSerCysLyAsnAspSerCysleuProProPheGly 753
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QY 753 yGluLeuProCysleuLySerleuGluLeuThrArgglySerAlaGluValglyTyra 773
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QY 773 lAsp-----SerglyPheProThrArgArgArgPheProSerle 786
Db 2989 TGAAGAAAGTGATATTGATGTTTCATTTCTGAGATCCCAAGAAATTAAGTTTCATCTT 3048
QY 786 uArgLyseuasnleuArgGluPheGlyAsnleuLyseGlyleuLeuLySgGluGly 806
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Db 3161 -ACCTTTCT----- 3169
QY 846 eSerSerllleSerAsnleuMetAlaenThrSerleuGlnlleArgTyraenlySgLuAs 866
Db 3170 -----TCATATCTTAGGAGCTCTTACTTCCCTCAGAAATTTGCTATAATTAAGTAGC 3219
QY 866 palAserleuProGluGluMetPheLySerleuAlaasnleuLyTyrlleuAsnilleSe 886
Db 3220 TACTTCAATTCACAAAGAGATGTTCAAAAACCTTGCAAAATCTCAAAATCTTGACAATCTC 3279
QY 886 rPheTyrlPheasnleuLySgLeuProThrSerleuAlaSerleuAsnAlaenlySgH 906
Db 3280 TCGGTGCAATATATCTCAAGAGCTGCTACCAAGCTTGCTAGTCTGATGCTTTGAAAG 3339
QY 906 sLeuGlnlleHisSerCysTyrlAlaenGluSerleuProGlnGluVallySgLyLe 926
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QY 946 yLeuGlnHisleuThralaenThrAsnleuSerValGluPheCysProThrleuVally 966
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QY 966 sArgCysGlnlyleGlylleGlyGluAspTrpTyrlleAlaHisllleProArgValPh 986
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QY 986 eilleTyrr 988
Db 3580 TATATAT 3586

RESULT 10
AX816333 AX816333 5191 bp DNA linear PAT 09-DEC-2003
LOCUS Sequence 50 from Patent WO03066675.
DEFINITION AX816333
ACCESSION AX816333
VERSION AX816333.1 GI:39646824
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Allefs,J.J. and van der Vossen,E.A.
AUTHORS Gene conferring resistance to phytophthora infestans (late-blight)
TITLE in solanaceae
JOURNAL Patent: WO 03066675-A 50 14-AUG-2003;
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location/Qualifiers
source
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4 present in pRC2-b1b"

ORIGIN
Alignment Scores:
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Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
Gaps: 9
US-10-647-268-2 (1-988) x AX816333 (1-5191)

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QY 21 leuGlyleuThrleuGlyPheLyAspGluPheGluLySleuGlnSerThrPheThr 40
Db 1251 CTGTATTCGCTTTTCGTTTTCAGATGATGATTCCAAAAGCTTTCACAGCATGTTTTCACA 1310
QY 41 lileGlnAlaValleuGluAspAlaGlnlySlyGlnleuLySAspLySAspAlaileGluAsn 60
Db 1311 ATTCAAGCGCTCTTGAAGATGCTCAGAGAACCACTCAACAAGACCTTAGAATAAT 1370
QY 61 TrpLeuGlnlySleuAsnAlaAlaAlaTyrgluAlaAspAspilleleuAspGluCyslys 80
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QY 81 ThrGluAlaProilleArgGlnlySlyAsnLySAspLySAspLySAspLySAspLySAsp 100
Db 1431 ACCAAGGCC--ACMAATTCCTCCAGTCTGAATATAGCGCGTTATCATCTCAAGGTTATC 1487
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Db 1548 GCTGAGAGAAAGAAAGATTTCATTTCGACGAAATAATTGTAGAGACAAAGCTGTAGA 1607
Oy 141 ArgInthrIyGIY----- 144
Db 1608 CCGGAAACAGGACTCATCTTAATAGATTACAAACAACCTAAGTTATATTATTTT 1667
Oy 144 ----- 144
Db 1668 TGGCAATTATCAAAATTCAGAAAAGGTTAAATATCATGATCTATGTAAATAGTGA 1727
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Db 2208 TATATGTCGAGAAATATCTCTATTTTCTGTGTCTCTAATAGATTGAATGAATA 2267
Oy 145 -----Phe-ValIeuaIngluProIngluValIyGI 154
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Db 2688 TAAATTAAGACACTTGAAGGTTGGAGCAAGGTGCTCTGTGTTCACCACTACTCG 2747
Oy 293 gIeugIuIy 313
Db 2748 TCTTGAAGAGGTTGATCAATATATGAGAAACATTCACCAATATGATCTGATCTGTC 2807
Oy 313 rGIIngluAspCyIrePheIeupIeuaIngluValIyIyIyIyIyIyIyIyIyIyIyIyIy 333
Db 2808 TCAAGAAAGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2867
Oy 333 nIeuaIngluValIy 353
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Oy 373 IArGIAspIeugIuIy 393
Db 2988 GAGAGACATCCGATTTGGAAATTTGCTCAAGATGAAATTTCTTCTGCTGCTGCTGAG 3047
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Db 3048 GCTTATACCATCAACTTCACTGATTTGAACAATGCTTTGCGATGTGCGGTGT 3107
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Db 3228 ATACTGAGCTCTTTTCCAGAGATTTGAAGTTAAAGATGTAATTTCAAGAT 3287
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Oy 493 nIleuIy 513
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Oy 513 IValIy 533
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Oy 533 uSerAspIleIy 553
Db 3468 AGTGATTCGACATTTAATAATGATTCATTTCCATGAGATCATGATCAATTAAGATA 3527
Oy 553 rIeuaIngluIy 573
Db 3528 CTTAAGCTGTATGCG---AGTGGCATGCGTATGTTCCAAAGCAATATCAAGCTTCA 3584
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ORIGIN

Alignment Scores:
Pred. No.: 2.3e-277 Length: 6824
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: 8 Gaps: 9

US-10-647-268-2 (1-988) x AY336128 (1-6824)

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DB 61 CTGTATTTGCTTTTCGCTTTCAGATGATGCTTCCAAAGCTTTCAGAGATGTTTCTCA 120
QY 41 IIeGlnAValLeuGlnAaspAaGlnLyLySerGlnLeuLyAaspLyAaIIeGlnAa 60
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DB 241 ACCAAGGCC---ACAAGATTCTCCACGCTGATGATGCGCTTATCTCAAGGATTTC 297
QY 101 ThrPheAargHISLySIIeGlyLyAaHISLySIIeMetGlnLyAaspValIIe 120
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QY 121 AIIaAaGlnAaGIIeLySPheHISLeuAaspGluAargThrIIeGlnAaGlnAIIaThr 140
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QY 141 AargGlnHISLySIIe----- 144
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QY 144 ----- 144
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QY 144 ----- 144
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Db      2038 ATACTGAGGCTCTTTTCCAAAGAGATTGAAGTTAAAGATGATAAACTTATTTCAAGAT 2097
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Qy      613 tProProArgIleGlySerLeuThrCysLeuIleThrIleuSerArgPheValIleGlyI1 633
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Qy      633 eGlnIysIysSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrlGlySerIleG1 653
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Db      2749 TGAATCGAAGAAAGTTAAAGTCTGAAGCCCTCAACACATCTCAATCTGACTTCTTT 2808
Qy      713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValIleuIy 733
Db      2809 AAAAATCATATGCTTCAGAGAAATCCATCTCCACAGAGGATGATCACTCAGATTTGAA 2868
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Qy      786 uArgIysLeuAsnIleArgGluPheGlyAsnLeuIysGlyIleuLeuIysGlyGluIyG1 806
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Qy      806 uGluGlnCysProValIleuGluGluIleGluIleIleCysCysProMetPheValIlePr 826
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Qy      826 oThrLeuSerSerValIysIysLeuValIleSerGlyAspIysSerAspAlaIleGlyPh 846
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Qy      966 sArgCysGluIysGlyIleGlyGluAspTrpTyrlIysIleAlaHisIleProArgValPh 986
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RESULT 12

AX814114 LOCUS 7349 bp DNA linear PAT 05-DEC-2003

AX814114 DEFINITION Sequence 37 from Patent EP1334979.

AX814114 ACCESSION

AX814114.1 GI:39103416

ORGANISM Solanum bulbocastanum

Solanum bulbocastanum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1

AUTHORS van der Vossen, E. A. and Allefs, J. J.

TITLE Gene conferring resistance to phytophthora infestans (late-blight) in solanaceae

JOURNAL Patent: EP 1334979-A 37 13-AUG-2003; Kweek-en Researchbedrijf Agrico B.V. (NL)

FEATURES

source 1..7349

/organism="Solanum bulbocastanum"

/mol_type="unassigned DNA"

/db_xref="taxon:147425"

ORIGIN

/note="BAC SPB4-Genomic Fragment"

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Pred. No.:	3638.50	Matches:	754
Percent Similarity:	68.03%	Conservative:	78
Best Local Similarity:	70.97%	Mismatches:	129
Query Match:	6	Indels:	262
DB:	6	Gaps:	9

US-10-647-268-2 (1-988) x AX814114 (1-7349)

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DB      2708 CTTGTAATGCTTTTCGTTTCGTTTCGAAGTGAATTCCTCAAGGCTTTCTCA 2767
QY      41  IleGlnIleValIleuPheLeuApeLeuGlnIlySerGlnLeuIlyApeIlyAlaIleGlnSer
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QY      61  TrpLeuGlnIlyLeuApeAlaIleAlaIleTyrgluIleApeApeIleLeuApeGluCysIlyS
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QY     214  IserGluApePheApeGlnIlyIlyApeGluIleIlyGluIleValIleGluSerIleGluGlu
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ACCESSION AY426259
VERSION AY426259.1 GI:39636704
KEYWORDS Solanum bulbocastanum
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 7349)
Van Der Vossen,E., Slikema,A., Hekkert Bt,B.L., Gros,J.,
Stevens,P., Muskens,M., Mouters,D., Pereira,A., Slikema,W. and
Allefs,S.
An ancient R gene from the wild potato species Solanum
bulbocastanum confers broad-spectrum resistance to Phytophthora
infestans in cultivated potato and tomato
Plant J. 36 (6), 867-882 (2003)
14675451
2 (bases 1 to 7349)
van der Vossen,E. and Allefs,S.
Direct Submission
Submitted (30-SEP-2003) Bioscience, Plant Research International,
Droevendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
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ORIGIN

Alignment Scores:

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Best Local Similarity: 61.65% Mismatches: 129  
Query Match: 70.97% Indels: 262  
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US-10-647-268-2 (1-988) x AY426259 (1-7349)

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AX814116
LOCUS AX814116 3971 bp DNA linear PAT 05-DEC-2003

DEFINITION Sequence 39 from Patent EP1334979.
ACCESSION AX814116
VERSION AX814116.1 GI:39103418
KEYWORDS
SOURCE Solanum bulbocastanum
ORGANISM Solanum bulbocastanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE
AUTHORS van der Vossen, E.A. and Alléle, J.J.
TITLE Gene conferring resistance to phytophthora infestans (late-blight)
in Solanaceae
JOURNAL Patent: EP 1334979-A 39 13-AUG-2003;
Kweek-en Researchbedrijf Agrico B.V. (NL)
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Best Local Similarity: 57.24% Mismatches: 137
Query Match: 70.34% Indels: 357
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 Db 2637 AACCTAATACAAATACCATCTTCCATGGAGATCTAATTAATTAAGATACCTGACCTTG 2696
 QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGln 576
 |||||
 Db 2697 TCTGGCAATTTTGAATTCGTAATCTTCCAAAGAGATTATGACAGGCTTCAAAATCTTCAG 2756
 QY 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysSerLeuProLysGluThrSerLysLeu 596
 |||||
 Db 2757 ACTTTATATCTACTATTTCGACTCTTCTTGTGTTGCAAAACAAACAAAGTAACCTT 2816
 QY 597 GlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArg 616
 |||||
 Db 2817 GGTAGTCTCCGAATCTTTTACTTGATGGCTGT---TCATTTGACGTCAACGCCAACAGG 2873
 QY 617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValIleGluIleGlnLys 636
 |||||
 Db 2874 ATAGGATTTGATGACATGCTTAAGTCTTAAGTTCCTTGTATGTGC---AAGAGAAA 2930
 QY 637 SerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHis 656
 |||||
 Db 2931 GGTTATCACTTGGTGAACCTTAACAAACCTAATCTCATGGCTCAATTTCAATCAACAAA 2990
 QY 657 LeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsn 676
 |||||
 Db 2991 CTTCAGCAGATGAAAGAAAGATAGCATGCAAAAGAGCTAATTTATCTGCTTAAGCAAT 3050
 QY 677 LeuHisSerLeuSerMetLysTrpAspAspGluArgProArgIleTyrGluSerGlu 696
 |||||
 Db 3051 CTGCACCTTTTATGCTGAGACTTGGACCTTGAAGAAACATGAA---TAGATTC--- 3104
 QY 697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArg 716
 |||||
 Db 3105 -----GAAGTTCTTGAAGCCCTCAAAACCACTCCCAATCTGAATATTAGAATCAAT 3158
 QY 717 GlyPheArgGlyIleArgLeuProArgTrpMetAsnHisSerValIleLysAsnValVal 736
 |||||
 Db 3159 GGCTTCGAGAGAAATCCGTCCTCCAGATGGATGAATCAACATTTTGAAGAAATGTGTC 3218
 QY 737 SerIleGluIleLeuSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuPro 756
 |||||
 Db 3219 TCTATTGAATTAGAGTGTGAAAACGTCTCATGCTTACCACTTGGTGGAGCTGCT 3278
 QY 757 CysLeuLysSerLeuGluLeuTrpArgGlySerAlaGluValGluTyrVal---AspSer 775
 |||||
 Db 3279 TGTCTAGAAAGTCTAAGATTACACACCGGGGTGAGAGATGTGAGATGTTGAAGATTAAT 3338
 QY 776 GlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArgGluPheGly 795
 |||||
 Db 3339 GTTCATCTC-----GGAAGGTTCCATCTTGAAGAACTGTATATAGGACCTTTAGT 3392
 QY 796 AsnLeuLysGlyLeuLeuLysLysGluGluGluGluCysProValIleGluGluIle 815
 |||||
 Db 3393 AACTTAAGAGATTCCTGAAAAAGAAAGAAAGAAACAAATCCCTGTGCTGAAGAGATG 3452
 QY 816 GluIleLysCysProMetPheValIleProThrLeuSerSerValLysLysLeuVal 835
 |||||
 Db 3453 ACATTTTACTGAGGCCCTAATGTTTGAATCCCAACCTTCTCTGCTCAAGACATTAAGAA 3512
 QY 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
 |||||
 Db 3513 GTTATTGCG-----ACAGATGCAACAGTTTGAAGGTCCATATCTTAATCTTGAAGGCTCTT 3566
 QY 856 ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluGluMetPheLys 875
 |||||
 Db 3567 ACTTCCCTTGACATTAGCAATTAACGTAGAAGCTACTTCACTCCCAAGAAAGATGTTCAAA 3626
 QY 876 SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895

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Db      3627 AGCTTGCAGAAATCTCAAAATTAATCTTTCTTTAGGAATCTCAAGAGTTGCCT 3686
Qy      896 ThrsSerLeuAlaSerLeuAsnAlaLeuIysHsLeuGluIleHisSerCysTyrAlaLeu 915
Db      3687 ACCAGCCTGGCTAGTCTCAATGCTTGAAGAAGTCTCAAAATTTGAATTTGTAAAGCAGCTA 3746
Qy      916 GluSerLeuProGluGluGlyValIysGlyLeuIleSerLeuThrGlnLeuSerIleThr 935
Db      3747 GAGAGTCTCCAGAGAGAGAGGGGTGAAGCTTTAACTTCACTCACCGAGTTGTCTCAGT 3806
Qy      936 TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnHisLeuThrAlaLeuThrAsn 955
Db      3807 AACTGTATGATGCTAAATGTTTACCGAGGGGATTCAGACACTTAACAGCCCTCACAAC 3866
Qy      956 LeuSerValGluPheCysProThrLeuAlaIysArgCysGluIysGlyIleGlyGluAsp 975
Db      3867 TTAAACAATTACTCAATGCTCAATAGTATTCAAGCGGTGTGAGAGAGGAATAGAGAAAGAC 3926
Qy      976 TrpTyrIysIleAlaHisIleProArgValPheIleTyr 988
Db      3927 TGGCAAAATTTGCTCAGATTCCATATTGACTCTATAT 3965
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Search completed: April 17, 2005, 03:01:42
Job time : 9559 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 20:33:57 ; Search time 1086 Seconds
(without alignments)
5385.547 Million cell updates/sec

Title: US-10-647-268-2
Perfect score: 5127
Sequence: 1 MAEAFQLVDLNLTCFIQGE.....EKIGEDMYKIAHPRVFIY 988

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Rgapop 6.0, Rgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 segs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlp
-O=/cgn2_1/USPTO_spool_p/US10647266/runat_15042005_154719_26465/app_query.fasta.1.1159
-DB=N_Geneseq_16Dec04 -QMT=faetap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPTCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdl
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=plc -NOEM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10647268_@CGN_1_1_708 @runat_15042005_154719_26465 -NCPUB=6 -ICPU=3
-NO MMAP -LARGEQUERRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5127	100.0	3193	12	ADK98516
2	5028.5	98.1	3595	12	ADK98518
3	5028.5	98.1	5028	12	ADK98524
4	4475	87.3	3347	12	ADK98520
5	3766.5	73.5	2913	10	ADK17759

6	3766.5	73.5	2913	12	ADH51531	Adh51531 S bulboca
7	3648	71.2	3260	10	ADP17762	Adp17762 S bulboca
8	3648	71.2	3260	12	ADH51534	Adh51534 S bulboca
9	3638.5	71.0	3592	10	ADP17760	Adp17760 Solanum b
10	3638.5	71.0	3592	12	ADH51532	Adh51532 S bulboca
11	3638.5	71.0	5191	12	ADH51533	Adh51533 S bulboca
12	3638.5	70.3	7349	10	ADP17761	Adp17761 Solanum b
13	3606.5	70.3	3971	10	ADP17763	Adp17763 S bulboca
14	3606.5	70.3	3971	12	ADH51535	Adh51535 S bulboca
15	3400	66.3	3899	10	ADP17764	Adp17764 S bulboca
16	3400	66.3	3899	12	ADH51536	Adh51536 S bulboca
17	3342	65.2	3222	12	ADK98522	Adk98522 S bulboca
18	1346.5	26.3	3879	8	ADA69439	Ada69439 Rice gene
19	1323	25.8	4149	8	ADA70126	Ada70126 Rice gene
20	1244	24.3	3801	3	AA59332	AA59332 Nucleotid
21	1244	24.3	6658	2	AAT79882	Aat79882 Tomato im
22	1235	24.1	4465	2	AAT42135	Aat42135 I2C-2 gen
23	1198	23.4	4948	2	AAT42134	Aat42134 I2C-1 gen
24	1028.5	20.1	4208	6	AAV44188	AAV44188 Lettuce r
25	1028.5	20.1	4208	6	ABK67786	ABK67786 Lettuce p
26	1008.5	19.7	4163	6	ABK67828	ABK67828 Lettuce p
27	1007.5	19.7	4163	2	AAV44230	AAV44230 Lettuce r
28	966.5	18.9	2353	2	AAV44189	AAV44189 Lettuce r
29	966.5	18.9	2353	6	ABK67787	ABK67787 Lettuce p
30	941	18.4	3852	2	AAZ20602	AAZ20602 Zea maye
31	937	18.3	3833	2	AAZ20601	AAZ20601 Zea maye
32	937	18.3	4390	2	AAZ20597	AAZ20597 Zea maye
33	937	18.3	5948	2	AAZ20596	AAZ20596 Zea maye
34	910	17.7	5763	2	AAZ20606	AAZ20606 Zea maye
35	908	17.7	5540	8	ADA71374	Ada71374 Rice gene
36	905.5	17.7	3855	2	AAZ20598	AAZ20598 Zea maye
37	904	17.6	5910	2	AAV66798	AAV66798 Rice bact
38	902	17.6	3853	2	AAZ20603	AAZ20603 Zea maye
39	901	17.6	3837	2	AAZ20600	AAZ20600 Zea maye
40	890	17.4	3879	2	AAZ20599	AAZ20599 Zea maye
41	852.5	16.6	4557	8	ADA71375	Ada71375 Rice gene
42	842	16.4	8206	2	AAZ20605	AAZ20605 Zea maye
43	821.5	16.0	4001	10	AA154262	AA154262 Movable g
44	782.5	15.3	2988	8	ADA71057	Ada71057 Rice gene
45	763.5	14.9	2559	6	AB213950	AB213950 Arabidops

ALIGNMENTS

RESULT 1
ID ADK98516 standard; cDNA; 3193 BP.
AC ADK98516;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE S Bulbocastanum Sbul1 cDNA sequence Segid1.
XX
XX
KW plant disease resistance polypeptide; solanaceous plant; potato;
late blight disease; fungus; Phytophthora infestans;
KM conferring pathogen resistance; Sbul1; gene; ss.
XX
XX
OS Solanum bulbocastanum.
XX
XX
FH Key Location/Qualifiers
FT CDS 52..3018
FT FT /*tag= a
FT FT /product= "S Bulbocastanum Sbul1 protein"
XX
XX
PD 11-MAR-2004.
XX
XX
PF 28-AUG-2003; 2003WO-US027045.
XX
XX
PR 29-AUG-2002; 2002US-0407100P.
PR 20-AUG-2003; 2003US-00647268.


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Oy 561 SerLeaGSerLeuProAsnGlnLeuCySlySleuGlnAsnLeuGlnThrLeuAspLeu 580
Db 1732 AGTATGCTGATGCTTCCAAACCAAGTATGCAAGCTTCAAAATCTGCAGACTCTGATCTA 1791
Oy 581 HisGlyCySHisSerLeuCySLeuProIysGlnThrSerIysLeuGlySerLeuArg 600
Db 1792 CATGGCTGATTCATCTTGTGTTGCTCCAAAGAAACAGCAAACTGGTAGTCTCGA 1851
Oy 601 AsnLeuLeuLeuAspGlyCySLeuGlyLeuThrCySmetProProArgIleGlySerLeu 620
Db 1852 AATCTTTACTGATGTTGCTGATGATGATCTGTGATGCCAACAGATAGGATCTTGTG 1911
Oy 621 ThrCysLeuIysThrLeuSerArgPheValIleGlyIleGlnIysLeuSesCySLeuGln 640
Db 1912 ACATGCTTAAAGACTTAAAGTAGATTTGTGGGAAATTCAGAGAAAGTTGTCACTT 1971
Oy 641 GlyIleLeuArgAsnLeuAsnLeuIysGlySerIleGlnIleThrHisLeuGlnArgVal 660
Db 1972 GGTGAATTAACGAAACCTGATCTGATGCTCAATGTAATCAGCATCTGAGAGAGTGTG 2031
Oy 661 LysAsnAspMetAspAlaIysGlnIleAsnLeuSerAlaIysGlnAsnLeuHisSerLeu 680
Db 2032 AAGAATGATATGAGTCAAAAGAACCAATTTATCTGCAGAAAGAAATCTGCATCTTTA 2091
Oy 681 SerMetIysTPAspAspAspGluArgProArgIleTyArgIuserGlnIysValIleVal 700
Db 2092 AGCATGAATGAGTACGACGATGACGTCACTATATATGATGAGAAAGTTGATGAGTGTG 2151
Oy 701 LeuGlnIleLeuIysProHisSerAsnLeuThrCySLeuThrIleArgGlyPheArgGly 720
Db 2152 CTGGAAGCTCTCAAAACCAACATCCCAATCTGACTGTTTAAACATGAGGGGCTTCAGAG 2211
Oy 721 IleArgLeuProAspTTPMetAsnHisSerValLeuIysAsnValIleSerIleGlnIle 740
Db 2212 ATCCGCTCCAGACTGATGATGATCATCAGTTTGAAGAAATGTGTCTATGTAATGATC 2271
Oy 741 IleSerCySLeuAsnCySLeuProProPheGlyIysLeuProCySLeuIysSer 760
Db 2272 ATCAAGTGCAGAAATGCTCATGCTTACCACTTGTGAGAGCTGCTGTCTTAAAGAT 2331
Oy 761 LeuGlnLeuTPArgGlySerAlaGlnValGlnTyValAspSerGlyPheProThrArg 780
Db 2332 CTAGAGTTGTGAGGGGCTCTGCGGAGTGGAGTATGTTGATTCCTGATTCCTTACAGA 2391
Oy 781 ArgArgPheProSerLeuArgIysLeuAsnIleArgGlnPheGlyAsnLeuIysGlyLeu 800
Db 2392 AGAAGTTTCCATCTCTGAGAAACTTAAATATACCGCAATTTGGTAAATCTGAAAGATGTG 2451
Oy 801 LeuIysIysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 820
Db 2452 CTGAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2511
Oy 821 PrometPheValIleProThrLeuSerSerValIysIysLeuValIleSerGlyAspIys 840
Db 2512 CTTATGTTGTTTATTCACACCTTCTTCTGTCAAGAAATGGTAGTATGAGGGAGACAG 2571
Oy 841 SerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIle 860
Db 2572 TCAGATGCAATAGGTTTCACTGATCTCAATCTCAATGAGGCTTACTTCCCTCAAAAT 2631
Oy 861 ArgTyValAsnIysGlnAspAlaSerLeuProGlnIysMetPheIysSerLeuAlaAsnLeu 880
Db 2632 CGCTATTAACAAAGAGATGCTTCACTCCAGAGAGATGTTCAAAAGCTTGCAGAAATCTC 2691
Oy 881 LysTyValAsnIleSerPheTyPheAsnLeuIysGlnLeuProThrSerLeuAlaSer 900
Db 2692 AAATATCTGAATATCTCTTTTACTTCAATCTTAAAGAGCTGCCACAGCTGCTAGT 2751
Oy 901 LeuAsnAlaLeuIysHisLeuGlnIleHisSerCySValIleLeuGlnIysLeuProGln 920
Db 2752 CTCAATGCTTGAACATCTGGAATTCATAGTTGTATGCACTGAGAGATCTCCCGAG 2811

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Oy 921 GlnGlyValIysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyCySLeuMetLeu 940
Db 2812 GAAGGTGGAAGGTTTAAATTTCACTACACAGTATTCATTAATCATATCTGGAATGCTA 2871
Oy 941 GlnCySLeuProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 960
Db 2872 CAATGTTTACCGGAGGATGTCAGACACTTAAACAGCTCTCACAAAATTAATCATGAGTTT 2931
Oy 961 CysProThrLeuAlaIysArgCySLeuGlyIleGlyGlnAspTTPTyIysIleAla 980
Db 2932 TGTCAACACTGCGCCAGCGGTGTGAGAGGAGATAGAGAGAGACTGATCAAAATTCCT 2991
Oy 981 HisIleProArgValPheIleTyR 988
Db 2992 CACATTCCTGTGTGTTTATTTAT 3015

RESULT 2
ADK98518
ID ADK98518 standard; DNA; 3595 BP.
XX
XX
XX
AC ADK98518;
XX
XX 03-JUN-2004 (first entry)
DE
XX
XX S Bulbocastanum Sbul1 gene genomic DNA sequence SegID3.
KW plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
XX conferring pathogen resistance; Sbul1; gene; de.
XX
XX Solanum bulbocastanum.
OS
XX
XX Key Location/Qualifiers
XX CDS 57..3432
XX FT /*tag= a
XX FT /product= "S Bulbocastanum Sbul1 protein"
XX FT intron 488..899
XX FT /*tag= b
XX
XX W02004020594-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027045.
XX
XX 29-AUG-2002; 2002US-0407100P.
XX 20-AUG-2003; 2003US-00647268.
XX
XX (USDA ) US SEC OF AGRIC.
XX (DREC-) DRY CREEK LAB.
XX
XX Osumi T, Belknap WR, Rockhold DR, Maccree MM;
XX
XX WPI; 2004-239179/22.
XX P-PSDB; ADK98519.
XX
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX molecule encoding a plant disease resistance polypeptide, useful for
XX conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Claim 1; SEQ ID NO 3; 103pp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum
XX bulbocastanum late blight resistance gene. The present sequence is the S
XX bulbocastanum gene sequence of the invention.
XX
XX Sequence 3595 BP; 1139 A; 614 C; 737 G; 1105 T; 0 U; 0 Other;
XX
XX Alignment Scores:

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Pred. No.: 0 Length: 3595
 Score: 5028.50 Matches: 987
 Percent Similarity: 87.66% Conservative: 0
 Best Local Similarity: 87.66% Mismatches: 1
 Query Match: 98.08% Indels: 138
 DB: 12 Gaps: 1

US-10-647-268-2 (1-988) x ADK98518 (1-3595)

QY 1 MetAlaGluAlaPheLeuGluValLeuLeuAspAsnLeuThrCysPheIleGlnGlyIle 20
 Db ATGGCTGAAAGCTTCTCTCAAGTTCGTAGACAACTGACTGTTTCATCCAGGGGAA 116
 QY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuLeuSerThrPheThrThr 40
 Db CTGGATTGATCTTGGTTTAAGATGAGCTTCGAAAGCTTCAAAGCAGCTTTACTACA 176
 QY 41 IleGlnAlaValLeuGluAspAlaGlnLeuLeuLeuAspLeuValIleGluAsn 60
 Db ATCCAGAGCTGCTGAGAGATGCTCGAAGCAATTCAGAGCAAGGCAATTAGAAAT 236
 QY 61 TrpLeuGlnLeuLeuAsnAlaAlaIleTyrgIleAlaAspAspIleLeuAspGluCysLeu 80
 Db TGGTTTCAGAACTCAATGCTGCTGATAGAGCTGATGACATCTTGACCAATGTAA 296
 QY 81 ThrGluAlaProIleArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
 Db ACTGAGGCACCAATTAGACAGAAAGAAATAGGGGTTCATCCAAAGCTTATC 356
 QY 101 ThrPheArgHisLeuLeuIleGlyLeuArgMetLeuLeuLeuLeuLeuLeuLeuLeu 120
 Db ACTTTTCGACAAATATGGGAAAGATGAAAGATTAAGAACTGATGTATAT 416
 QY 121 AlaAlaGluArgIleLeuPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
 Db GCAGGGGAACGAATTAACTTTCATTTGATGAAGAGCTATAGAGACCAAGTTCCTACA 476
 QY 141 ArgGlnThr----- 143
 Db CGCCAAACAGGTGCTCATCTTATGATATTTTCTGAAAAAAGCTTTATCATCAAT 536
 QY 143 ----- 143
 Db 537 CATGTGTTTGGGAATTCGTTAATCTAAATGTTGCTGCAAGCTTAAGTAGATAGT 596
 QY 143 ----- 143
 Db 597 GATCCAGCTTGGATTATTAATCTATTAAGCTAAATCTGTTTAGTAGAGTTTAAAT 656
 QY 143 ----- 143
 Db 657 ATATTAACCTGATTAATCATAGCTTAATCTAGATTAAGATTAAGCCCCAAGCTTAA 716
 QY 143 ----- 143
 Db 717 ATGACAGATAAACCAGAGTTGTTTAGCTCTTAATAATTAAACAATGATTAATATGTA 776
 QY 143 ----- 143
 Db 777 ATTCAAAAAGTGATTTTAAATTGAATAATTTTCGTGCTTCTCAAGCTTATCAT 836
 QY 143 ----- 143
 Db 837 GTCTTTTACTGTGCAAAATTTCTAATTGATTTTTCGTGACTTCCTAACGAGCTTGGCC 896
 QY 144 -GlyPheValLeuAsnGluProGlnValTyrgIleArgAspLeuGluLeuAspGluIleVal 163
 Db AGGTTTGTGTTTGAATGAACCAAGTTTATGAGAGACAAAGAAAGACAGATAGT 956
 QY 163 IlyValIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlu 183
 Db GAAATTCCTGATTAACAATGTAGCAATGCCCAAAACACTTCCAGTCTCCCAATATCTGG 1016

QY 183 YMetGlyCylLeuGlnGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIle 203
 Db TATGGGGGAGCTTGAAGAAAGACACTTGGCCCAATGCTTTCAATGATCGAAGAT 1076
 QY 203 eGluHisPheHisProIleLeuThrIleCysValSerGluAspPheAsnGluLeuArgLe 223
 Db TGAGCATTTCCATCCCAAAATATGGAATTTGTCCTCGAAGATTTTAAATGAAAGAGCTT 1136
 QY 223 uIleLeuGluIleValGluSerIleGluGluLeuSerLeuGlyCylMetAspLeuAlaPr 243
 Db GATAAAGAAATTTGATGATCTATTTGAAGAAAGTCACTTGTCGATGAGACTGCTCC 1196
 QY 243 OLeuGlnLeuLeuAspLeuArgAspLeuLeuAsnGlyLeuLeuThrLeuLeuValLeuAspAs 263
 Db ACTTCAAAGAGCTTGGGACTTGGGACTTGAATGAAAAAATATTGCTCGCTTAGATGA 1256
 QY 263 PValTrpAsnGluAspGlnAspLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 283
 Db TGTTCGATGATGATGATCAAGATTAAGTGGGCTAAGTTAAGCAAGTCTTGAAGGTGAGC 1316
 QY 283 aSerGlyAlaSerValLeuThrThrThrArgLeuGluLeuValGlySerIleMetGlyThr 303
 Db AAGTGGGCTTCTGTTTCAACCACTACTCGTCTTGAAAAAGTTGATCAATTAATGGGAAAC 1376
 QY 303 rLeuGlnProTyrgIleuLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlu 323
 Db ATTGCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1436
 QY 323 nArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLeuGluIle 343
 Db ACGTGACTTGGGACCAAGAAAGAAATTAATCTTAATCTTGTGCTATCCGAAAGAGAT 1496
 QY 343 eValLeuLeuSerGlyCylValProLeuAlaAlaLeuThrLeuGlyGlyIleLeuArgPr 363
 Db TGTGAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1556
 QY 363 eLysArgGluGluArgGlnTrpGluHisValArgAspSerGluIleTrpLeuProGlu 383
 Db TAAAGAGAGAGAAAGACAGTGGACATGTGAGATGATGATGATGATGATGATGATGATGAT 1616
 QY 383 nGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrgHisIleuProLeuAspLe 403
 Db AGAAGAAAGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1676
 QY 403 uArgGlnCysPheThrTyrgCysAlaValPheProLysAspThrGluMetGluLeuGlyAs 423
 Db GAGACAAATGCTTACATATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736
 QY 423 nLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerTyrgLysAsnLeuGluLeuGlu 443
 Db TCTAATCTCTCTGATGAGCAGATGTTTATTTATCGAAAGAACTTGGAGCTTACA 1796
 QY 443 uAsnValGlyAsnGlnValTrpAsnGluLeuTyrgLeuAspSerPhePheGlnGluIleGlu 463
 Db GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1856
 QY 463 uValLeuSerGlyGlnThrTyrgPheLeuMetHisAspLeuIleHisAspLeuAlaThrSe 483
 Db AGTTAATCTGGTCAAACTTATTTCAAGATGATGATGATGATGATGATGATGATGATGAT 1916
 QY 483 rLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrgIle 503
 Db TCTAATTTGGGAGAGCAGATCAAGAGCAATATCCAGAAATTAATTTGTAAGAAATTTACAT 1976
 QY 503 eHisMetSerIleGlyPheThrIleValValSerSerTyrgSerLeuSerHisLeuGlu 523
 Db ACHTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2036
 QY 523 nLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLeuGlnLeuProSe 543
 Db GAAATTTGCTCGTGAAGGCTCTTAATCTAAGTACATTAAGCAATTAAGCAATTAAGCAAT 2096
 QY 543 rSerIleGlyAspLeuValHisLeuArgTyrgLeuAsnLeuSerGlyAsnThrSerIleArg 563

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Db      2097 TTCCATTGGAATCTAGTACATTTAAAGTACTTAACCTTGCTGGCAATACAGTATCG 2156
Qy      563  GSerLeuProLeuGlnLeuCybLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCy 583
Db      2157 TAGTCTTCCAAACCGATTATGACAGCTTCAAAATGTGACACTTGTATCTAAGTGGCTG 2216
Qy      583  sHisSerLeuCybLeuProLeuGlnThrSerLeuGlnGlySerLeuAspLeuLeu 603
Db      2217 TCATTCACTTTGTTGTTTGGCCAAAAGAAACAAAGCAACTGGTACTTCCAAATCTTT 2276
Qy      603  uLeuAspGlyCybTyrglyLeuThrCybMetProProArgIleGlySerLeuThrCyb 623
Db      2277 ACTGATGCTGCTATGATTGACTTGTATGCCCAAGAGATAGGATCTTGACATGCTC 2336
Qy      623  uLyThrLeuSerArgPheValValGlyIleGlnLyblySerCybGlnLeuGlyGlu 643
Db      2337 TAAAGACTTAAGTATGATTGTGGTGGAAATCAGAAAGAAAGTTGTCAACTGTGTAAT 2396
Qy      643  uArgAsnLeuAsnLeuTyrglySerIleGlnIleThrHisLeuGlnuArgValLybAsnAs 663
Db      2397 ACGAAACCTGATCTCTATGGCTCAATTGAAATCGCATCTTGAGAGAGTGAAGATGA 2456
Qy      663  pMetAspAlaLybGlyuAlaAsnLeuSerAlaLybGlnuAsnLeuHisSerLeuSerMetLy 683
Db      2457 TATGGATGCAAAAGAGCAATTTATCTGCAAAAGAAATCTGCATCTTTAAGCATGA 2516
Qy      683  sTrpAspAspAspGluArgProArgIleTyrglySerGlyblybValGluValLeuGluAl 703
Db      2517 ATGGGATACACATGAACTGCCACGTATATGAAACCAAAAAGTTGAAGGCTTGAAGC 2576
Qy      703  aLeuLybProHisSerAsnLeuThrCybLeuThrIleArgGlyPheArgGlyIleArgLe 723
Db      2577 TCTCAACCACTCACTCAATCTGACTTGTTTAACAATCGGGGCTTCAAGAGATCCGCT 2636
Qy      723  uProAspTrpMetAsnHisSerValLeuLybAsnValSerIleGlnIleIleSerCy 743
Db      2637 CCCAGACTGGATGATCACTGAGTTTGA AAAAGTTGCTCTATTTGAATCATCAGTTG 2696
Qy      743  bLybAsnCybSerCybLeuProProPheGlyGlyLeuLeuProCybLeuLybSerLeuGlu 763
Db      2697 CAAAAACCTGCTCATCTTACCCACCTTGTGGAGCTGCTGTCAAAAAGCTCAGACTT 2756
Qy      763  uTrpArgGlySerIleGlnuAlaGlnTybValAspSerGlyPheProThrArgArgPh 783
Db      2757 ATGGAGGGGGTCTGGGAGAGTGAAGTATGATTTCTGATTTCCCTACAGAGAGGTT 2816
Qy      783  eProSerLeuArgLybLeuAsnIleArgGlybPheGlybAsnLeuLybGlyLeuLeuLybLy 803
Db      2817 TCCATCTCTGAGAAACTTAATATACGGCAATTTGATATCTGAAAGAGATTGCTGAAAA 2876
Qy      803  sGlnuGlyGlnuGlnuCybProValLeuGlnuIleGlnIleLybCybCybProMetPh 823
Db      2877 GGAAAGAAAGAGCAATGCCCTGTGCTTGAAGAGATTAAGATTAATGTGGCCCTATGTT 2936
Qy      823  eValIleProThrLeuSerSerValLybLybLeuValSerGlybAspLybSerAspAl 843
Db      2937 TGTATTCACACCCCTTCTTCTGTCAAGAAATGTGATGTGGGGACAAAGTCAAGATGC 2996
Qy      843  aIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTybAs 863
Db      2997 AATAGGTTTCAAGTTCCATATCTAATCTCATGCTTTTACTTCCCTCCAAATTCGCTAADA 3056
Qy      863  nLybGlnuAspAlaSerLeuProGlnuGlnuMetPheLybSerLeuAlaAsnLeuTybLe 883
Db      3057 CAAGAAAGATGCTTCACTCCCAAGAGAGATGTTCAAAAAGCCCTTGCAAAATCTCAATACTT 3116
Qy      883  uAsnIleSerPheTybPheAsnLeuLybGlnuLeuProThrSerLeuAlaSerLeuAsnAl 903
Db      3117 GAATATCTCTTTTACTTAATCTTAAGAGAGCTGCTACCGGCTGAGTCAAGTCAAGTGC 3176
Qy      903  aLeuLybHisGlnuGlnuIleHisSerCybTybAlaLeuGlnuSerLeuProGlnuGlnuIyVa 923

```

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Db      3177 TTTAAGACATCTGGAATTCATAGTGTATGACTAGAGAGTCTCCCGAGAGAGTGT 3236
Qy      923  lLybGlyLeuIleSerLeuThrGlnLeuSerIleThrTybCybGlnuMetLeuGlnCybLe 943
Db      3237 GAAAGGTTTAAATTCATCTACACAGTTATCCATATACGTGTAATGCTAACAATGTT 3296
Qy      943  uProGlnuLybGlnuHisLeuThrAlaLeuThrAsnLeuSerValGlnuPheCybProTh 963
Db      3297 ACCGAGGAGATTGACAGCACTTAACAGCCCTCAAAATTTATCAGTTGTTGTCNAAC 3356
Qy      963  rLeuAlaLybArgCybGlnuLybGlyIleGlyGlnuAspTrpTybTybIleAlaHisIlePr 983
Db      3357 ACTGGCCAAAGCGGTGTGAAGAGGAATAGAGAGACTGTACAAAAATGCTCAATTC 3416
Qy      983  oArgValPheIleTyb 988
Db      3417 TCGTGTGTTTATTTAT 3432

RESULT 3
ADK98524
ID   ADK98524 standard; DNA; 5028 BP.
AC   ADK98524;
NC   03-JUN-2004 (first entry)
DE   S Bulbocastanum Sbul protein-related chimeric transgene Segid9.
KW   plant disease resistance polypeptide; solanaceous plant; potato;
KW   late blight disease; fungus; Phytophthora infestans;
KW   conferring pathogen resistance; gene; ds; transgenic; Ubi 3 promoter.
OS   Solanum bulbocastanum.
XX   Chimeric.
XX
XX   Key Location/Qualifiers
FH   CDS 1029..4404
FT   /tag= a
FT   /product= "S Bulbocastanum Sbul1 protein"
FT   intron 1460..1871
FT   /*tag= b
PN   WO2004020594-A2.
PD   11-MAR-2004.
XX
XX   28-AUG-2003; 2003WO-US027045.
PF   29-AUG-2002; 2002US-040710P.
PR   20-AUG-2003; 2003US-00647268.
XX
XX   (USDA ) US SEC OF AGRIC.
XX   (DREC-) DRY CREEK LAB.
XX
XX   Osumi T, Belknap WR, Rockhold DR, Maccree MW;
XX   WPI: 2004-239179/22.
XX   P-PSDB; ADK98525.
XX
XX   New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX   molecule encoding a plant disease resistance polypeptide, useful for
XX   conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX   Claim 1; SEQ ID NO 9; 103bp; English.
XX
XX   This invention relates to a novel isolated nucleic acid molecule encoding
XX   a plant disease resistance polypeptide. The preferred plant is a
XX   solanaceous plant that is potato. The resistance is to late blight
XX   disease, caused by the fungus Phytophthora infestans. The invention is
XX   useful for conferring pathogen resistance in plants using a Solanum
XX   bulbocastanum late blight resistance gene. The present sequence is that
XX   of a chimeric transgene (Sbul1 gene with a potato Ubi1 promoter sequence)
XX   of the invention.

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XX Sequence 5028 BP; 1647 A; 847 C; 958 G; 1576 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 5028
Score: 5028.50 Matches: 987
Percent Similarity: 87.66% Conservative: 0
Best Local Similarity: 87.66% Mismatches: 1
Query Match: 98.08% Indels: 138
DB: 12 Gaps: 1
US-10-647-268-2 (1-988) x ADR98524 (1-5028)
QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 1029 ATGGCTGAAGCTTCTCTCAAGTCTGTTAGCAATCTGACTGTTTCATCCAAAGGGGAA 1088
QY 21 LeuGlyLeuIleLeuGlyPheLeysAspGluPheGluLeuGlnSerThrPheThrThr 40
Db 1089 CTTGGATTGATTCTTGTTTAAAGATGAGTTCGAAAGACCTTCAAGCAGTTTACTACA 1148
QY 41 IleGlnAlaValLeuGluAspAlaGlnIleLeuLeuAspAlaIleGluAsn 60
Db 1149 ATCCAAAGCTGCTGAAGATGCTCAGAAAGCAATTGAAGCAGCAATTGAAAT 1208
QY 61 TrpLeuGlnIleLeuAsnAlaIleAlaIleTyrGluAlaAspAspIleLeuAspGluCysLeu 80
Db 1209 TGGTTGCAAGAACTCATAGCTCTGCTCATATGAGCTGATGACATTTTGGACAAATGTAA 1268
QY 81 ThrGluAlaProIleArgGlnIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
Db 1269 ACTGAGGACCAATTGACAGAAAGAAACAATGAGGTGTTTATCATCCAAACGTATAC 1328
QY 101 ThrPheArgHisIleValIleGlyLeuArgMetLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 1329 ACTTTTCTGTCACAAATTTGGGAAAGAAAGAAAGAAATTTAGGAAACCTGATGTAAT 1388
QY 121 AlaIleArgIleValIleLeuPheHisIleLeuAspGluArgThrIleGluArgGlnValAlaThr 140
Db 1389 GCAAGGGAACCAATTAACTTTCATTGATGAAGACCTATAGAGACCAAGTTCCTACA 1448
QY 141 ArgGlnThr----- 143
Db 1449 CGCCAAACAGGTGCTCATATGATATTTTCTGAAAAACAGCTTATATCATCAAAAT 1508
QY 143 ----- 143
Db 1509 CATGTGCTTTGGGAATTCGTCTAATCTAAATGTTGCTCAAGTCTAAGTAGATAAGT 1568
QY 143 ----- 143
Db 1569 GGATCCAGCTTTGATTTATTAATCTATTAAGTAAATCTGTTTAGTGAAGTTTAAACAT 1628
QY 143 ----- 143
Db 1629 ATATAACCTCAGATAAATCCATAGCTTACTCATAGATTAGAGATGAGCCCCCAAGCTTAA 1688
QY 143 ----- 143
Db 1689 ATGACAGATAAAGCCAGAGTTGTTTAGCTCTTAATAATTAAACATGATATAATGTGA 1748
QY 143 ----- 143
Db 1749 ATTCAAAAAAGTCATTTTAAATTGAATATTTCTGCTGCTTCTCAAGCTTATCATAT 1808
QY 143 ----- 143
Db 1809 GTCTTTTACTGTCAAAAATTTACTCTTGATTTTTCGTGACTCTCAAGCTTGGGCC 1868
QY 144 -GlyPheValLeuAsnGluProGlnValIleTyrGlyArgAspLeuLeuLeuLeuLeuLeu 163
Db 1869 AGGTTTGTGTTTGAATGACCAAGATTATGGAAGAGCAAGAAAGAAAGACAGATAGT 1928

QY 163 IlySerIleLeuIleAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlu 183
Db 1929 GAAAAATCCGTGATTAACAATGTTTACCAATGCCCCAAACCTTCACATCTCCCAATACTGG 1988
QY 183 YMetGlyGlyLeuGlyIleThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIle 203
Db 1989 TATGGGGGAGCTTAGGAAGAAGACACTCTTGCCCAATGCTCTTCAATGATCAGAGATAT 2048
QY 203 eGluHisPheHisPProIleIleTyrIleCysValSerGluAspPheAsnGluIleValGle 223
Db 2049 TGAGCATTTTCATCCCAAAATATGATTTGTCTCCGAGATTTTAATGAGAGAGGTT 2108
QY 223 uIleLeuGlnIleValGlnSerIleGlnGluLeuSerLeuGlyGlyMetAspLeuAlaPro 243
Db 2109 GATTAAGGAATTTTGAATCTTATTTAGAAAGAAAGTCACTTGAGGCAATGGACTGGCTCC 2168
QY 243 OleuGlnIleLeuLeuArgAspLeuLeuAsnGlyLeuLeuLeuLeuValLeuLeuAspAs 263
Db 2169 ACTTCAAAAGAGCTTCGGGACTTGCTGAATGGAAAAAATATTTGCTCGCTTAGATGA 2228
QY 263 pValTrpAsnGluAspGlnAspIleTyrAlaValLeuArgGlnValLeuLeuValGlyAl 283
Db 2229 TGTTTGAATGAAGATCAAGATTAAGTGGCTTAAGTCAAGTCTTGAAGGTTGAGC 2288
QY 283 aSerGlyAlaSerValLeuThrThrArgLeuGluLeuValGlySerIleMetGlyThr 303
Db 2289 AAGTGGCGCTTCTGTTTAAACCACTACTCGTCTTGAAGAGTTGACATTAATGGGAC 2348
QY 303 rLeuGlnProTyrGluLeuSerAsnLeuSerGlnIleAspCysTrpLeuLeuPheMetGlu 323
Db 2349 ATTGCAACCAATGAAATTTGCAATTTGCTCAAGAAAGATTGTGGTTGTGTTCAATGCA 2408
QY 323 nArgAlaPheGlyHisGlnGlnGluIleAsnLeuAsnLeuValAlaIleGlyLeuGlyGlu 343
Db 2409 ACGTGATTTGGGACCAAGAAAGAAATAATCTTAATCTTGCTGCTATCGAAAGAGAT 2468
QY 343 eValIleLeuCysGlyGlyValProLeuAlaAlaValThrLeuGlyGlyIleLeuArgPhe 363
Db 2469 TGTGAAAAAATGTGTGTGTGCTCTGACAGCTAAACCTTGAGAGTATTTTGGCCTT 2528
QY 363 eLysArgGlnGluArgGlnTrpGluHisValArgAspSerGluIleTrpIleLeuProGlu 383
Db 2529 TAAAGAGAAAGAAAGACAGTGGCAACATGAGATGATGAAATTTGGCCTCA 2588
QY 383 nGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTyrHisHisIleuProLeuAspLe 403
Db 2589 AGAAGAAAGTCTTATTTCTGCTGCTGCTGACATTAAGTACATCACCTTCCACTGATTT 2648
QY 403 uArgGlnCysPheThrTyrCysAlaValPheProLeuAspThrGluMetGluLeuGlyAs 423
Db 2649 GAGCAATGCTTACATATTTGTCAGATATCCCAAGGATACCGAAATGGAAAAAGGAAA 2708
QY 423 nLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerIleValAsnLeuGluLeuGlu 443
Db 2709 TCTAATCTCTCTGATGAGCAGATGTTTATTTATGAAAGAAACCTTGAGGCTTAA 2768
QY 443 uAsnValGlyAsnGlyValTrpAsnGluLeuTyrLeuAspSerPhePheGlnGluIleGlu 463
Db 2769 GAATGTAGGTAAGAGTATGAAATTAATTAATCTGAGGCTTTTCTTCCAGAGATTGA 2828
QY 463 uValIleSerGlyGlnThrTyrPheLeuMetHisAspLeuIleHisAspLeuAlaThrSe 483
Db 2829 AGTTAATCTGGTCAAACTTATTTCAAGTGCATGATTCATTCATGATCTGGCAACATC 2888
QY 483 rLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrIle 503
Db 2889 TCTAATTTGGCAAGACATCAAGCAGCAATATCCAGAAATATTTGTAATAATTTACAT 2948
QY 503 eHisMetSerSerIleGlyPheThrIleValIleSerSerTyrSerLeuSerHisIleuGlu 523
Db 2949 ACHTATGATGTCATGTTGTTTCACTTAAAGTGTATCTTCACTCTTCTTCCACTTGA 3008
QY 523 nLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLeuGlnLeuProSe 543

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Db 3009 GAAAGTTGTCTGAGGGTGGCTTAATCTAAGTACATAAACTTAAGCAGTACCGTC 3068
Qy 543 rSer11eGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThrSer11eAr 563
Db 3069 TTCAATGGAGATCTAGTACATTTTAAGTAACTTAACCTTGCTGGCAATCTAGATTGCG 3128
Qy 563 gSerLeuProAsnGlnLeuCybLeuGlnAsnLeuGlnThrLeuAspLeuHisgLyCy 583
Db 3129 TAGCTTCCAAACCAAGTATATGCAAGCTTCAAATCTGACAGCTCTGATCTACAGTGGTG 3188
Qy 583 gHisSerLeuCybLeuProGlyLeuThrSer11eGlyLeuGlnSerLeuAspLeuLe 603
Db 3189 TCATTCACCTTGTTGTTGCCAAAAGAAACAAGCAACTGTGAGTCTTCCAAATCTTTT 3248
Qy 603 uLeuAspGlyCybTyrGlyLeuThrCybMetProProArg11eGlySerLeuThrCybLe 623
Db 3249 ACTTGATGGTTGCTATGATGACTTGATGCAACAAGATAGATCTTGACATGCGCT 3308
Qy 623 uLybThrLeuSerArgPheValValGly11eGlnLybLeuSerCybGlnLeuGlyLe 643
Db 3309 TTAAGCTTAAGTATGATTTGGTGGGAAATTCAGAAAGAAAGTTGTCAACTGGTGAAT 3368
Qy 643 uArgAsnLeuAsnLeuTyrGlySer11eGln11eThrHisLeuGlnArgVal11yAsnAs 663
Db 3369 ACGAAACCTGATCTCTATGGCTCAATTGAATCAAGCATCTTGAGAGATGAAGAATGA 3428
Qy 663 pMetAspAla1yGlyuAlaAsnLeuSerAla1yGlyuAsnLeuHisSerLeuSerMetLy 683
Db 3429 TATGATGCAAAAGAACCAATTTATCTGCAAAAGAAATCTGCAATCTTTAAGATGAA 3488
Qy 683 sTrpAspAspAspGluArgProArg11eTyrGlnSerGlnLybVal11eGlnGluAl 703
Db 3489 ATGGAGATGACATGACATGACCTCACTATATGATACAAAGAAAGTTGAAGTGGCTTGAAGC 3548
Qy 703 aLeuLybProHisSerAsnLeuThrCybLeuThr11eArgGlyPheArgGly11eArgLe 723
Db 3549 TCTCAACCAACATCTCATCTGACTTGTTAAACAATCAAGGGCTTCAAGAACTCCGCT 3608
Qy 723 uProAspTrpMetAsnHisSerValLeuLybAsnVal11eSer11eGln11eLeuSerCy 743
Db 3609 CCCGAGACTGATGATCACTCACTGATTTGAAAAATGTTCTCTATTTGAATCATCAGTTG 3668
Qy 743 sLybAsnCybSerCybLeuProProPheGlyGlnLeuProCybLeuSerLeuGlnLe 763
Db 3669 CAAATACTGCTCACTGCTTACCACTCTTGAGAGTGGCTTGCTTAAAAAGCTTAGAGCT 3728
Qy 763 uTrpArgGlySerAlaGlnValGlnTyrValAspSerGlyPheProThrArgArgArgPh 783
Db 3729 ATGAGAGGGGCTCTCGGAAAGTGAAGTATGTTGATTCGATTCCTTACAAAGAAAGGTT 3788
Qy 783 eProSerLeuArgLybLeuAsn11eArgGlnPheGlyAsnLeuLybGlyLeuLeuLybLy 803
Db 3789 TCCATCTCTGAGAAAACTTAATATATACGCAATTTGATATCTGAAGAAGATTGCTGAATAA 3848
Qy 803 sGlnGlyGlnGlnGlnCybProValLeuGlnGln11eGln11eLybCybCybProMetPh 823
Db 3849 GGAAGGAGAAAGCAATGCTCTGCTTGAAGAGATGAAGATTAATTTGCTCCCTAATGTT 3908
Qy 823 eVal11eProThrLeuSerSerVal11yLybLeuVal11eSerGlyAspLybSerAspAl 843
Db 3909 TGTATTTCCAACTCTTTCTCTGTCAGAAATTTGTTATTTAGTGGGCAAGTCAAGTCAAGC 3968
Qy 843 a11eGlyPheSerSer11eSerAsnLeuMetAlaLeuThrSerLeuGln11eArgTyrAs 863
Db 3969 AATAGGTTTCACTTCAATATCAATCTCATGCTTCTTCTTCCCTCCAAATTCGCTATAAA 4028
Qy 863 nLybGlnAspAlaSerLeuProGlnGlnMetPheLybSerLeu11aAsnLeuLybTyrLe 883
Db 4029 CAAAGAAATGCTTCACTCCCAAGAAAGATGTTCAAAAGCTTGAAGATTCCAAAATCTT 4088
Qy 883 uAsn11eSerPheTyrPheAsnLeuLybGlnLeuProThrSerLeuAlaSerLeuAsnAl 903

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Db 4089 GAATATCTCTTTTACTTCAATCTTAAAGAGCTGCTACAGCCTGCTACTCAATGC 4148
Qy 903 aLeuLybHisLeuGln11eHisSerCybTyrAlaLeuGlnSerLeuProGlnGlnLybA 923
Db 4149 TTTAAGCATCTGAAAATTTCAATGTTTATGCTAGAGAGTCTCCCGAGAGAGTGT 4208
Qy 923 11yGlyLeu11eSerLeuThrGlnLeuSer11eThrTyrCybGlnMetLeuGlnCybLe 943
Db 4209 GAAAGTTTATTTCACTCAACAGTTATTCATATACATAGTGAATGCTACAAATGTTT 4268
Qy 943 uProGlnGlyLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGlnPheCybProth 963
Db 4269 ACCGAGAGATTTGACAGCACTTACAGCCCTTCAAAATTTATCAGTTTGTCCAAAC 4328
Qy 963 rLeuAla1yAspArgCybGlnLybGly11eGlyuAspTyrTyr11eAlaHis11ePr 983
Db 4329 ACTGGCCAGCGGTGTAGAGAGGAAATAGAGAAAGATCTGTACAAATTTGCTCACATTC 4388
Qy 983 cArgValPhe11eTyr 988
Db 4389 TCGTGTGTTATTTAT 4404

RESULT 4
ID ADK98520 standard; DNA; 3347 BP.
XX ADK98520;
AC ADK98520;
XX 03-JUN-2004 (first entry)
DT
XX
DE S Bulbocastanum Sbul2 gene sequence SegID5.
XX
KW plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
KW conferring pathogen resistance; Sbul2; gene; ds.
XX
OS Solanum bulbocastanum.
XX
FH Key Location/Qualifiers
FT CDS 57..3344
FT FT /*tag= a
FT FT /product= "S Bulbocastanum Sbul2 protein"
FT FT 510..788
FT FT /*tag= b
XX
XX WO2004020594-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027045.
XX
XX 29-AUG-2002; 2002US-0407100P.
XX 20-AUG-2003; 2003US-00647268.
XX
XX (USDA ) US SEC OF AGRIC.
XX (DRYC-) DRY CREEK LAB.
XX
XX Osuni T, Belknap WR, Rockhold DR, Maccree MM;
XX
XX MPI; 2004-239179/22.
XX P-PSDB; ADK98521.
XX
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX molecule encoding a plant disease resistance polypeptide, useful for
XX conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Example; SEQ ID NO 5; 103bp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum

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CC buldocastanum late blight resistance gene. The present sequence is the S
CC buldocastanum Shul 2 gene sequence which was used in the exemplification
CC of the invention.

XX Sequence 3347 BP; 1070 A; 577 C; 693 G; 1007 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	3347
Score:	4475.00	Matches:	883
Percent Similarity:	83.94%	Conservative:	37
Best Local Similarity:	80.57%	Mismatches:	66
Query Match:	87.28%	Indels:	110
DB:	12	Gaps:	2

US-10-647-268-2 (1-988) x ADK98520 (1-3347)

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OY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAenLeuThrCysPheIleGlnGlyGlu 20
DB 57 ATGGCTGAAGCTTTCTTCATCAAGTCTGTAGACATCTGACTGTTTCATCCAAAGGGAA 116
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThrThr 40
DB 117 GTTGATTTGATCTTGTTTAAAGATAGATTCGAAAAGCTTCGAAAGCAATTAACTACA 176
OY 41 ILeGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaIleGlnLysn 60
DB 177 ATCCAAAGCTGCTGTAAGAGATGCTCAGAAAGCAATTGAAGGACAAAGCAATGAAAT 236
OY 61 TrpLeuGlnLysLeuAsnAlaAlaAlaIleGlyGluAlaAspAspIleLeuAspGluCysLys 80
DB 237 TGGTGGCAAGAACTCAATGCTGCTGTATATGAAAGCTGACGACATCTTGGAAGATGTAAA 296
OY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTrpGlyCysTrpHisProAsnValIle 100
DB 297 ACTAGGACCAATTAAGACAGAAAGAAACAATATGAGGTATCATCCAAAGCTTATC 356
OY 101 ThrPheArgHisLysIleGlyLysArgNecLysLysIleMetGluLysLeuAspValIle 120
DB 357 GCTTCCCTGCACAGATTGGGAAAAAGATGAAAAAATTATGGAATTAAGATGATATT 416
OY 121 AlaAlaGluArgIleLysPheHisLeuAspGluLysThrIleGluLysGlnValAlaThr 140
DB 417 GCACGGGAAACGAATTAAGTTTCATTTGGCTGAAAGCACTACAGAGAGCAAGTTGCTACA 476
OY 141 ArgGlnThr----- 143
DB 477 CGCCAAACAGGTGCTCATCTTATGATATTTCTAAAAAACAAGCTTATATCATGAATTT 536
OY 143 ----- 143
DB 537 CANTGTGTTTGGGATTTTCTAATCTAAATGTTGCTCAAGTCTAAGTATGATTAAGTGG 596
OY 143 ----- 143
DB 597 ATCCAGATTGGATATATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 656
OY 143 ----- 143
DB 657 AAAGCTGAGTTGTTTAAACATTATAAATTAAACATGATTAATTAATTAATTAATTA 716
OY 143 ----- 143
DB 717 GTGCAATTATGCTGCTCTCTCAAGCTTATCATTTGCTTTATTTGCAAAATTTCTTC 776
OY 144 -----GlyPheValLeuAsnGluProGln 151
DB 777 TTGCTTTTTCGCTGACTCTCTACTGAGCTTGACACAGGTTTGTTTAAATGAACCAAA 836
OY 152 ValTrpGlyArgAspLysGlnLysAspGluIleValLysIleLeuIleAsnValSer 171
DB 837 GTTATGAGAGAGCAAAAGAAAGATGAGATGTAATAATCCGATTAATAACATTTGTTAGC 896
OY 172 AsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrThr 191
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DB 897 GATGCCAAACACTTTCAGTCTCCCAATACTTGATATGGGGGATTAAGAAACACACA 956
OY 192 LeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrp 211
DB 957 CTTCGCCAAATGCTCTTCAATGATCAGAGATATTAAGCATTTCTTCCAAAATATGG 1016
OY 212 IleCysValSerGluAspPheAsnGlnLysArgLeuIleLysGluIleValGlnSerIle 231
DB 1017 ATTTGTCTTCGAAAGATTTTAAATGAAGAGATGTGTAAGAAATTTGATGATCTATT 1076
OY 232 GlnGluLysSerLeuGlyGlyMetAspLeuAlaProLeuGlnLysLysLeuAspAspLeu 251
DB 1077 GAAGAAAAGTCACTTGCTGACATGAGACTTGCTCCACTTCAAAAGAGCTTCAGGACTTG 1136
OY 252 LeuAsnGlyLysLysTrpLeuLeuValLeuAspAspValTrpAsnGluAspGlnAspLys 271
DB 1137 CTGAATGCAAAAAATATTTGCTTGTAGATGATATTTGGAATGAAGATCAAGATTAAG 1196
OY 272 TrpAlaLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThr 291
DB 1197 TGGCTAAGTTTACGAAAGGTTGAAGTTGAGCAAGTGCTCTTATCTTAACTCAACACT 1256
OY 292 ThrArgLeuGluLysValGlySerIleMetGlyThrLeuGlnProTrpGluLeuSerAsn 311
DB 1257 ACTGCTTTGAAAAGCTTGAGTCAATTAATGCAAACTTTGCACCAATATGATTTGCTAAC 1316
OY 312 LeuSerGlnGluLysAspTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlnGlu 331
DB 1317 TTGTGTCAAAGAAATGCTGCTGTTGTTGTTTCATCAACGTCATTTGGGCCCAAGAAAGAA 1376
OY 332 IleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLysCysGlyGlyValPro 351
DB 1377 ATTAATATATAATCTTGCTGCTATCGAAAGAGATAGTGAATAATGTGCTGTGGTCCCT 1436
OY 352 LeuAlaAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlnGluLysArgGlnTrpGlu 371
DB 1437 CTAGCAGCTTAAACTCTTGAGGATATTTGGCACTTCAAGAGACAAAGAAAGACGTGGGAA 1496
OY 372 HisValArgAspSerGluIleTrpLysLeuProGlnGlnGlnSerSerIleLeuProAla 391
DB 1497 CATTGAGAGATGATGATGATTTGGAAATTTGCCCAAGAAAGTTCTTATTCGCCGGCC 1556
OY 392 LeuArgLeuSerTrpHisLeuProLeuAspLeuArgLysPheThrTrpCysAla 411
DB 1557 CTGAACCTTAAGTACATCATCTTCACTTGATTTAGACAAATGCTTTTCATATGTGCA 1616
OY 412 ValPheProLysAspThrGlnMetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHis 431
DB 1617 GTATCCCAAGAGATACCAAAATGGAAGAAATCTAATCTCTCTGGAATGGACAT 1676
OY 432 GlyPheIleLeuSerLysGlyAsnLeuGluLeuAsnValGlyAsnGluValTrpAsn 451
DB 1677 GGTTCCTTTTATCGAAAGAACTTGAGCTAGAGAGTGAATATGAATGAATGAAT 1736
OY 452 GluLeuTrpLeuArgSerPhePheGlnGluIleGluValLysSerGlyGlnThrTrpPhe 471
DB 1737 GAATTAATCTTGAAGCTTTCTTCCAAAGATTTGAAGTTACATATGTAATAAATTAATTC 1796
OY 472 LysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerLysSerThrSerSer 491
DB 1797 AAGATCAATGATCTCATCATGATTTGGCTACATCTCTATTTTCGCAAGCCATCAAGC 1856
OY 492 SerAsnIleArgGlnIleIleValGluAsnTrpIleHisMetMetSerIleGlyPheThr 511
DB 1857 AACAAATATCCGTAATAATTAATTAATAAGTTAACCCCAATATATGTCGATTTGCTTGA 1916
OY 512 LysValIleSerSerTrpSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeu 531
DB 1917 AAAGTGCTCTTTTAACTCTGTTCTCACTTCCAAAAGTTTGCTCGTAAGGTTGCTT 1976
OY 532 AsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeu 551
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Db      1977 AATCTAAGTAACTGAACCTCAGACGATTACCATCTTCATAGGGAGCTGATACATTAA 2036
Qy      552 ArgTyrLeuAenLeuSerGlyYasnThrSerIleArgSerLeuProAenGlnLeuCysIlys 571
Db      2037 AGATACCTTAACCTTGTCTGACAAATAATAGAAATTCCTTAAGTCTTCCAGACAGTATGCAAG 2096
Qy      572 LeuGlnAenLeuGlnThrLeuAenLeuHiseGlyCysHiseSerLeuCysLeuAenProlys 591
Db      2097 CTTCAAAATCTGCACAGACTCTTGATCTACGTTGTTCTCTACAGACTTCTGTGTTTGCCAAA 2156
Qy      592 GlnThrSerIysLeuGlnIleSerLeuArgAenLeuLeuAenAenGlyCysArgIleLeuThr 611
Db      2157 GAAACAAACCAACCTTGATAGTCTCCGAAATCTTTTACTGATCGTTGCCAGATGATGACT 2216
Qy      612 CysMetProProArgIleGlySerLeuThrCysLeuIysThrLeuSerArgPheValVal 631
Db      2217 TGTATGCCACCAAGATAGATCATTCATTCCTTAAAGCTCTAGATCGCTTTCCAATG 2276
Qy      632 GlyIleGlnIysSerCysGlnLeuGlnIleLeuAenArgAenLeuAenLeuIysIleSer 651
Db      2277 GGA---AGGAGAGAAAGTCTCAATGTTGATTAACGAAACCTGAATCTGTATGCTCA 2333
Qy      652 IlegIuIleThrIleLeuGlnArgValIlyAenAenAenAenAenAenAenAenAenAen 671
Db      2334 ATTCAATCACGCACTTGAGAGAGATGAATGATGATGATGATGATGATGATGATGATGAT 2393
Qy      672 SerIalysGluAenLeuHiseSerLeuSerMetIysTPAenAenAenAenAenAenAen 691
Db      2394 TCTTCAAAAGAAATCTGATTTCTTTAAGTATGATGATGATGATGATGATGATGATGAT 2453
Qy      692 IleTyrGlnSerGlnIysValGlnValIleGlnIleLeuIysProHiseAenLeuThr 711
Db      2454 AGATATGATCAGAGATGTTGAAGTGGCTTGAAGCCCTCAACCACTCCATCTGACT 2513
Qy      712 CysLeuThrIleArgGlyPheArgGlyIleArgLeuProAenTPRMetAenHiseVal 731
Db      2514 TGTTTAACTAATTTATGGCTTCAGAGAAATCCGTCCTCCAGCTGATGAATCACTCACTT 2573
Qy      732 LeuIysAenValIleSerIleGlnIleIleSerCysIysAenCysSerCysLeuProPro 751
Db      2574 TTGAAAAATGTGTCTCTTGAATCAACGCAATTCGAAATGCTCAATGCTTACCCACC 2633
Qy      752 PheGlyGlnLeuProCysLeuIysSerLeuGlnLeuTPRArgGlySerIleGlnValGln 771
Db      2634 TTTGGTGAAGTCCCTGTCTTAATAGTCTACAGTATGAGAGGGCTCTGCAAGAGTGAAG 2693
Qy      772 TyrValAenSerGlyPheProThrArgArgPheProSerLeuArgIysLeuAenIle 791
Db      2694 TATATGATTCGTGATCCCTCAAGAAAGAGTTTCCATCTCTGAGAAACTTATATTA 2753
Qy      792 ArgGlnPheGlyAenLeuIysGlyLeuLeuIysGlyGlnIleGlnCysProVal 811
Db      2754 GCGCAATTTGATTAATCTGAAGGATGGTGAAGAAAGAAAGAAAGAAAGCAATTCCTGTG 2813
Qy      812 LeuGlnGlnIleGlnIleCysCysProMetPheValIleProThrLeuSerSerVal 831
Db      2814 CTTGAAGAGATGAGATTAACCTGCGCCCTATGTTTATTCCAGCCCTTCTTCTGTC 2873
Qy      832 LysIysLeuValIleSerGlyAenIysSerAenAenIleGlyPheSerSerIleSerAen 851
Db      2874 AACAAATTTGATTAATGAGGAGAGATGAGATGCAATGAGCTTCAATTAATCTTAAT 2933
Qy      852 LeuMetIleLeuThrSerLeuGlnIleArgTyrAenIysGlnAenAenAenAenAenAen 871
Db      2934 CTCAGGCTCTTACTTCTCTCAATTAATGATTAATCTGAAAGCTACTTCCCAAA 2993
Qy      872 GluMetPheIysSerLeuAenAenLeuIysTyrLeuAenIleSerPheTyrPheAenLeu 891
Db      2994 GAGATGTTCAAAAGCTTGCAAATCTTAATAATCTTGAATATCTATTAATCTCAAGATTC 3053
Qy      892 LysGlnLeuProThrSerLeuAenAenLeuAenAenAenAenAenAenAenAenAen 911
Db      3054 AAAGAGCTGCTTCAACCACTGGCTAGTCTTAATGCTTGAAGAAATCTGGAATTTGAAGT 3113

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Qy      912 CysTyrAlaLeuGlnSerLeuProGlnGlnIlyValIysGlyLeuIleSerLeuThrGln 931
Db      3114 TGTATGACATGAGAGATCTCCCGAGAGAGTGTGAAGGTTTAATCTTACCTTACACA 3173
Qy      932 LeuSerIleThrTyrCysGlnMetLeuGlnCysLeuProGlnIlyLeuGlnHiseLeuThr 951
Db      3174 TTATTCATTAACATCTGCACGATCTCAATGTTATTCGAGGAGATTCACACCTTAACA 3233
Qy      952 AlaLeuThrAenLeuSerValGlnPheCysProThrLeuAenAenAenAenAenAenAen 971
Db      3234 GCCCTCAAAATTTATCAATTAATGAGATGTCACACCTGCGCAAGCTGTGAAGAGGA 3293
Qy      972 IlegIyGlnAenTPRTPYIysIleAlaHiseIleProArgValPheIle 987
Db      3294 ATAGAGAAAGACTGTACAAATTTGCTACATTCCTGATGTGTTATC 3341

RESULT 5
ADP17759
ID      ADP17759 standard; DNA; 2913 BP.
XX
XX      ADF17759;
AC
XX      12-FEB-2004 (first entry)
DT
XX
DE      Solanum bulbocastanum Rpi-b1b DNA sequence.
XX
KW      gene, ds; Rpi-b1b; Rpi-b1b gene cluster; growth regulant;
KM      oomycete infection; introgression breeding; plant; late blight.
XX
XX      Solanum bulbocastanum.
OS
XX
FH      Key
FT      1..2913
FT      CDS
FT      /tag= a
FT      /product= "Rpi-b1b protein"
PM
XX      EP1334979-A1.
XX
PD      13-AUG-2003.
XX
XX      08-FEB-2002; 2002EP-00075565.
PF
XX      08-FEB-2002; 2002EP-00075565.
PR
XX
PA      (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
PI
XX      Van Der Vossen BAG, Allefs JHM;
XX
DR      MPI: 2003-714439/68.
XX
XX      P-PSDB: ADF17765.
XX
PT      New resistance gene conferring resistance against an oomycete pathogen,
PT      useful for producing plants, especially potatoes and tomatoes, resistant
PT      against oomycete pathogens such as Phytophthora infestans.
XX
XX      Example 5; SEQ ID NO 35; 86pp; English.
XX
XX      This invention relates to novel isolated polynucleotides that confer
XX      resistance against late blight caused by the oomycete pathogen
XX      Phytophthora infestans, which threatens both tomato and potato crops.
XX      Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX      leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX      and which cause disease resistance to bacteria, fungi, nematodes etc.
XX      These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
XX      described as plant growth regulants. They are useful in providing
XX      resistance to Phytophthora infestans, especially in Solanum tuberosum
XX      (potato) plants to protect against oomycete infection or to demonstrate
XX      disease susceptibility. Resistance can be conferred by transformation of
XX      existing potato and tomato cultivars with the gene, a procedure that is
XX      more straightforward and faster than conventional introgression breeding.
XX      This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b DNA of
XX      the invention.

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XX Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2,796-314 Length: 2913
Score: 3766.50 Matches: 753
Percent Similarity: 83.43% Conservative: 78
Best Local Similarity: 75.60% Mismatches: 130
Query Match: 73.46% Indels: 35
DB: 10 Gaps: 8
US-10-647-268-2 (1-988) x ADF17759 (1-2913)
QY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspLeuThrCysPheIleGlnGlyGlu 20
DB 1 ATGGGTGAAGCTTTCATTCAAGTTCGTACAGCAATCTCACTTCTTCTCAAGGGGAA 60
QY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGlyLeuGlnSerThrPheThrThr 40
DB 61 CTGTGATTGCTTTCGTTTCAAGATGATCCAAAGGCTTTCAGCATGTTTCTCA 120
QY 41 IleGlnAlaValLeuGlnAspAlaGlnGlySerGlnLeuLysAspLysAlaIleGlnAsn 60
DB 121 ATTCAGCGCTTCCTTGAAGATGCTCAGAGAAAGCACTCAACAAAGCCCTTGAATAAT 180
QY 61 TrpLeuGlnLysLeuAsnAlaAlaAlaTyrGlnAlaAspAspIleLeuAspGluCysLys 80
DB 181 TGGTTGCAAAAATCTAATGCTGCTCATATGACATGACATCTTGGATTAATAA 240
QY 81 ThrGlnAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
DB 241 ACCAAGGCC--ACMAAGATTCCTCCAGCTGAATGAGCCGTATCATCCAAAGGTTATC 297
QY 101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
DB 298 CCTTTCCTCCACAAAGTCGGAAGAAAGATGACCAAGATGAAGAAATCTAAGGCAATT 357
QY 121 AlaAlaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
DB 358 GCTGAGGAAAGAAAGAAATTTTCATTGTCACGAAATAATGTAAGAGCAAGCTGTAGA 417
QY 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValTyrGlyArgAspLysGluLysAsp 160
DB 418 CGGAAACAGAGTTCGTATTACCGAACCGCAGGTTTATGGAAGAAGCAAGAAAGAT 477
QY 161 GluIleValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
DB 478 GAGATAGTGAAGAAATCTTAATAAACATGTATGATGCCCAACCTTTCAGTCTCCCA 537
QY 181 IleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGln 200
DB 538 ATACTGGTATGGGGGGGATTAGGAAAAAGCACTCTGCTCCAAAGGCTTCAATGACAG 597
QY 201 ArgValIleGlnHisPheHisProLysIleTyrIleCysValSerGluAspPheAsnGlu 220
DB 598 AGAGTTTCTGAGCAATTCATTCCAAAATATGATTTGTCTCGGAAAGATTTGTAGAG 657
QY 221 LysArgLeuIleLysGluIleValGlnSerIleGluGlnLysSer---LeuGlyGlyMet 239
DB 658 AAGAGGTTAATAAAGGCAATTGTAGAACTTAATTAAGAGAGGCCCATCTTGTGAGATG 717
QY 240 AspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeu 259
DB 718 GACTTGCTCCACTTCAAAAGAACCTTCAGAGATGCTGAAATGAAAAAGATCTTCTT 777
QY 260 ValLeuAspAspValTyrAsnGluAspGlnAspLysTyrAlaLysLeuArgGlnValLeu 279
DB 778 GTCTTAATGATGATGTTTGAATGAAAGATCAACAGAAAGGCGCTAATTAAAGAGCAGTCT 837
QY 280 LysValGlyLysAsnGlyLysValSerValLeuThrThrArgLeuGlnLysValGlySer 299
DB 838 AAGGTGGAGCAAGTGGTGCTTCTGTCTAACCACTACTGCTTGTGAAGAGTTGATCA 897

QY 300 IleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeu 319
DB 898 ATTATGGAACTTTCGCAACCATATGAACTGTCAAAATCTGTCTCAAGAAAGATTTGGTGG 957
QY 320 LeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIle 339
DB 958 TTGTTTCATGCAACCTGCACTTTGGACACCAAGAAATAATCCAAACTGTGTGGCAATC 1017
QY 340 GlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGly 359
DB 1018 GAAAGAGAGATTGAAAAAAGTGGTGCTGTCTTACAGGCCCAAACTTGTGGAGGT 1077
QY 360 IleLeuArgPheLysArgGluGluArgGlnTyrGlnHisValArgAspSerGluIleTyr 379
DB 1078 ATTTTGTGCTTCAAGAGAGAAAGAAAGCATGGGAAATGTGAGAGACAGTCCGATTTGG 1137
QY 380 LysLeuProGlnGlnLysSerSerIleLeuProAlaLeuArgLeuSerTyrHisIleLeu 399
DB 1138 AATTGGCTCAAGATGAAAGATTTCTATCTGCTGCTGCCCTGAGGCTTAGTTCAATCAACT 1197
QY 400 ProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGlnMet 419
DB 1198 CCAGTTGATTTGAAACATGCTTTCGATTTGTGGGTGTTCCTCAAGAGATGCCAAATG 1257
QY 420 GlyLysGlyAsnLeuIleSerLeuTyrMetAlaHisGlyPheIleLeuSerLysGlyAsn 439
DB 1258 GAAABAAGAAAGCATATCTCTCTGTGATGGCCGATGCTTTCTTTATCAAAAGAAAC 1317
QY 440 LeuGluLeuGlnLysAsnValGlyAsnGluValTyrAsnGluLeuTyrLeuArgSerPhePhe 459
DB 1318 ATGAGGCTTGAAGATGAGGCGAGATGGAAGTATGGAAGAAATTAATATACCTTGTTC 1377
QY 460 GlnGluIleGluValLysSerGlyGlnThrThrPheLysMetHisAspLeuIleHisAsp 479
DB 1378 CAAAGATTAAGTTAAGATGGAATACTTATTTCAAGATGATGATTCATCCATGAT 1437
QY 480 LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleLeuAl 499
DB 1438 TTGGCAACATCTCTGTTTCAGCAAAACATCAAGAGCAATTCGTTGAATAATAATAA 1497
QY 500 GluAsnTyrIleHisMetMetSerIleGlyPheThrLysValAlaSerSerTyrSerLeu 519
DB 1498 CACAGTTACACACATATGATGATTCATTTGTCGCGAAGTGGTGTGTTTTCACCTCT 1557
QY 520 SerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLys 539
DB 1558 CCCCCCTGGAAAGATTATCTGTTAAGAGTCTTAATCTAGATGATGACATTTAAT 1617
QY 540 GlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsn 559
DB 1618 AAGTTACCATCTTCCATTTGAGATCTAGTACATTTAAAGATTAATTGAACCTGATGGC--- 1674
QY 560 ThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAsp 579
DB 1675 AGTGGCATGTGTGCTTCCAAAGCAGTTATGCAACCTTCMAAATCTGCAACTCTTGAT 1734
QY 580 LeuHisGlyCysHisSerLeuCysLysProLysGluThrSerLysLeuGlySerLeu 599
DB 1735 CTACAAATATTCGACCAAGCTTTGTGTGTCGCAAAAGAAACAAGTAACTTGTAGTCTC 1794
QY 600 ArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySer 619
DB 1795 CGAAATCTTTTACTTATGATGGTACCGCATTCATTCATTTGATGCAACCAAGATAGATCA 1854
QY 620 LeuThrCysLeuLysThrLeuSerArgPheValValGlyTyrIleGlnLysLysSerCysGln 639
DB 1855 TTGACATGCTTAAAGCTCTAGGTCAATTTGTGTGGA---AGGAAGAAAGGTTATCA 1911
QY 640 LeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHisLeuGluArg 659
DB 1912 CTGTGTAACCTAGAAACCTTAATCTTATGCTCATTAATAATCTGCAATCTTGGAGA 1971
QY 660 ValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSer 679

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Db      1972 GTGAAGAAATGATPACAGACGCAAAAGACCAATTATATGCAAAAGGAATCTGCATCT 2031
Qy      660 LeuserMetLysTrpAspAspGluArgProArgIleTyrGluSerGluValGlu 699
Db      2032 TTAAACCAAGAGTTGG--AAATACCTTGGACCACTATATATGAAAGCAAGAACTTAA 2088
Qy      700 ValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArg 719
Db      2089 GTGCTTGAAGCCCTCAAAACCACTCCATCTGACTTCTTAAATCATATGCTTCA 2148
Qy      720 GlyIleArgLeuProAspTrpMetAsnHisSerValLeuLysAsnValValSerIleGlu 739
Db      2149 GGAATCCACTCTCCAGAGTGTGATGATCATCATGATATGAAATAATATGCTCTATTTCTA 2208
Qy      740 IleIleSerCysLysAsnCysSerCysLeuProPheGlyGluLeuProCysLeuLys 759
Db      2209 ATTAGCAACTTCAGAACTGCTCATGCTTACCACTTGTGGATCTGCTGTCTAGAA 2268
Qy      760 SerLeuGluLeuTrpArgGlySerIleGluValGluTyrValAsp----- 774
Db      2269 AGTCAAGATTACACTGGGGGCTGCGGATGTGAGATATGTTGAAGAAGTGATATTGAT 2328
Qy      775 -----SerGlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArg 792
Db      2329 GTTCATCTGATTCCTCCCAAGAAATAGATTTCATCTCTGAGAAACTGATATATG 2388
Qy      793 GluPheGlyAsnLeuLysGlyLysLeuLysGlyGluGluGluGluGluGluGluGlu 812
Db      2389 GACTTGTGTAGTCTGAAAGATGCTGTAAGAAAGAAAGAAAGCAATTCCTGTGCTT 2448
Qy      813 GluGluIleGluIleLysCysCysProMetPheValIleProThrLeuSerSerValLys 832
Db      2449 GAAAGAGATGATATTCACGAGTGCCTTTCTG-----ACCTTTCT----- 2490
Qy      833 LysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeu 852
Db      2491 ----- 2499
Qy      853 MetAlaLeuThrSerLeuGluIleArgTyrAsnLysGluAspAlaSerLeuProGluGlu 872
Db      2500 AGGCTCTTACTTCCCTCAGAAATTTGCTATATTAAGCTTACTTCCCAAGAAAG 2559
Qy      873 MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
Db      2560 ATGTTCAAAAACCTTGCAATCTCAAAATCTTGACAATCTTCGGTGCATATATCTCAA 2619
Qy      893 GluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysAsnIleSerCys 912
Db      2620 GAGCTGCTTACAGCTTGGTCTAGTCTGAATGCTTTGAAAAGCTTAAATAATTCATTGTGT 2679
Qy      913 TyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLeuIleSerLeuThrGluLeu 932
Db      2680 TGCACACTAGAGAGTCTCCCTGAGAAAGGCTGAAAGGCTTATATCTTCACTCACAGATTA 2739
Qy      933 SerIleThrTyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnHisLeuThrAla 952
Db      2740 TTGTGTAAACCTGTACATCTAAATGTTTACAGAGGGAATGACACCTAAACACC 2799
Qy      953 LeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIle 972
Db      2800 CTCACAAGTTAAAAAATTCGGGAGATGTCACAACATGATCAAGCGGTGTGAAGAGGATA 2859
Qy      973 GlyLysAspTrpTyrLysIleAlaHisIleProArgValPheIleTyr 988
Db      2860 GGAAGAGCTGSCACAAAATTTCTACATTCCTAATGTGAATATATAT 2907

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RESULT 6
 ADH51531 standard; DNA; 2913 BP.
 XX AC ADH51531;
 XX

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DT      25-MAR-2004 (first entry)
DE      XX
XX      S bulbocastanum Rpi-b1b gene SeqID48.
XX      plant disease; oomycete infection; Phytophthora infestans; fungicide;
XX      Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
XX      ds.
OS      Solanum bulbocastanum.
XX      XX
XX      US2003221215-A1.
XX      XX
XX      27-NOV-2003.
XX      XX
XX      07-FEB-2003; 2003US-00360522.
XX      XX
XX      07-FEB-2003; 2003US-00360522.
XX      XX
XX      (KWE-) KWEER EN RESEARCHBEDRIJF AGRICO BV.
XX      XX
XX      Allele JHM, Van Der Vossen EAG;
XX      XX
XX      WPI; 2004-010903/01.
XX      XX
XX      P-PSDB; ADH51537.
XX      XX
XX      New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
XX      PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
XX      PT with resistance against oomycete infection.
XX      XX
XX      Claim 6; SEQ ID NO 48; 98bp; English.
XX      XX
XX      This invention relates to a novel DNA sequence in the field of plant
XX      CC disease, in particular oomycete infections. The DNA sequence encodes a
XX      CC protein which may provide a plant or its progeny with at least partial
XX      CC resistance against an oomycete infection caused by Phytophthora
XX      CC infestans. The invention may be useful for the development of compounds
XX      CC with a fungicide activity. The DNA sequence of the invention encodes an
XX      CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
XX      CC cell, protein or binding molecule is useful for providing a plant or its
XX      CC progeny with resistance against an oomycete infection such as late blight
XX      CC (a disease of major importance to production of Solanaceae such as potato
XX      CC and tomato cultivars). The present sequence is that of the S
XX      CC bulbocastanum Rpi-b1b gene of the invention.
XX      XX
SQ      Sequence 2913 BP; 925 A; 531 C; 628 G; 829 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,79e-314 Length: 2913
Score: 3766.50 Matches: 753
Percent Similarity: 83.43% Conservative: 78
Best Local Similarity: 75.60% Mismatches: 130
Query Match: 73.46% Indels: 35
DB: 12 Gaps: 8

US-10-647-268-2 (1-988) x ADH51531 (1-2913)
Qy      1 MetAlaLeuAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db      1 ATGGCTGAAGCTTTCATCAAGTTGCTGACAAATCTCACTTTCCTCAAGGGGAA 60
Qy      21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
Db      61 CTGTATTTGCTTTTGGGTTTTCAGATGATGATTCCAAGGCTTTTCAAGCATGTTTCTACA 120
Qy      41 IleGlnAlaValLeuGlnAlaPalaGlnLysLysGlnLeuLysAspLysAlaIleGlnAsn 60
Db      121 ATTCAGCCGCTCTTGAAGATGCTCAGAGAAAGCACTCAACAACAAGCCTTAGAAAT 180
Qy      61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
Db      181 TGGTTGCAAAAACCTCAATGCTGTACATATATGAAAGTGATGATCTTGGATGAAATATAA 240
Qy      81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100

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Db 241 ACCAAGGCC---ACAAGATTCCTCCAGCTCGAATATGCGCGCTTATCATCAAAAGGTTATC 297
Qy 101 ThrPheArgHisLeuYsIlleGlyIysArgMetLysLysIlleMetGluLysLeuAspValIle 120
Db 298 CCTTCCCGTCACAGAGTCGGGAAAAGATGACCAAGGATGATGATGATGATGATGATGATGATGAT 357
Qy 121 AlaIaIaGluArgIleLysPheHisLeuAspGluArgThrIleGluArgGluValAlaThr 140
Db 358 GCTGAGAAAGAAAGAAATTTTCAATTTGACGAAAATTTGTAGACAGACAGACAGCTGTTAGA 417
Qy 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValIlyGlyArgAspLysGluLysAsp 160
Db 418 CGGAAACAGGTTCTGTATTAACCGAACCGGAGTTTATGAAAGACAAAGAGAAAGAT 477
Qy 161 GluIleValLysIleLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
Db 478 GAGATAGTGAATAATCTTAATAAACAATGTAGTGTGCGCAACACCTTTCAGTCCCTCCA 537
Qy 181 IleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGln 200
Db 538 ATACTTGATAGGGGGGAGTTAGAAAAGACTCTTGCCCAATGCTTCAATGACAG 597
Qy 201 ArgValIleGluHisPheHisProLysIleTrrIleCysValSerGluAspPheAsnGlu 220
Db 598 AGAGTACTGAGCAATTCATCCAAATATGATGATTTGTCTCGAAGATTTTGATGAG 657
Qy 221 LysArgLeuIleLysGluIleValGluSerIleGluLysSer--LeuGlyGlyMet 239
Db 658 AAGAGGTAAATAAGCAATGTAGATCTATGAAAGAGCCATACCTTGAGTGAAGT 717
Qy 240 AspleuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysThrLeuLeu 259
Db 718 GACTTGCTCCACCTTCAAAAGAGCTTCAGAGTTGCGAATGAGAAAAGATCTTGCTT 777
Qy 260 ValLeuAspAspValTrrAsnGluAspGluAspLysTrrAlaLysLeuArgGluValLeu 279
Db 778 GTCTTAAGTGAATGTTTGAAGATGAAATCAACAGAAAGGCGCTAAATTTAAGACAGTCTTG 837
Qy 280 LysValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGluValGlySer 299
Db 838 AAGGTGAGCAAGTGTGCTTCTGTCTTCAACACTACTCGTCTTGAAGAGTTGAGTCA 897
Qy 300 IleMetGlyThrLeuGlnProTrrGluLeuSerAsnLeuSerGlnLysAspCysTrrLeu 319
Db 898 ATATAGGAAATGCAACCATGAACTGTCAATCTGTCAAGAAAGATGTGTGTTG 957
Qy 320 LeuPheMetGlnArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIle 339
Db 958 TTGTTCAAGCAACGTGATTTGACACCAAGAAATAAATCCAAACCTTGTGCGCATC 1017
Qy 340 GlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGly 359
Db 1018 GGAAGAGAGATTTGAAAAAAGTGTGTGTCTCTAGACAGCAAACTCTTGAGAGT 1077
Qy 360 IleLeuArgPheLysArgGluGluArgGlnTrrLysIleValAlaArgAspSerGluIleTrr 379
Db 1078 ATTTTGTCTTCAAGAGAGAAAGAAAGCATGGAAATGTGAGACAGTCCGATTTGG 1137
Qy 380 LysLeuProGlnGluGluSerSerIleLeuProAlaLeuArgLeuSerTrrHisIleLeu 399
Db 1138 AATTGCTCTCAAGATGAAAGTTCTATTCCTGCTGCTGCTGAGGCTTATTCACATCACTT 1197
Qy 400 ProLeuAspLeuArgGlnCysPheThrTrrCysAlaValPheProLysAspThrGlnMet 419
Db 1198 CCACTTATTTGAACAATGCTTTGCGATTTGTGCGGTTCCTCAAGAGATGCCAAATG 1257
Qy 420 GluLysGlyAsnLeuIleSerLeuTrrMetAlaHisGlyPheIleLeuSerLysGlyAsn 439
Db 1258 GAAAAAAGAAAGCTAATCTCTCTGATGCGCATGTTTCTTTATCAAAAAGAAAC 1317
Qy 440 LeuGluLeuGluAsnValGlyAsnGluValTrrAsnGluLeuTrrLeuAspSerPhePhe 459
Db 459
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Db 1318 ATGAGCTAGAGATGTCGGCGGATGAAGTATGAAAAGATTTATCTGAGCTCTTTTTC 1377
Qy 460 GlnGluIleGluValLysSerGlyGlnThrTrrPheLysMetHisAspLeuIleHisAsp 479
Db 1378 CAAGAGATTTGAAGTTAAAGATGTAAACCTATTTCAAGATGATGATGATGATGATGATGATGAT 1437
Qy 480 LeuAlaThrSerLeuPheSerSerAlaSerThrSerSerSerSerIleArgGluIleIleVal 499
Db 1438 TTGGCAACATCTCTGTTTTCAGCAACACATCAAGCAGCATATCTCGTGAATAATAATAA 1497
Qy 500 GluAsnTrrIleHisMetMetSerIleGlyPheThrLysValIleSerSerTrrSerLeu 519
Db 1498 CACAGTAAACACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1557
Qy 520 SerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLys 539
Db 1558 CCCCCCTTGAAAAGTTATCTGTTAAGATGCTTAAATGATGATGATGATGATGATGATGATGAT 1617
Qy 540 GlnLeuProSerSerIleGlyAspLeuValHisLeuArgTrrLeuAsnLeuSerGlyAsn 559
Db 1618 AAGTTACCAATCTTCATTTGAGATCTAGTACATTTAAGATTAATCTTGAACCTGTATGATG 1674
Qy 560 ThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAsp 579
Db 1675 AGTGCAATGCGTATGCTTCCAAAGCAGTTATGCAAGCTTCAAAATCTGCAAACTTGAT 1734
Qy 580 LeuHisGlyCysHisSerLeuCysGlyLeuProLysGluThrSerLysLeuGlySerLeu 599
Db 1735 CTACAAATATTTGCAACCAAGCTTGTGTTGCGCAAAAGAAACAAGTAACTTGTGATGCTC 1794
Qy 600 ArgAsnLeuLeuLeuAspGlyCysTrrGlyLeuThrCysMetProProArgIleGlySer 619
Db 1795 CGAAATTTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1854
Qy 620 LeuThrCysLeuLysThrLeuSerArgPheValIleGlyIleGlnLysLysSerCysGln 639
Db 1855 TTGACATGCTCTTAAGACTTACGTCATTTGTTGTTGA---AGAAAGAAAGGTTATCA 1911
Qy 640 LeuGlyGluLeuArgAsnLeuLeuTrrGlySerIleGluIleThrHisLeuGluArg 659
Db 1912 CTGTGGAATGAGAAACCTTAATCTCTATGCTCAATTAATAATCTGCAATCTTGAGAGA 1971
Qy 660 ValLysAsnAspMetCysPalaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSer 679
Db 1972 GTGAAGATGATTAAGACGGAAGAAAGCAATTTATCTGCAGAAAGAGATCTGCATTTCT 2031
Qy 680 LeuSerMetLysTrrPheAspAspGluArgProArgIleTrrGluSerGlnLysValGlu 699
Db 2032 TTAAAGATGATGTTGG---AATAACTTTGACCCACATATATATGAATCAGAGAAAGTTAA 2088
Qy 700 ValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArg 719
Db 2089 GTCTTGAAACCTTCAACCACTCCAAATCTGACTTCTTTTAAATCTATGAGCTTCA 2148
Qy 720 GlyIleArgLeuProAspTrrMetAsnHisSerValLeuLysAsnValIleSerIleGlu 739
Db 2149 GGAATCCATCTCCCAAGAGTGAATGATCACTCAGTATGAAAAATGTGTCTTATTTCA 2208
Qy 740 IleIleSerCysLysAsnCysSerCysLeuProProPheGlyGluLeuProCysLeuLys 759
Db 2209 AATTAGCACTTCAAGAAATGCTCATGCTTACCACTTTGAGATGCTGCTGTGTAGAA 2268
Qy 760 SerLeuGluLeuTrrArgGlySerAlaGluValGluTrrValAsp----- 774
Db 2269 AGCTTGAATTTACACTGCGGGGCTCTCGGATGTGAGATATGTTGAAGAGATGATTTGAT 2328
Qy 775 -----SerGlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArg 792
Db 2329 GTTCATTTCTGATTCCTCCCAAGAAATTAAGTTTTCATCTTGAAGAACTTATATATG 2388
Qy 793 GluPheGlyAsnLeuLysGlyLeuLeuLysLysGluGluGlnGlnCysProValLeu 812
Db 2389 GACTTTGTAGTCTGAAGAGATTTGCTGAAGAAAGAGAGAACCAATTCTCTGTGCTT 2448
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QY      813  GluGluIleGluIleLysCysCysProMetPheValIleProThrLeuSerSerValLys 832
DB      2449  GAAAGATGATATATTCACGAGTGCCTTTCTG-----ACCTTTCT----- 2490
QY      833  LysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeu 852
DB      2491  -----TCTATATCTT 2439
QY      853  MetAlaLeuThrSerLeuGluIleArgTyrAsnLysGluAspAlaSerLeuProGluLys 872
DB      2500  AGGGCTTACTACTCCCTCAGAAATTCCTATATTAAGTACCTTCACTTCCCGAAGAG 2559
QY      873  MetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLys 892
DB      2560  ATGTTCAAAAACCTTGCAATCTCAAAATCTGCAATCTCTCGGTGCAATATCTCAA 2619
QY      893  GluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCys 912
DB      2620  GAGCTGCCTACCAAGCTTGCTGCTGTAATGCTTGAATGCTTGAATGCTTGAATGCTG 2679
QY      913  TyrAlaLeuGluSerLeuProGluGluLysValLysGlyLeuIleSerLeuThrGluLeu 932
DB      2680  TCGCGACTAGAGAGTCTCCCTGAGGAGAGGCTGAGAGGCTTATCTTCACTCAGAGTTA 2739
QY      933  SerIleThrTyrCysGluMetLeuGlnCysLeuProGluGluLysLeuGlnHisLeuThrAla 952
DB      2740  TTCTGTGAACACTGTAACATCTGTAATAATCTTACCAAGGAGATGCGACACTTAACACC 2799
QY      953  LeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyLe 972
DB      2800  CTCACAGATTAAAAATTCGGGGATGTCTCACACACTGATCAACGGGTGAGAGAGGAAATA 2859
QY      973  GlyGluAspTyrTyrLeuIleAlaHisIleProArgValPheIleTyr 988
DB      2860  GGAAGAGACTGGCACAAATTTCTCACATCTTAAATGTAATATATAT 2907

RESULT 7
ADFI17762
ID  ADFI17762 standard; DNA; 3260 BP.
XX
AC  ADFI17762;
XX
DT  12-FEB-2004 (first entry)
XX
DE  S_bulbocastanum RGCI-b1b coding DNA containing an intronic sequence.
XX
KW  gene; ds; RGCI-b1b; Rpi-b1b gene cluster; growth regulator;
KM  oomycete infection; introgression breeding; plant; late blight.
XX
OS  Solanum bulbocastanum.
XX
FH  Key
FT  CDS
FT  1..3260
FT  /tag= a
FT  /product= "RGCI-b1b protein"
FT  /note= "This coding sequence contains one intron"
FT  /transl_except= (pos: 709..710, aa: Gly)
FT  intron
FT  428..708
FT  /tag= b
FT  /number= 1
XX
XX  EP1334979-A1.
XX
XX  13-AUG-2003.
XX
XX  08-FEB-2002; 2002EP-00075565.
XX
XX  08-FEB-2002; 2002EP-00075565.
XX
XX  (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
XX  Van Der Vossen BAG, Allefa JHM;
PI

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XX      XX  MPI: 2003-714439/68.
DR      DR  P-PSDB; ADFI17767.
XX      XX
PT      PT  New resistance gene conferring resistance against an oomycete pathogen,
PT      PT  useful for producing plants, especially potatoes and tomatoes, resistant
PT      PT  against oomycete pathogens such as Phytophthora infestans.
XX      XX
PS      PS  Example 5; SEQ ID NO 38; 86bp; English.
XX      XX
CC      CC  This invention relates to novel isolated polynucleotides that confer
CC      CC  resistance against late blight caused by the oomycete pathogen
CC      CC  Phytophthora infestans, which threatens both tomato and potato crops.
CC      CC  Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
CC      CC  leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
CC      CC  and which cause disease resistance to bacteria, fungi, nematodes etc.
CC      CC  These R genes, namely Rpi-b1b, RGCI-b1b, RC3-b1b and RC4-b1b, can be
CC      CC  described as plant growth regulators. They are useful in providing
CC      CC  resistance to Phytophthora infestans, especially in Solanum tuberosum
CC      CC  (potato) plants to protect against oomycete infection or to demonstrate
CC      CC  disease susceptibility. Resistance can be conferred by transformation of
CC      CC  existing potato and tomato cultivars with the gene, a procedure that is
CC      CC  more straightforward and faster than conventional introgression breeding.
CC      CC  This polynucleotide sequence is the Solanum bulbocastanum RGCI-b1b coding
CC      CC  DNA containing an intronic sequence in an exemplification of the
CC      CC  invention.
XX      XX
SQ      SQ  Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;
XX      XX

Alignment Scores:
Pred. No.: 5,44e-304 Length: 3260
Score: 3648.00 Matches: 745
Percent Similarity: 76.58% Conservative: 92
Best Local Similarity: 68.16% Mismatches: 143
Query Match: 71.15% Indels: 114
DB: 10 Gaps: 9

US-10-647-268-2 (1-988) x ADFI17762 (1-3260)
QY      QY  1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyLys 20
DB      DB  1 ATGGCTTAACCTTCTCTCAAGTTCGTGCTAGATATCTCACTTTTTCATCCAGGGGAA 60
QY      QY  21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
DB      DB  61 CTTCGATTGGTTTGTGTTTCGAGAGGAGTTTAAATCTTCAAGTATCTTTTCATG 120
QY      QY  41 IleGlnAlaValLeuGluAlaPheAlaGlnLysLeuLysAspLysAlaIleGluAsn 60
DB      DB  121 ATCCAACTGTGCTAGAGATGCTCAAGAGACGAATGAAAGTACAAAGCAATTAAGAAC 180
QY      QY  61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
DB      DB  181 TGGTTACAGAACTCAATGTTGCTGCATATGATGATGATGATGATGATGATGATGATG 240
QY      QY  81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIle 100
DB      DB  241 ACTGAGGCA--GCMAATTCAGACAGGCTGTATGGGGCTTATCTCAACGAGCAATC 297
QY      QY  101 ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspValIle 120
DB      DB  298 ACTTTCGTTACAAAGGTGGGAAAAAGATGAAGAATGATGAAAAAAGTATGATGCAAT 357
QY      QY  121 AlaAlaGluArgLysPheHisLeuAspGluArgThrIleGluAlaGlnValAlaThr 140
DB      DB  358 GCAGAGGAAAGGAGAAATTTTCAATTATGATGAAGATTATAGAGAGACAAGCTGCTAGA 417
QY      QY  141 ArgGlnThr----- 143
DB      DB  418 CGGCAAC-AGGTCCTCATTTATTTATTTTAAAACAAATAAGTATACAAATTCGAG 476
QY      QY  143 ----- 143

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Dh 477 AGAAGAGAAATTTATATCATTTTATTTTGGCAATATCAAGTCATTTGTGTT 536
Qy 143 ----- 143
Dh 537 TTAAGCTGGGGAGATTCAAAATATTTTCTCTAGCTTAATGTTGTCTCACTCACTCA 596
Qy 143 ----- 143
Dh 597 GCATGATTTTCTCAATCCCTTCATCACTCCCTCTACTGCAATATCTCTCTAT 656
Qy 144 -----GlyPheVal 146
Dh 657 TTCTGTGATCTCTTAATGAGCTTGAATGTAAACAATCTTGTGAGAGAGTTTCTT 716
Qy 147 LeuAenGIuProGIuValTyrGIuYArgAspGluValAspGluIleValIleValIleu 166
Dh 717 TTAACGTAGCCAAAGCTTTATGAGAGAGAGAGAGAGAGATGATAGATGAGAAATCTTG 776
Qy 167 IleAenValSerAsnIleGIuThrLeuProValLeuProIleLeuGIuMetGIuGIy 186
Dh 777 ATAAACATGTATGTTATTCGAGAGAGTCCAGTACTCCCAATACCTGGTATGGGGGA 836
Qy 187 LeuGIuYThrThrLeuValAGIuMetValPheAenAspGIuArgValIleGIuIlePhe 206
Dh 837 CTAGAGAAAGAGACTCTGAGCCCAATGGTCTTCAATGATCAAGATTAAGAGCATTTTC 896
Qy 207 HisProIleTyrPheValSerGIuAspPheAenGIuYArgLeuIleuGIu 226
Dh 897 AATCAAGATATGGGTTTGTCTCAGATGATTTTGTAGAGAGAGGTTATTTAGGCA 956
Qy 227 IleValGIuSerIleGIuGIuYSerLeuGIuMetAspLeuValProLeuGIuYs 246
Dh 957 ATTGAGATCTAATGAGAGAAAGCATCGGGTGACATGAGCTTGCTCCCTCAGAAA 1016
Qy 247 LysLeuAArgAspLeuLeuAsnGIuYLeuYThrLeuValLeuAspAspValTyrAsn 266
Dh 1017 AAGCTTGGAGGTTGTGATGAGAGAGAGAGATCTTCTGTGTTGGAGATGTTTGAAT 1076
Qy 267 GIuAspGIuAspLeuYThrPheValLeuLeuArgGIuValLeuYsValGIuYAspGIuVal 286
Dh 1077 GAAGTCAAGAGAGAGAGAGAGATCTTATGAGCAGATTTGAAAGATTTGAGAGTGTCT 1136
Qy 287 SerValLeuThrThrThrArgLeuGIuYValGIuSerIleMetGIuYThrLeuGIuPro 306
Dh 1137 TCAATTTCAATTAATCTACTCTCTGAGAGAGAGAGAGATTAATGAGAGATCTTCACTA 1196
Qy 307 TyrGIuLeuSerAsnLeuSerGIuAspCysThrLeuLeuPheMetGIuArgValPhe 326
Dh 1197 TATCATTTATCAAAATTTGTCTCAAGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1256
Qy 327 GIuYHisGIuGIuGIuIleAsnLeuAsnLeuValIleGIuYsGIuIleValIleYs 346
Dh 1257 TGCCACCAAAACCGAGAGAGAGAGAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1316
Qy 347 CysGIuYGIuValProLeuValIleYsThrLeuGIuGIuIleLeuArgPheYsArgGIu 366
Dh 1317 TGTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1376
Qy 367 GIuArgGIuThrGIuIleValArgAspSerGIuIleThrYsLeuProGIuGIuGIuSer 386
Dh 1377 GAAAGTCAAAATGAGAGAGAGAGAGATGAGATTTGAGATTTAATCTCAAGAGAGAGAT 1436
Qy 387 SerIleLeuProIleLeuArgLeuSerTyrHisIleLeuProLeuAspLeuArgGIuYs 406
Dh 1437 TCTGTGTTGCTGCTGAGAGAGAGATTAATCATCATCTTCACTTGAATTTGAGAGAGAT 1496
Qy 407 PheThrTyrCysIleValIlePheProYsAspThrGIuMetGIuYsGIuAsnLeuIleSer 426
Dh 1497 TTTGCAATATGCGAGATTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGATTTTCATCGCT 1556
Qy 427 LeuTyrPheMetIleHisGIuIleLeuSerIleGIuYsAsnLeuGIuGIuGIuValIleGIy 446
Dh 1557 CTCTGATGCGACACAGATTTCTTTTATCAAAAGAGAGAGATGAGAGATGAGAGATGAGGCT 1616

Qy 447 AsnGIuValTyrPheAsnGIuLeuTyrLeuArgSerPhePheGIuGIuIleGIuValIleYsSer 466
Dh 1617 AATGAGATGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1676
Qy 467 GIuGIuThrTyrPheYsMetHisAspLeuIleHisAspLeuValIleThrSerLeuPheSer 486
Dh 1677 GGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1736
Qy 487 AlaSerThrSerSerAsnIleArgGIuIle----- 497
Dh 1737 GCAAGCCCATCAACAGAGATTAATCCCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1796
Qy 498 ---IleValGIuAsnTyrIleHisMetSerIleGIuYThrThrYsValIleSerSer 516
Dh 1797 TTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1856
Qy 517 TyrSerLeuSerHisIleGIuGIuYsPheValSerLeuArgValIleAsnLeuSerAspIle 536
Dh 1857 TACTCTCTCTGCTCTTAAGAGTTGTCTCGTTAAGGAGGCTTAATCTTAAGTAACTCA 1916
Qy 537 LysLeuYsGIuLeuProSerSerIleGIuYsPheValHisIleuArgTyrLeuAsnLeu 556
Dh 1917 GAATTTGAACAGTAACTGCTCTCCGTGAGATCTAGTACATTAAGATCACTTGACCTG 1976
Qy 557 SerGIuYsAsnThrSerIleArgSerLeuProAsnGIuLeuCysYsIleGIuAsnLeuGIu 576
Dh 1977 TCTGTGAT---AAATTTTATGCTCTTCAAGAGGTTGCAAGCTTCAAAATCTGACG 2033
Qy 577 ThrLeuAspLeuHisGIuYsHisIleSerLeuYsCysLeuProYsGIuThrSerYsLeu 596
Dh 2034 ACTCTGATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2093
Qy 597 GIYSerLeuArgAsnLeuLeuAspGIuYsTyrGIuYLeuThrCysMetProProArg 616
Dh 2094 TGTAGTCTCCGAGATCTGACTGTGATCACTGT---CCATTAATCTTAAGCCACAGAG 2150
Qy 617 IleGIYSerLeuThrCysLeuYsThrLeuSerArgPheValIleGIuIleGIuYs 636
Dh 2151 ATAGAGATGTTGACATGCTCTTAAGACATGATGATCTTCTGTTAGGCT---GAGAGAGAG 2207
Qy 637 SerCysGIuLeuGIuLeuLeuArgAsnLeuAsnLeuTyrGIYSerIleGIuIleThrHis 656
Dh 2208 GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2267
Qy 657 LeuGIuArgValIleYsAsnAspMetAspIleYsGIuValAsnLeuSerIleYsGIuAsn 676
Dh 2268 CTGAGAGAGTGAAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2327
Qy 677 LeuHisSerLeuSerMetYsTyrPheAspAspGIuArgProArgIleTyrGIuSerGIu 696
Dh 2328 CTACACTCTTAAGAGATGAGTTGGAT-----AGACCAAGAGATGATGATCGAG 2378
Qy 697 LysValGIuValLeuGIuValLeuYsProHisSerAsnLeuThrCysLeuThrIleArg 716
Dh 2379 GAAGTTAAAGTGTCTTAAGCCCTCAACACATCCCAATCTGAATATTAATTAAGATCAAT 2438
Qy 717 GIuYArgGIuYIleArgLeuProAspTyrPheAsnHisSerValLeuYsAsnValIle 736
Dh 2439 GACTTTGTGAGATTTCTGTCTCCCTGACGTGAGATGATCACTGATTTGAGAGAGATGATG 2498
Qy 737 SerIleGIuIleIleSerCysYsAsnYsSerCysLeuProProPheGIuGIuLeuPro 756
Dh 2499 TCTATTCTAATTAAGCGGTTGTGAAGAGCTCTGTGTTTCAACACCTTGTGTGAGCTGCT 2558
Qy 757 CysLeuYsSerLeuGIuLeuThrArgGIuYsArgIleGIuValIleGIuYVal---AspSer 775
Dh 2559 TGTCTTAAGAGCTGAGATTAACAGACGGGTCTGTGGAGGTGAGAGATGATTAAGAGATCT 2618
Qy 776 GlyPheProThrArgArgArgPheProSerLeuArgYsLeuAsnIleArgGIuPheGIy 795
Dh 2619 GGAATTCCTCAAGAGAGAGATTTTCATCTCTGAGAGAGAGATTAATTAATTAATTAATTAAT 2678
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QY 796 AsnLeuYsglyLeuLeuYsglyGluGluGlnCysProValLeuGluGlu 815
 DB 2679 AATCTGAAGAGATTGACAGAAATGAAAGACAGACATTCCTCGCTTGAAGAGATG 2738
 QY 816 GluIleYsgCysProMetPheValIleProThrLeuSerSerValValLeuVal 835
 DB 2739 AAGATTTCGAGATCCCTATGTTGTTTCCGACCCCTTTCTTGTCMAAATTGAA 2798
 QY 836 ValSerGlyAspIlySerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
 DB 2799 ATTGGGGGGG---GCAGATCGAGAGGTTTGAGCTTCATATCTAATCTGACACTCTT 2855
 QY 856 ThrSerLeuGlnIleArgTyrAsnIlysgIuAspAlaSerLeuProGluGluMetPheIys 875
 DB 2856 ACATCCCTCAAGATTTCAGTACACACAGAGTCACTTCACTGGAAGAGATGTTCAA 2915
 QY 876 SerLeuAlaAsnLeuYsgTyrLeuAsnIleSerPheTyrPheAsnLeuYsgIleuPro 895
 DB 2916 AACCTTGAAATCTCATATACCTTGAAGTCTCTTCTTGAGAAATCTCAAGAGCTGCT 2975
 QY 896 ThrSerLeuAlaSerLeuAsnAlaLeuYsgIleuGlnIleHisSerCysTyrAlaLeu 915
 DB 2976 ACCGAGCTCGCTAGCTCAACAATTGAAAGTCTGAGTATTCGTTATTGTTACGCACTA 3035
 QY 916 GluSerLeuProGluGluGlyValIlysgIlyLeuIleSerLeuThrGlnLeuSerIleThr 935
 DB 3036 GAGAGTCTCCCGCAGAGAGGCTGGAAGTTTATCTTCACTCAAGACTTATTGTTGAA 3095
 QY 936 TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnIleHisSerCysTyrAlaLeu 955
 DB 3096 CACTGTAAATGCTAAATGTTTACAGAGGAGATGCGACACTTAACAACCTCAAGT 3155
 QY 956 LeuSerValGluPheCysProThrLeuAlaIlyArgCysGlyIlyGlyIleGlyGluAsp 975
 DB 3156 TTTAAATAATTCGGGAGTGTCCAACTGATCAAGCGGTGTGAAGAGGAATGAGAAAGAC 3215
 QY 976 TrpTyrIlyIleAlaIleAlaIleProArgValPheIleTyr 988
 DB 3216 TGGCAAAAATTTCTCACATTCCTTAATGTGAATATATAT 3254
 RESULT 8
 ID ADH51534 standard; DNA; 3260 BP.
 XX ADH51534;
 AC
 XX 25-MAR-2004 (first entry)
 DT
 XX
 DE S bulbocastanum RGCl-b1b gene SeqID51.
 XX
 KM plant disease; oomycete infection; Phytophthora infestans; fungicide;
 KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
 KM des; RGCl-b1b.
 XX
 OS Solanum bulbocastanum.
 XX
 US2003221215-A1.
 XX
 XX 27-NOV-2003.
 PD
 XX 07-FEB-2003; 2003US-00360522.
 PF
 XX 07-FEB-2003; 2003US-00360522.
 PR
 XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
 PA
 XX AlJefe JHM, Van Der Vossen EAG;
 PI
 XX WPI; 2004-010903/01.
 DR
 XX
 XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.

XX
 PS Claim 6; SEQ ID NO 51; 98bp; English.
 XX
 CC This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of the S
 CC bulbocastanum RGCl-b1b gene which is related to the invention.
 XX
 SQ Sequence 3260 BP; 1012 A; 555 C; 706 G; 987 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,44e-304 Length: 3260
 Score: 3648.00 Matches: 745
 Percent Similarity: 76.58% Conservative: 92
 Best Local Similarity: 68.16% Mismatches: 143
 Query Match: 71.15% Indels: 114
 DB: 12 Gaps: 9
 US-10-647-268-2 (1-988) x ADH51534 (1-3260)
 QY 1 MetAlaGluAlaPheLeuGlnValLeuAspAsnLeuThrCysPheIleGlnGly 20
 DB 1 ATGCTGAAGCTTTCCTTCAAGTCTCTAATATCTCACTTTTTCATCAAGGGGAA 60
 QY 21 LeuGlyIleuIleuGlyPheIlyAspGluIlysgIlyLeuGlnSerThrPheThrThr 40
 DB 61 CTTCGATTGGTTTGGTTTGGTTTGCAGAGAGGTTTAAACCTTCAAGTATTTTCATG 120
 QY 41 IleGlnAlaValLeuGlnAspAlaGlnIlysgIlyLeuYsgIlyAspIlyAlaIleGluAsn 60
 DB 121 ATCCAGCTGTGCTAGAAAGATGCTCAAGAGAGCACTGAAGTCAAGGCAATAAAGAAC 180
 QY 61 TrpLeuGlnIlyLeuAsnAlaAlaIlyArgValIleAspPheIleuAspGluCysIys 80
 DB 181 TGGTTACAGAAATCTCAATGTTGCTGCAATGATGATGATGATGATGATGATGATGAT 240
 QY 81 ThrGluAlaProIleArgGlnIlysgIlyAsnIlysgIlyCysTyrHisProAsnValIle 100
 DB 241 ACTGAGGCA---GCAAGTTTCAAGCAGGCTGATTTGGGCGTTATCATCCAGACCATC 297
 QY 101 ThrPheArgHisIlysgIlyIlyArgMetIlysgIlyIleMetGluYsgLeuAspValIle 120
 DB 298 ACTTTCTGTTCAGAGTGGGAAAAAGATGAAGAAATGATGAAAGAACTAGATGCATTT 357
 QY 121 AlaIleGluArgIlysgIlyPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
 DB 358 GCAGAGGAAACGAGAAATTTTCATTAGATGAAGATTATAGAGACAAGCTGCTAGA 417
 QY 141 ArgGlnThr----- 143
 DB 418 CGGAAAC-AGTGCTCATCTTAATTTTAAACAAATTAAGTATTACAAATTGCGAG 476
 QY 143 ----- 143
 DB 477 AGAAACGAGAAATTTATATCTTTTATTTTGGCAATTATCAAGATCATTTGTGTTT 536
 QY 143 ----- 143
 DB 537 TTAAGCTGGGGGAAGTTCAATATTTTCTAGTCTTAATGTTTGTCTGACTCATCA 596
 QY 143 ----- 143
 DB 597 GCATGATTCTCAATCTTCACTTCAACTCCCTCACTGCTGCAAAATATCTTCTCTATT 656
 QY 144 -----GlyPheVal 146

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Db 657 TTCTGTGACTCTTAATGAGCTTGAATGTAACAACATCTTGTGTGAGCAGGTTTGT 716
Qy 147 LeuAnsgluProGlnValTyrGlyArgAspIleGlySerGluValLeuValSer 166
Db 717 TTAACGTAGCCCAAAAGTTATGAGAGGAAAAGAGAGATGATGATAAATCTGTG 776
Qy 167 IleAsnValSerAsnIleGlnThrLeuProValLeuProIleGlnGlyVal 186
Db 777 ATAAACAATGTTAGTATTCGAGAAAGTCCAGACTCCCAATCTTGATGGGGA 836
Qy 187 LeuGlyThrThrLeuValGlnMetValPheAsnArgIleValIleGlnIlePhe 206
Db 837 CTAGAAAGACGACTCTAGCCCAATGCTTCAATGATCAAGAATTAAGACATTC 896
Qy 207 HisProIleIleThrIleCysValSerGluAspPheAsnGluValArgLeuIle 226
Db 897 AATCTAAAGATATGGTTGTGTCTCAGATGATTTGATGAGAAAGGTATTAAGCA 956
Qy 227 IleValGlnSerIleGlnGluSerLeuGlyMetAspLeuValProLeuGlnIle 246
Db 957 ATGTGATGATCTATTGAGAAAGCACTGGGTGACATGACTGGCTCCCTCCAGAA 1016
Qy 247 LysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeuValLeuAspAspVal 266
Db 1017 AAGCTTCAGAGAGTTGTAATGAGAAAAGATACCTTCTGTTTGGATGATGTTGGAAT 1076
Qy 267 GluAspGlnAspLysThrAlaLysLeuArgGlnValLeuLysValGlyValSer 286
Db 1077 GAAAGTCAAGAAAAGTGGAGTAATCTTAGAGCAGATTAAGAGATTGGAGCTAG 1136
Qy 287 SerValLeuThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeu 306
Db 1137 TCATTTCAATTAATTAATCTGCTCTTGAATAAATGGATCAATTAAGCAATTTG 1196
Qy 307 TyrGluLeuSerAsnLeuSerGlnGluAspCysThrLeuLeuPheMetGlnArg 326
Db 1197 TATCAGTTATCAAAATTTGCTCAAGAAAGATTGTTGTTTCACCAACAGTGCAT 1256
Qy 327 GlyHisGlnGlnGluIleAsnLeuAsnLeuValAlaIleGlyLysGlnIleVal 346
Db 1257 TGCCACCAAAACCGAAACAGTCTTAATCTTAAGAAATCGAAAGAGATGTGAAG 1316
Qy 347 CysGlyGlyValProLeuValAlaLysThrLeuGlyGlyIleLeuArgPheLys 366
Db 1317 TGTGGGGGTGTGCTCTAGACAGCAAACTCTTGAAGCTTTTACGCTTCAAGAG 1376
Qy 367 GluArgGlnThrGluHisValArgAspSerGluIleTyrLysLeuProGlnGlu 386
Db 1377 GAAAGTGAATGGAAACATGATGATGATGATGAAATTTTCAACCAAGATCAAA 1436
Qy 387 SerIleLeuProAlaLeuArgLeuSerTyrHisIleLeuProLeuAspLeuArg 406
Db 1437 TCTGTTTGTGCTGCTGAGCTGAGGTATCATCTTCCACTTGATTTAGACAAAT 1496
Qy 407 PheThrTyrCysAlaValPheProLysAspThrGluMetGluLysGlyAsnLeu 426
Db 1497 TTTCGATATTCGCGAGTATTCGCAAGACACCAAAATAGAAAAGAAATCTCAT 1556
Qy 427 LeuThrMetAlaHisGlyPheIleLeuSerLysGlyAsnLeuGluLeuAsnVal 446
Db 1557 CTCGAGATGGCACACAGTTTCTTTATCAAAAGGAAACATGAGCTGAGAGCTG 1616
Qy 447 AsnGluValTTPAsnGluLeuThrLeuArgSerPhePheGlnGluIleGluVal 466
Db 1617 AATAGAGATGAGAAATTAATCTTGAAGCTTTTTCAGAGAGATTGAAGTTAAAT 1676
Qy 467 GlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeu 486
Db 1677 GGTAAACTTATTTCAAGATGATCTCATTCATGATTTGGGTACATCATATGTTT 1736
Qy 487 AlaSerThrSerSerSerAsnIleArgGluLeu----- 497
Db 1737 GCAAGCGATCAACAGAGATTAACGCCAAATAATGTAAGATGATGAATATGAT 1796
Qy 498 ---IleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysValSer 516
Db 1797 TTCAATTGACAAATTTATTAAGATATGATGTCATTTGGTTTCTCCGAAGTGT 1856
Qy 517 TyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeuSer 536
Db 1857 TACTCTCCTTGCTCTTAAAGAGTTGTCTCGTTAAGGGGTCTTAATCTTAAGTA 1916
Qy 537 LysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeu 556
Db 1917 GAATTTGAACAGTATCCGCTCTTCGTTGAGATGTAGACATTTTAAGATACCT 1976
Qy 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsn 576
Db 1977 TCTGTATAT---AAATTTGATGCTTCCAAAGAGCTTGCCAGCTTCABAATCT 2033
Qy 577 ThrLeuAspLeuHisGlyCysHisSerLeuCysLeuProLysGluThrSerLeu 596
Db 2034 ACTCTTGATCTATTAATTAATGTCAGTCACTTCTGTTGCGGAAACAACAAGTA 2093
Qy 597 GlySerLeuArgAsnLeuLeuAspGlyCysTyrGlyLeuThrCysMetProArg 616
Db 2094 TGTAGTCTCCGAAATCTTGATCTGATCACTGT---CCATTAAGCTTATGACC 2150
Qy 617 IleGlySerLeuThrCysLeuLysThrLeuSerArgPheValGlyIleGlnLys 636
Db 2151 ATAGAGATTTGATGATCCCTTAAGACATGATTAATCTTGTGTGAAGC---GA 2207
Qy 637 SerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGlu 656
Db 2208 GGTATATCAACTGTTGTAACATCAAGAAATTAACCTCGTGTGCAATTTCAAC 2267
Qy 657 LeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLys 676
Db 2268 CTTAGAGAGTGAAGAAATGATATGAGACAAAGACCAATTAATCTGCAAAAGCA 2327
Qy 677 LeuHisSerLeuSerMetLysThrAspAspGluArgProArgIleTyrGluSer 696
Db 2328 CTACACTCTTTAAGCAATGATGGGAT-----AGACCAACAGATTAAGATCC 2378
Qy 697 LysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysLeu 716
Db 2379 GAACTTAAGGTCTGGAAGCCCTCAACACATCCCATCTGAATTTAAGAATATT 2438
Qy 717 GlyPheArgGlyIleArgLeuProAspThrMetAsnHisSerValLeuLysAs 736
Db 2439 GACTTGTGTGATTTCTGTCTCCCTGACTGGATGATCACTCAGTTTGAAAAAT 2498
Qy 737 SerIleGluIleIleSerCysLysAsnCysSerCysLeuProPropheGlyGlu 756
Db 2499 TCTATTTCAATTAAGCGGTGTGAAGAACTGCTCGTCTTACACCTTTGGTGA 2558
Qy 757 CysLeuLysSerLeuGluLeuThrPArgGlySerAlaGluValGlyVal---As 775
Db 2559 TGTCTAGAAAGTCTGAGTTACAGACGGGCTCTGTGAGGGAGTATGTGAAGATT 2618
Qy 776 GlyPheProThrArgArgArgPheProSerLeuArgLysLeuAsnIleArg 795
Db 2619 GGAATTCCTGACAGAAAGAAAGATTCATCCCTGAAAACCTCATATAGCTGT 2678
Qy 796 AsnLeuLysGlyLeuLeuLysLysGluGlyGlnGlnCysProValLeuGluGlu 815
Db 2679 AATCTGAAGAGATTTGACAGAGATGAAGAGACAGCAATCCCGCTTGAAGAGAT 2738
Qy 816 GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLeu 835
Db 2739 AAGATTTTCGAGTTGCCATGTTGTTTTCGACCCCTTCTCTGTCAGAAATTTGA 2798
Qy 836 ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMet 855
Db 2799 ATTTGGGGGGAG--GCAGATGACGAGGTTTGAAGCTTCATTAATCTCAGAC 2855
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Qy	856	ThisSerLeuGlnIleArgTyrAsnIlySerIuAspAlaSerLeuProGluIuMetPheIys	875
Db	2856	ACATCCCTCAAGATTTCAGTAAACAACAAGTACTTACTGAAAGAGATGTTCAA	2915
Qy	876	SeuLeuAlaAsnLeuIysTyrLeuAsnIleSerPheTyrPheAsnLeuIysGluLeuPro	895
Db	2916	AACCTTGAAATTCATATACCTTAGAGTCTCTTCTTGGAGAAATCTCAAGACCTGCT	2975
Qy	896	ThisSerLeuAlaSerLeuAsnAlaLeuIysHisIleuGluIleHisSerCysTyrAlaLeu	915
Db	2976	ACCAAGCCCTGGCTAGCTCAACAATTTGAAGTCTGGATATTCGTTATGTTAGGCACTA	3035
Qy	916	GluSerLeuProGluGluGluValIlySerIlyLeuIleSerLeuThrGlnLeuSerTlleThr	935
Db	3036	GAGAGTCTCCCGAGAGAGGCTGGAAAGCTTATCTTACTCAACAAGTAAATTTGTGA	3095
Qy	936	TyrCysGluMetCLeuGlnCysLeuProGluIlyLeuGlnHisIleuThrAlaLeuThrAsn	955
Db	3096	CACGTGTAACAAGCTAAATGTTTACAGAGGGAATTGCAGCAACTTAACAACCTCAACA	3155
Qy	956	LeuSerValGluPheCysProThrLeuAlaIysArgCysGluIlySerIlyGluAsp	975
Db	3156	TTAAAAATTCCGGGAGTGTCCACAATCATGATCAAGCGGTGTGAGAAAGGAAATGAGA	3215
Qy	976	TrpTyrIlySerIleAlaHisIleProArgValPheIleTyr	988
Db	3216	TGGCACTAAATTTCTCACATTCCTTAATGTGAATATATAT	3254
RESULT 9			
ID	ADP17760	standard; DNA; 3592 BP.	
XX	ADP17760;		
XX	12-FEB-2004	(first entry)	
DE	Solanum bulbocastanum Rpi-b1b genomic DNA.		
XX	Solanum bulbocastanum.		
XX	Key	location/Qualifiers	
FT	CDS	1..3592	
FT		/*tag= a	
FT		/product= "Rpi-b1b protein"	
FT		/note= "this coding sequence contains one intron"	
FT		/transl_except= (pos: 1107..1108, aa: Gly)	
FT	Intron	428..1106	
FT		/*tag= b	
FT		/number= 1	
XX	EPI334979-A1.		
XX	PD	13-AUG-2003.	
XX	PF	08-FEB-2002; 2002EP-00075565.	
XX	PR	08-FEB-2002; 2002EP-00075565.	
XX	PA	(KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.	
PI	Van Der Vossen EAG, Allefs JHM;		
XX	WP1; 2003-714439/68.		
DR	P-PSDB; ADP17765.		
PT	New resistance gene conferring resistance against an oomycete pathogen, useful for producing plants, especially potatoes and tomatoes, resistant against oomycete pathogens such as Phytophthora infestans.		
XX			

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OY 144 ----- 144
Db 658 CATCACTACCAATCCCTTGGTAATCTTTCTTACCTAATAA CTTGAACACT 717
OY 144 ----- 144
Db 718 CGATCCGTTTGTCTTTCTTAACAAGACGCTCAGAGAAAAGGTTTCTTATTCG 777
OY 144 ----- 144
Db 778 TTTCTGTGTGCTGCACTTGGGTCCTTAATCCCAATTAAAAACAGGCAATGTAATCCA 837
OY 144 ----- 144
Db 838 ACAGAGGTAGCCTTCTCAGACGCTGACTTAATTTGTTCTAACAAGAAAAAAGA 897
OY 144 ----- 144
Db 898 TTAGACATGTTTTCTTGTCAATGATTAGGCTGATTTCTTCAGAGTGAACATAGG 957
OY 144 ----- 144
Db 958 GATATATTGACCAAAAGTAGAATGGTAATATTAAAGTATTTCTGATAGAACAGAG 1017
OY 144 ----- 144
Db 1018 TATATTGCGCAAAATATCTCTATTTCTGTGTCTCTAATGAGTTGAATGTAATA 1077
OY 145 -----Phe-ValLeuSngInuProGlnValTyrG1 154
Db 1078 TATTCATGTCGACATTTGTCGACCAAGTTCTGTATTAAACCGACGAGTTTAGG 1137
OY 154 YARAspLysGluLysAspGluLeuValLysIleLeuIleAspAsnValSerAsnAlaG1 174
Db 1138 AAGAGACAAAGAAAGATGAGATGATAAATCTTAATAACAATGTTAGTAGGCCA 1197
OY 174 nThrLeuProValLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrThrLeuAlaG1 194
Db 1198 ACACCTTTCAGTCTCCCAATACTTGTAATGGGGGANTTAGAAAAAGCATCTTGCCA 1257
OY 194 nMetValPheAsnAspGlnArgValIleGluHisPheHisProLysIleTrrIleCysVa 214
Db 1258 AATGTCCTTCATATACCAAGAGTTACTGACATTTCCATCCAAATATAGATTGTGTG 1317
OY 214 LSeGluAspPheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLys 234
Db 1318 CTCGGAAGATTTTATGAGAAAGAGGTTAATAAGGCATGTGTAGAACTTATGAAGAG 1377
OY 234 sSer--LeuGlyGlyMetAspLeuAlaProLeuGluLysLysLeuArgAspLeuAs 253
Db 1378 GCCACTACTTGTGAGATGACACTTGGCTCCACTCAAAAAGAGCTTCAGAGAGTTG 1437
OY 253 nGlyLysLysThrLeuLeuValLeuAspAspValTrrAsnGluAspGlnAspLysTrrAl 273
Db 1438 TGGAAAAAGATATCTGTCTGTCTTATGATGATGTTGAAATGAATCAACAGAGTGG 1497
OY 273 alyLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrTr 293
Db 1498 TAATTTAAGGCACTCTTGAAGAGTTGAGACAGAGGAGGCTTCTGTCTTAACCACT 1557
OY 293 gLeuGluLysValGlySerIleMetGlyThrLeuGlnProTrrGluLeuSerAsnLeu 313
Db 1558 TCTTGAAGAGGTGGATCAATTATGGGACATTCGACACCATATGAACGTCAATCTG 1617
OY 313 rGlnGluAspCysThrLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluLea 333
Db 1618 TCAGAGAGATTTGTGTGTGTTCATGCAACGTCATTTGACACCAACAAAGAAATAA 1677
OY 333 nLeuAsnLeuValAlaIleGlyLysGluIleValLysCysGlyGlyValProLeuAl 353
Db 1678 TCACAAACCTTGTGGCAATCGGAAAGAGATTTGTGAAAAAAGTGTGTGTGCTTAC 1737
OY 353 aAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGluLysGluIleTrrGluHisVa 373
Db 1738 AGCCAAACCTTGTAGAGTATTTGTCTCAAGAGAAAGAAAGACATGGGAACATGT 1797
OY 373 LArgAspSerGluIleTrrLysLeuProGlnGluSerSerIleLeuProAlaLeuAr 393
Db 1798 GAGAGACAGTCCCATTTGGAAATTTGCCCTCAAGATGAAGATTCATTTCTGCTGCC 1857
OY 393 gLeuSerTrrHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPh 413
Db 1858 GCTTAGTTACCATCAATCCACTTGATTTGAAACAATGCTTTGCCGATTTGGGGGTT 1917
OY 413 eProLysAspThrGluMetGluLysGlyAsnLeuIleSerLeuTrrPheAlaHisGlyPh 433
Db 1918 CCAAGAGATGCCAAATATGAAAAAGAAAGCTAATCTCTCTGATGGCGCATGGTTT 1977
OY 433 eIleLeuSerLysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTrrAsnGluLe 453
Db 1978 TCTTTATCAAAAGGAACAATGAGCTAGAGATGTGGCGCATGAACTATGAAAGATT 2037
OY 453 uTyrLeuArgSerPhePheGlnGluIleGluValLysSerGlyGlnThrTyrPheLysMe 473
Db 2038 ATACTGAGGCTTTTTCACAGAGATTGAAGTTAAAGATGTAATAACTTATTTCAAGAT 2097
OY 473 tHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSer 493
Db 2098 GCATGATCTCATCATGATGATTTGGCAACATCTCTGTCTTTCAGCAACACATCAAGCA 2157
OY 493 nIleArgGluIleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrLysVa 513
Db 2158 TATCCGTAATTAATTAACAACAGTTACACACATATGATGTCATTTGGTTCGCGCAAG 2217
OY 513 LValSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLe 533
Db 2218 GGTGTTTTTTTACACTTCTCCCTCCCTGGAAAGTTATCTCTGTAAAGTGTTAATCT 2277
OY 533 uSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyr 553
Db 2278 AGGTGATTCGACATTTAATAATGATTAACATCTTCCATTTGAGATCTAGTACATTAA 2337
OY 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuG1 573
Db 2338 CTTGAACCTGTATGAGC---AGTGCATGCGTAGTCTTCCAAAGACAGATTTGCAAGCT 2394
OY 573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGluPh 593
Db 2395 AAATCTGCAAACTTGTGATCTACATATATGACCAACAGCTTTGTGTTCACAAAAGAA 2454
OY 593 rSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMe 613
Db 2455 AAGTAACCTTGGTATGATCTCGAAATCTTTTACTTGAATGATGACATTTGATGTAT 2514
OY 613 tProProAlaGlyIleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGlyI1 633
Db 2515 GCCACCAAGATAGATGATCAATTAACATGACCTTAAAGCTTAAAGCTAATTTGTTGGA 2572
OY 633 eGluLysLysSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleG1 653
Db 2573 -AGAGAAAGGTTATCACTTGTGAACTAGGAAACCTTAATCTCTAATGGCTCAATTA 2631
OY 653 uIleThrHisLeuGluLysArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAl 673
Db 2632 AATCTGCACTTTGAGAGAGTGAAGATGATGAAGCGCAAAAAGAACCAATTATTCGC 2691
OY 673 alyGluAsnLeuHisSerLeuSerMetLysTrrAspAspAspGluLysArgIleTyr 693
Db 2692 AAAAGGGAATCTGCAATCTTTAAGCATGAGTTGG---AATAACTTTGACCAATATATA 2748
OY 693 rGluSerGluLysValGluValLeuGluAlaLeuLysProHisSerAsnLeuThrCysIle 713
Db 2749 TGAATCAAGAAAGTTAAAGTCTTGAAGCCTTCAAAACCAACATCTGACTTCTTT 2808
OY 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrrPheAsnHisSerValLeuLys 733
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Db 358 GCTGAGAAAGAAAGATTTTCATTTCGACGAAAAAATTGTAGAGACAAGCTGTAGA 417
Qy 141 ArgGlnThrGly----- 144
Db 418 CGGGAACAGAGTACTCATCTTAATAATGATTAACAACAATAAGTTATATTCATTTT 477
Qy 144 ----- 144
Db 478 TGGCAATTATCAAAATTCAGAAAAAGGTTAAATATCTCATGTCCTATGCTAAATAGTGA 537
Qy 144 ----- 144
Db 538 TATATACCTCTGTTGTACTTTCGATCGAATATACCTTGCAAACTGGCAAGCTGAGA 597
Qy 144 ----- 144
Db 598 TCAATTAATCAACCCCACTTTTAATAATCTGATATCTTAGAAATCCACCTGTCTAAT 657
Qy 144 ----- 144
Db 658 CATCACTACCAATTCCTTTGCTTGAATCTTTCTTTACCTATAAATCTTGAACT 717
Qy 144 ----- 144
Db 718 CGATCCGTTTGTCTTTCTTAACAAGCAGCTCAGAAAAAGGTTTCTTCTATTTCTG 777
Qy 144 ----- 144
Db 778 TTTCTCTGTGCTGCACTTGGGCTTAATCCATTAATAAACAAGGAGCTTAATCCCA 837
Qy 144 ----- 144
Db 838 ACGACGTAAGCTTCTCTGACAGCTGATAAATTTTGTCTAACAAGAAAAAAGA 897
Qy 144 ----- 144
Db 898 TTAGACATGTTTTCTTTCATGATTAGGCTGAGATTTCTTTCAGAGTGAGACATAGG 957
Qy 144 ----- 144
Db 958 GATATATTGACCAAAAGTAGAATGGATATATTAAAGTATTTCTGATAGAACAGAG 1017
Qy 144 ----- 144
Db 1018 TATATTGCGAAATATCTCTATTTTCTGTGCTCTAATGATTTGAATTAATAA 1077
Qy 145 ----- 145
Db 1078 TATTCTCATGTGACATTTGCTTGACCAAGGTTCTGTATTAACCGAACCGAGTTATAG 1137
Qy 154 YArgAspLysGlnLysAspGlnLeuValLysIleLeuIleAsnAsnValSerAsnIle 174
Db 1138 AAGAGACAAAGAGAAAGATGATGATGAAAAATCTAATAAACAATGTATGATGCCA 1197
Qy 174 nThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLysThrThrLeuIle 194
Db 1198 AACACCTTCAAGTCTCCCAATACCTTGATATGGGGGATAGGAAAAACGACTCTGCCA 1257
Qy 194 nMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrpIleCysVa 214
Db 1258 AATGCTCTTCAATACACAGAGAGTACTGACATTTCCATTTCCAAAATATAGATTTGT 1317
Qy 214 LserGlnAspPheAsnGlnLysArgLeuIleLysGlnIleValGlnSerIleGlnGly 234
Db 1318 CTGCGAAGATTTTGATGAGAAAGGTTATATTAAGCAATTTGTAATCTTATTAAGAGAG 1377
Qy 234 sSer---LeuGlyGlyMetAspLeuValAspLeuGlnLysLeuArgAspLeuLeu 253
Db 1378 GCCACTAATCTTGATGAGATGAGCTTGCTCCACTTCAAAAGAGAGCTTACAGAGTTGCTGAA 1437
Qy 253 nGlyLysLysThrLeuLeuValLeuAspAspValTrpAsnGlnAspGlnAspLysTrp 273
Db 1438 TGGAAAAAGATATCTTGTGTCTTATGATGATTTGGAAATGAAATCAACAAGATGGGC 1497

Qy 273 aLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThr 293
Db 1498 TAATTTAAGACACTCTTGAGAGGTTGAGCAAGGAGGCTTCTGTCTTCAACCTACTCG 1557
Qy 293 GLeuGlnLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLeuSerAsnLeu 313
Db 1558 TCTTGAAAGGTTGGATCAATTAAGGAACTTGCAACCATATGACATGTCAAATCTGTC 1617
Qy 313 rGlnGlnAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlnGlnIle 333
Db 1618 TCAAGAAAGATTTGTTGTTGTTTCATGCAACGCTTGCGACCAACAAGAAATATA 1677
Qy 333 nLeuAsnLeuValAlaIleGlyLysGlnIleValLysLysCysGlyGlyValProLeu 353
Db 1678 TCNAACCTTGTCATTCGAAAGAGATTTGAAAGAAAGAGTGCTGCTGAGC 1737
Qy 353 aAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGlnLysArgGlnTrpGlnHisVa 373
Db 1738 AGCCAAAACCTTGAGAGTATTTTGTGCTTCAAGAGAAAGAAAGACATGGGAACATGT 1797
Qy 373 LArgAspSerGlnIleTrpLysLeuProGlnGlnLysSerIleLeuProAlaLeu 393
Db 1798 GAGAGACAGTCCGATTTGGAATTTGCTCAAGATGAAAGTTCTATCTGCTGCCCTGAG 1857
Qy 393 GLeuSerTyrHisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaVal 413
Db 1858 GCTTAGTTACCATCAACTTCCACTTGATTTGAAACAAATGCTTTCGATTTGGGCTGT 1917
Qy 413 eProLysAspThrGlnMetGlnLysGlnAsnLeuIleSerLeuTrpMetAlaHisGly 433
Db 1918 CCCAAAGATGCCAAATATGAAAAAGATCAATCTCTCTGATGGCGATGGTT 1977
Qy 433 eIleLeuSerLysGlyAsnLeuGlnLeuGlnAsnValGlyAsnGlnValTrpAsnGly 453
Db 1978 TCTTTATCAAAAGAAACATGAGCTAGAGATGGGAGATGAAGATGAGAAAGAT 2037
Qy 453 uTyrLeuArgSerPhePheGlnGlnIleGlnValLysSerGlyGlnThrTyrPheLys 473
Db 2038 ATACTGAGGCTCTTTTCCAAAGATGAAAGTTAAAGATGTAATAAATTATTTCAAGAT 2097
Qy 473 cHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSer 493
Db 2098 GCATGATCTCATCAATGATTTGGCAACATCTCGTTTTCAGCAACAACATCAAGCAGCA 2157
Qy 493 nIleArgGlnIleIleValGlnAsnTyrIleHisMetMetSerIleGlyPheThrLysVa 513
Db 2158 TATCCGTAATTAATAATAACACATTAACACATATGATGTCATTTGGCGCAAGT 2217
Qy 513 ValSerSerTyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsn 533
Db 2218 GGTGTTTTTTTACACCTTCCCTGGGAAAGTTTATCTGTTAAGAGTCTTATATCT 2277
Qy 533 uSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArg 553
Db 2278 AGGTGATTCGACATTAATTAATGATTCATCTTCATTTGAGATCTGATTAAGATA 2337
Qy 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeu 573
Db 2338 CTTGAACTGTATGGC---AGTGGCATGGCTTACTCTTCCAAAGCACTTATGCAAGCTTCA 2394
Qy 573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGln 593
Db 2395 AATCTGCAAACTCTTGATCTACAAATATTTGACCAACAAGCTTTGTGTTGCCAAAAGAAC 2454
Qy 593 rSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCys 613
Db 2455 AAGTAAACTTGATGATCTCGAAATCTTTTACTGTATGATGATCCACATTAAGACTTGTAT 2514
Qy 613 cProProArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheValValGly 633
Db 2515 GCCACCAAGATAGATCAATTAATGATGCTTAAAGACTTAAGTCAATTTGTTGGA--- 2572
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Qy 633 eGlnLysLeuSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleG 653
Db 2573 -AGGAAGAAAGGATATCACTTGGTGAAGACTGAAGAACTTAATCTTAATGGCTCAATTA 2631
Qy 653 uIleThiHileuGluLysValLysAsnAspMetAspAlaLysGluLysAlaAsnLeuSerAl 673
Db 2632 AATCTCCGACATCTTGAAGAGATGAAGAAATGAATAGACGCAAAAGCAATTTATCTGC 2691
Qy 673 aLysGluAsnLeuHiseSerLeuSerMetLysTyrAspAspAspLysLysProArgIleTyr 693
Db 2692 AAAAGGAATCTGCAATCTTTAAGCATGAGTTGG--AAATACCTTGGACCAATATATA 2748
Qy 693 rGluSerGluLysValGluValLeuGluAlaLeuLysProHiseSerAsnLeuThrCysLe 713
Db 2749 TGAATCGAAGAAATTAAGTCTTGAAGCCCTCAAGCCATCCATCGATCGATCTTCTT 2808
Qy 713 uThiLysGlyPheArgGlyLysLeuProAspTyrPheAsnHiseSerValLeuLys 733
Db 2809 AAAAATCTATGGCTTCAGAGGAATCCATCTCCAGAGGAGTGAATCATCATGATATTGAA 2868
Qy 733 sAsnValValSerIleGluIleIleSerCysLysAsnCysSerCysLeuProPheG 753
Db 2869 AAAATATTGCTCTTAATCTTAATAGCAACTTCAGAAACTGCTCATGCTTACCACTTTGG 2928
Qy 753 YGluLeuProCysLeuLysSerLeuGluLeuTyrPArgLysSerAlaGluValGluTyrVa 773
Db 2929 TGATCTGCTTGTCTTAAGAACTCTAGACTTACATCGGGGGCTCGGATGCGAGTATGT 2988
Qy 773 lAsp-----SerGlyPheProThrArgArgPheProSerLe 786
Db 2989 TGAAGAATGGAATATGATGATTCATCTGAGATCCCAAGAAATTAAGTTTCATCTT 3048
Qy 786 uArgLysLeuAsnLysLeuGluPheGlyAsnLeuLysGlyLeuLeuLysGlyLysGlyLys 806
Db 3049 GAGGAAATCTGATATATGCGACTTGTGATCTGAAGAGATGCTGAAGAAAGAGAGAGA 3108
Qy 806 uGluGluCysProValLeuGluGluIleGluIleLysCysCysProMetPheValIlePr 826
Db 3109 AGACCAATCTCTGCTGCTTGAAGATGATTAATTCACAGAGTCCCTTTTCG----- 3160
Qy 826 oThiLeuSerSerValLysLysLeuValValSerGlyAspLysSerAspAlaIleGlyPh 846
Db 3161 -ACCTTTCT----- 3169
Qy 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGluLysArgLysValLysGluAs 866
Db 3170 -----TCTAATCTTAGGGCTCTTACTTCTCCCTCAGAATTTGCTAATTAAGTAGC 3219
Qy 866 pAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSe 886
Db 3220 TACTTCAATCCCAAGAGATGTCMAAAACCTTGCAATCTCAAAATCTTGACCAATCTC 3279
Qy 886 rPheTyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysH 906
Db 3280 TCGGTGCAATATCTCAAGAGCTGCCCTACAGCTGCTAGTCTGATGATGTTGAAGA 3339
Qy 906 sLeuGluIleHiseSerCysTyrAlaLeuGluSerLeuProGluGlyValLysGlyLe 926
Db 3340 TCTAAATTAATCAATGCTTCCGCACTAGAGAGTCTCCCTGAGAGAGGGCTGAGAGGTTT 3399
Qy 926 uIleSerLeuThrGluLeuSerIleThrTyrCysGluMetLeuGluCysLeuProGluG 946
Db 3400 ATCTTCACTCAAGAGATATTGTTGAACACTGTAACATGCTTAATAAGTTTACCAAGGG 3459
Qy 946 YLeuGluHiseLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLys 966
Db 3460 ATTGACAGACTTAACAACCTCAACAAGTTTAAATTCGGGGAGTCCCAACATGATCA 3519
Qy 966 sArgCysGluLysGlyLysGlyLysGlyLysArgLysLysLysLysLysLysLysLysLys 986
Db 3520 GCGGTGAGAGAGGAAATGAGAAAGACTGCGACAAATTTCTCAATTTCTTAATGTGA 3579
Qy 986 eIleTyr 988

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Db 3580 TATATAT 3586
RESULT 11
ID ADH51533
ID ADH51533 standard; DNA; 5191 BP.
XX
AC ADH51533;
XX
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum Rpi-b1b partial gene SeqID50.
XX
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KW de.
XX
OS Solanum bulbocastanum.
XX
PN US2003221215-A1.
XX
PD 27-NOV-2003.
XX
PF 07-FEB-2003; 2003US-00360522.
XX
PR 07-FEB-2003; 2003US-00360522.
XX
PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX
PI Allefs JHM, Van Der Vossen EAG;
XX
DR WPI; 2004-010903/01.
XX
PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
PS Claim 6; SEQ ID NO 50; 98bp; English.
XX
CC This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a fragment of the
CC S bulbocastanum Rpi-b1b protein which is related to the invention.
XX
SQ Sequence 5191 BP; 1673 A; 877 C; 941 G; 1700 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7,03e-303 Length: 5191
Score: 3638.50 Matches: 754
Percent Similarity: 68.03% Conservative: 78
Best Local Similarity: 61.65% Mismatches: 129
Query Match: 70.97% Indels: 262
DB: 12 Gaps: 9
US-10-647-268-2 (1-988) x ADH51533 (1-5191)
Qy 1 MetAlaGluAlaPheLeuGluValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db 1191 ATGCGTGAAGCTTTCATTTCAAGTCTCTGAGACATCTCACTTCTTCTCAAGAGGGGAA 1250
Qy 21 LeuGluLeuLeuGluGlyPheLysAspGluLysPheLysLeuGluGlnSerThrPheThrThr 40
Db 1251 CTTGTATTGCTCTTTCGATTTTCAAGATGAGTTCAGAGGCTTTCAGAGCATGTTTCTACA 1310
Qy 41 lIleGluAlaValLeuGluAspAlaGlnLysLeuLysAspLysAlaIleGluAsn 60

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Qy 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCybLysLeuG 573
Db 3528 CTTBAACCTGATGGC---ACTGGCAGCCGATGCTTCCAAAGCATTAATCAAGCTTCA 3584
Qy 573 nAsnLeuGlnThrLeuAsnLeuH1sglyCybH1SerLeuCybLeuProLysGln 593
Db 3585 AAATCTCAAACTCTGATCTTCAAAATATTGGACCAAGCTTTGTTGTCGCAAAAGAAC 3644
Qy 593 rSerLysLeuGlySerLeuAsnLeuLeuLeuAsnGlyCybGlyLeuThrCysMe 613
Db 3645 AAGTAACTGGTAGTCTCCAAATCTTTACTGATGAGCCAGTCATTGACTGTAT 3704
Qy 613 tProPArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheValIleGly 633
Db 3705 GCCACCAAGGATAGATATTAAGATGCTTAAGACTTAAGCTTAATGTTGTTGGA-- 3762
Qy 633 eGlnLysLysSerCysGlnLeuGlyGlnLeuArgAsnLeuAsnLeuTyrgLysSerIleG 653
Db 3763 -AGGAGAAAGGTTATCAACTGGTGAACCTAGAAACCTAAATCTCTATGCTCAATTAA 3821
Qy 653 uIleThrH1sLeuGlnLysValIleAsnAspMetAspAlaIleGlyAlaAsnLeuSer 673
Db 3822 AATCTCGCATCTTGAAGAGAGAAAGATAGGACGCAAAAGACCAATTATATTCGC 3881
Qy 673 aLysGlnAsnLeuH1sSerLeuSerMetLysTrpAspAspArgIleArgProArgIleTy 693
Db 3882 AAAAGGGAATCTGCATCTTTTAAGCATGAGTTGG---AATACTTTGAGACCATATATA 3938
Qy 693 rGlnSerGlnLysValGlnValLeuGlnAlaLeuLysProH1sSerAsnLeuThrCysLe 713
Db 3939 TGAATCGAAGAGATTAAAGTCTTGAAGCCCTCAACACATCCATCTGACTTCTTT 3998
Qy 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnH1sSerValLeu 733
Db 3999 AAAAATCTATGCTTCAGAGAAATCCATCTCCAGAGGATGATCACTCAGATTGAA 4058
Qy 733 sAsnValIleSerIleGlnIleIleSerCysLysAsnCysSerCysLeuProPheG 753
Db 4059 AAAATGTCCTCTTCTTAATTAAGCACTTCAAGAACTGCTTCAACCCCTTGG 4118
Qy 753 yGlnLeuProCysLeuLysSerLeuGlnLeuTrpArgLysIleValGlnValIleGly 773
Db 4119 TGAATCGCTTGTCTAGAAAGCTTAGATTAACATCGGGGCTGGGATGAGATATCT 4178
Qy 773 lAsp-----SerGlyPheProThrArgArgPheProSerIle 786
Db 4179 TGAAGAGTGGATATTGATGTTCAATCTGAGATCCCAAGAAATAAAGTTTCATCCTT 4238
Qy 786 uArgLysLeuAsnIleArgGlnPheGlyAsnLeuLysGlyLeuLysLysGlnGly 806
Db 4239 GAGGAAACTTGATATATGAGGACTTGGTAGTCTGAAAGAGATTGCTGAAAGAAAGAGGA 4298
Qy 806 uGlnGlnCysProValLeuGlnGlnIleGlnIleLysCysCysProMetPheValIlePr 826
Db 4299 AGAGCAATTCCTGCTGCTTGAAGAGATGATATTACAGAGCGCTTTTTCG----- 4350
Qy 826 oThrLeuSerSerValLysLysLeuValIleSerGlyAspLysAspAlaIleGlyPh 846
Db 4351 -ACCCCTTCT----- 4359
Qy 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTrpAsnLysGlnAs 866
Db 4360 -----CTATATCTTAGGGCTCTTACTTCCCTCTCCCTAATTCCTAATTAAGTAGC 4409
Qy 866 pAlaSerLeuProGlnGlnMetPheLysSerLeuAlaAsnLeuTyrgLysAsnIleSe 886
Db 4410 TACTTCATTCAGAGAGAGATTCAAAACCTTCAAAATCTCAAAATCTTGACATATCTC 4469
Qy 886 rPheTyrrPheAsnLeuLysGlnLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysH 906
Db 4470 TCGGTGCAATATCTCAAAAGAGCTGCTACAGACTTGGCTAGTCAATGCTTTGAAAG 4529

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Qy 906 sLeuGlnIleH1sSerCysTrpAlaLeuGlnLeuProGlnGlnValLysGlyLe 926
Db 4530 TCTAAATTCATATGTTGTTGGCCTAGAGAGCTCCCTCAGAGAGGGCTGAAAGCTTT 4589
Qy 926 uIleSerLeuThrGlnLeuSerIleThrTyrgCysGlnMetLeuGlnCysLeuProGln 946
Db 4590 ATCTTCACTCAAGAGATTATTTGTGAACACTGTAACTGTAAATGTTTAAACAGAGGG 4649
Qy 946 yLeuGlnH1sLeuThrAlaLeuThrAsnLeuSerValGlnPheCysProThrLeuAlaL 966
Db 4650 ATTGAGACCTTAACAACCTCAACAGATTAAATTCGGGAGTCCACAACTGATGAA 4709
Qy 966 sArgCysGlnLysGlyIleGlyGlnAspTrpTyrgLysIleAlaH1sIleProArgValPh 986
Db 4710 GCGGTGTGAGAAAGGAATAGAGAAAGACTGGCAAAATTTCTCAATTCCTAATGTGAA 4769
Qy 986 eIleTyrr 988
Db 4770 TATATAT 4776

RESULT 12
ADFI7761
ID ADFI7761 standard; DNA; 7349 BP.
XX
AC ADFI7761;
XX
DT 12-FEB-2004 (first entry)
XX
DE Solanum bulbocastanum BAC SPB4 genomic DNA fragment.
XX
KW ds; BAC SPB4; Rpi-b1b gene cluster; growth regulant; oomycete infection;
XX introgression breeding; plant; late blight.
XX
OS Solanum bulbocastanum.
XX
PN EP1334979-A1.
XX
PD 13-AUG-2003.
XX
PF 08-FEB-2002; 2002EP-00075565.
XX
PR 08-FEB-2002; 2002EP-00075565.
XX
PA (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
XX
PI Van Der Voosen EAG, Alléfs JHM;
XX
DR WPI; 2003-714439/68.
XX
PT New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes and tomatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX
PS Example 5; SEQ ID NO 37; 86pp; English.
XX
CC This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
XX described as plant growth regulants. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum BAC SPB4
XX genomic DNA fragment, present in RGC2-b1b of the invention.
XX
Sequence 7349 BP; 2508 A; 1139 C; 1218 G; 2484 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.:	1.16e-302	Length:	7349
Score:	3638.50	Matches:	754
Percent Similarity:	68.03%	Conservative:	78
Best Local Similarity:	61.65%	Mismatches:	129
Query Match:	70.97%	Indels:	262
DB:	10	Gaps:	9

US-10-647-268-2 (1-988) x ADF17761 (1-7349)

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Oy      1 MetIaGluaIaPheLeuGlnValIleuAspAsnLeuThrCysPheIleGlnIyGlu 20
Db      2648 ATGGCTGAAGCTTTTCATTCAGAGTCTGCTAGACAACTTCACCTCTTCTCTCAAGGGGAAA 2707
Oy      21 LeuGlyLeuIleLeuGlyPheLysAspGluPheGluIyLysLeuGlnSerThrPheThrThr 40
Db      2708 CTTGATTTGCTTTGGTTTTCAGAGTGAATCCAAAGCTTTCAAAGCATGTTTCTTACA 2767
Oy      41 IlegIaIaValIleuGlnAspAlaGlnIyLysGlnLeuIyAspLysAlaIleGlnAsn 60
Db      2768 ATTCAAGCCGTCCTTGAAGATGCTCAGAGAGCAACTCAACAAACAGCTCTAGAAAT 2827
Oy      61 TrpLeuGlnIyLysLeuAsnAlaAlaIaIyGlnIaAspAspIleLeuAspGluCysLys 80
Db      2828 TGGTTGCAAAACCTCAATGCTGCTCAATGACATGACATGATCTTGATGAATATAA 2887
Oy      81 ThrGlnIaProIleArgGlnIyLysAsnIySyrGlyCysTyrHisProAsnValIle 100
Db      2888 ACCAAGGCC---ACAAGATTCTCCACGCTGCAATGAGCCGTTATCAATCAAGAGTTATC 2944
Oy      101 ThrPheArgHisIyLysIleGlyLysArgMetLysIyIleMetGlnLysLeuAspValIle 120
Db      2945 CCTTTCGTCACAAAGGTGCGGAAAGAGAGACCAAGATGATGAAACCTAAAGCAATT 3004
Oy      121 AlaIaGlnArgIleLysPheHisLeuAspGlnArgThrIleGlnArgGlnValaIaThr 140
Db      3005 GCTGAGAAAGAAAGAAATTTTCATTTGACGAAAAAATTGTAGAGACAAAGCTGTAGA 3064
Oy      141 ArgGlnThrGly----- 144
Db      3065 CGGGAACAGGATCACTCATCTTAATTAATTAACAACAATAAGTTTATTCATTTT 3124
Oy      144 ----- 144
Db      3125 TGGCAATTATCAAAATTCAGAAAAAGGTTAATAATCTCATGTCATGTAATAGTGA 3184
Oy      144 ----- 144
Db      3185 TATATACCTCTGTTGATCTTCGATCTGAATATACTTGCAATCTGGCAGACTCAGAA 3244
Oy      144 ----- 144
Db      3245 TCAAATATTCACCCCAACTTTTAATACTCGATATCTTTAGAAATCCACCTGTCTAACT 3304
Oy      144 ----- 144
Db      3305 CATTCACATACCAATCCCTTTGCTTGAATCTTTTCTTACCTATTAACCTTGAAACAT 3364
Oy      144 ----- 144
Db      3365 CGATCCGTTTGGTTTCTTAAACAAGACGTCAGAGAAAGAGTTTCTTCTATTTCTG 3424
Oy      144 ----- 144
Db      3425 TTTCTCTGTGTGTGCTGACCTTGGTCTTAATCCCATTAACAAAGGCAATGTTAATCCA 3484
Oy      144 ----- 144
Db      3485 AGGACGGTAGCCCTTTCTCTACAGCTGACTGTAAATTTTGTCTAACAAGAAAAAGAGAG 3544
Oy      144 ----- 144
Db      3545 TTAGACATGTTTTTCTTGTGATGTAGAGCTGATTTCTTTCAAGATGGAACATAGGG 3604

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Oy      144 ----- 144
Db      3605 GATATATTGGACCAAAAGTAGATGGGTATATTTAAAGTATTTTCGATAGAACAGAG 3664
Oy      144 ----- 144
Db      3665 TATATTGTGCAAAATATCTCTATTTTCTGTGTCTCTAATAGATGATGATATATA 3724
Oy      145 ----- 144
Db      3725 TATTTCAATGTGACATTTGCTTGACCAAGGTCTGTATTAACCGAACCGAGTTTATGG 3784
Oy      154 YArgAspIyGlnIyAspGluIleValIySileLeuIleAsnAsnValSerAsnIaG 174
Db      3785 AAGAGCAAGAGAAAGATGATGATGAAATCCATATTAACAATGTTAGTATGCCCA 3844
Oy      174 nThrLeuProValIleuProIleLeuGlyMetGlyIyLeuGlyLysThrThrLeuIaG 194
Db      3845 ACACCTTTCAGTCTCCCAATTACTTGATGGGGAGATTAGAAAAACGACTCTTGCCCA 3904
Oy      194 nMetValPheAsnAspGlnArgValIleGlnHisPheHisProLysIleTrpIleCysVa 214
Db      3905 AATGCTCTTAATGACCAAGAGTTACTGACATTTCCATTCCAAATATGATTTGTGT 3964
Oy      214 LserGlnAspPheAsnGlnIyAspArgLeuIleLysGlnIleValIaGlnSerIleGlnIy 234
Db      3965 CTGGAAGATTTTTCATGATGAGAGAGTTTATTAAGGCAATTTGTAATCTATGAAGGAG 4024
Oy      234 sSer---LeuGlyIyMetAspLeuAlaProLeuGlnIyLysLeuArgAspLeuAs 253
Db      4025 GCCACTACTTGTGATGATGACCTTGCTCCACTTCAAAAGCACTTCAAGAGTTGCGAA 4084
Oy      253 nGlyIyLysIyThrLeuValIleuAspAspValITrPAsnGlnAspGlnAspIyTrpAl 273
Db      4085 TGGAAAAAGTACTGCTGCTGTTAGTATGTTTGAATGAAGATCAACAGAAAGTGGC 4144
Oy      273 alyLeuArgGlnValIleuLysValIaIaSerGlyValaIaSerValIleuThrThrAr 293
Db      4145 TAATTTAAGAGCATCTTGAAGGTTGAGCAAGGGCTTGCTTCTTCAACCACTACTCTG 4204
Oy      293 gLeuGlnIyLysValIySerIleMetGlyThrLeuGlnProTyGlnLeuSerAsnLeu 313
Db      4205 TCTTGAAGAGGTTGATCAATTAATGAGAACATTCGCAACATTAATCTGATCTGTC 4264
Oy      313 rGlnGlnAspCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnIyGlnIyLeas 333
Db      4265 TCAAGAAAGATTGTTGTTGTTGTTTCATCCAAAGTGCATTTGACACCAAGAGAAATATA 4324
Oy      333 nLeuAsnLeuValaIaIleGlyIyGlnIyLeValIyLysCysGlyIyValProLeuAl 353
Db      4325 TCCAAACTTGTGCAATCGGAAGAGAGATTGTAAAAAAGTGGTGTGTGCTTACG 4384
Oy      353 aAlaIySerThrLeuGlyIyLysIleLeuArgPheLysArgGlnGlnArgIyTrpGlnHisVa 373
Db      4385 AGCCAAAACCTTGAAGGATTTTGTGCTTCAAGAGAGAGAGAGAGATGGAACATGT 4444
Oy      373 lArgAspSerGlnIyLysTrpLysLeuProGlnIyGlnIySerSerIleLeuProAlaLeuAr 393
Db      4445 GAGAGACGTCGCAATTTGGAATTTTGCTTCAAGAGAGAGAGAGATCTTATTTGCTGCGCTGAG 4504
Oy      393 gLeuSerTyHisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValaIaPh 413
Db      4505 GCTTAGTTACATCAACTTCACCTTGATTGAAACAATAGCTTTCGTAATGTGGGGGTT 4564
Oy      413 eProLysAspThrGlnMetGlnIyLysGlnIyAsnLeuIleSerLeuThrPheMetAlaHisGlyPh 433
Db      4565 CCCAAAGGATCCAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4624
Oy      433 eIleuSerIySgIyAsnLeuGlnIyLysValaIyAsnGlnValITrPAsnGlnLe 453
Db      4625 TCTTTTATCAAAAGAGAAACATGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4684

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QY 453 uTyrLeuArgSerPheheGInGluIleGluValIysSerGlyGlnThrTyrrhPheIysMe 473
 Db 4685 ATACTTGGAGCTCTTTTCCAAAGAGATTGAAGTTAAAGATGTAAGTTAACTTATTCAGAGAT 4744
 QY 473 tHiaAspLeuIleHisaPheLysAlaThrSerLeuPheSerAlaSerThrSerSerSerSAs 493
 Db 4745 GCATGATCTCATTCATGATTTGGCAACATCTCTGTTTCACACAAACATCAATCAACAGCA 4804
 QY 493 nIleArgGluIleIleValAlaAsnTyrrIleHiseMetSerIleGlyPheThrIysVa 513
 Db 4605 TATCCGTAATTAATAACACAGTTACACACATrGATGTCATTCGTTGTTCCGCGAAGT 4864
 QY 513 lValSerSerTyrrSerLeuSerHiseLeuGlnIysPheValSerLeuArgValIleuAsnLe 533
 Db 4665 GGTGTTTTTATACACTTCCCTTGGAAAGTTATCTCGTTAAGAGGCTTAATCT 4924
 QY 533 uSerAspIleIysLeuIysGlnLeuProSerSerIleGlyAspIleValHiseLeuArgTy 553
 Db 4925 AGGTGATTCGACATTTAATAGTTAACCATCTTCATTCAGATCTAGTACATTTAAGATA 4984
 QY 553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCyIysIleuG 573
 Db 4985 CTTAAACCTGATATGCG--AGTGCATGCGTATGCTTCCAAAGCAGTTATCAGAGCTTCA 5041
 QY 573 nasnLeuGlnThrLeuAspLeuHiseGlyCyHiseSerLeuCySyleuProIysGluTh 593
 Db 5042 AAATCTCGAAACTCTTGATCTCAAAATATTCGACCAAGCTTGTGTTGCCAAAGAAAC 5101
 QY 593 rSerIysLeuGlySerLeuAsnLeuLeuLeuAspGlyCyStryGlyLeuThrCyMe 613
 Db 5102 AAGTAAACTGGTATGCTCCCAAACTTTTACTTGATGTTAGCCAGTCATTCAGCTTGAT 5161
 QY 613 tProPArgIleGlySerLeuThrCyIysLeuThrLeuSerArgPheValIleGlyI 633
 Db 5162 GCCACCAAGATAGATCATTTGACATGCTTAAAGCTCTAGCTCAATTTGTTGG-- 5219
 QY 633 eGlnIysIysSerCySglnLeuGlyGluLeuArgAsnLeuAsnLeuTyrrGlySerIleG 653
 Db 5220 -AGGAAGAAAGGTATATCACTTGATGTAAGTGAACCTTAATCTCATATGCTCAATTA 5278
 QY 653 uIleThrHiseLeuGluArgValIysAsnAspMetAspAlaIysGluAlaAsnLeuSerAl 673
 Db 5279 AATCTCGCATCTTGAAGAGATGAAGAAATGATAGACGCAAAAGCAATTTATCTGCG 5338
 QY 673 aIysGluAsnLeuHiseSerLeuSerMetIysTrpAspAspAspGluArgProArgIleTy 693
 Db 5339 AAAAGGGAATCTGATCTTTAAGCATGAGTTG--ATAATCTTGACCACTATATA 5395
 QY 693 rGluSerGluIysValGluValIleuGluAlaLeuIysProHiseAsnLeuThrCySle 713
 Db 5396 TGAATCAGAGAATTAAGTCTTGAAGCCCTCAACCACTCAATCTGACTTCTTT 5455
 QY 713 uThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHiseSerValIleuTy 733
 Db 5456 AAAAATCTATGCTTCAGAGGAATCCATCTCCAGAGAGATGATCACTCAGATTGA 5515
 QY 733 aAsnValIysSerIleGluIleIleSerCyIysAsnCySerTyrrLeuProProPheG 753
 Db 5516 AAAATATTGCTCTAATCTTAATTAAGCACTTCAAGAACTGCTCAATCTTCAACCCCTTGG 5575
 QY 753 yGluLeuProCySyleuIysSerLeuGluLeuTrpArgGlySerAlaGluValIleuTyrrVa 773
 Db 5576 TGATCTGCTTGTCTAAGAACTCTAGATTCACCTGGGGGCTCGGATGCGAGTATGT 5635
 QY 773 lAsp-----SerGlyPheProThrArgArgArgPheProSerIle 786
 Db 5636 TGAAGAAAGTGATATTGATGTTCACTTCGATTCGCCCAAGAAATAAGTTCCATCTT 5695
 QY 786 uArgIysLeuAsnIleArgIuPheGlyAsnLeuIysGlyIysLeuIysIysGlyGluI 806
 Db 5696 GAGGAAACTTATATATAGGACTTTGGTAGCTTAAGAGATTTGCTGAAGAAAGAGAGAGA 5755
 QY 806 uGluGlnCySproValIleuGluGluIleGluIleIysCySAspProMetPheValIlePr 826

Db 5756 AGAGCAATCTCCCTGCTTGAAGATGATTAATTCACAGAGCCCTTTCTG----- 5807
 QY 826 oThrLeuSerSerValIysIysLeuValIserGlyAspIysSerAspAlaIleGlyPh 846
 Db 5808 -ACCTTCT----- 5816
 QY 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgTyrrAsnIysGluAs 866
 Db 5817 -----TCTATCTTAGGCGCTTCTTACTTCCCTCAGAAATTGCTATATAAAGTAGC 5866
 QY 866 pAlaSerLeuProGluIleuMetPheIysSerLeuAlaAsnLeuIysTyrrLeuAsnIleSe 886
 Db 5867 TACTTCATTCGCCAGAGAGATGTTCAAAAACCTTGAAATCTCAAAATACCTGACAAATCTC 5926
 QY 886 rPheTyrrPheAsnLeuIysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuIysH 906
 Db 5927 TCGGTGCAATTAATCTCAAGAGCTGCTTACCGAGTTGCTAGTCTGAAATGCTTGAAGA 5986
 QY 906 sLeuGluIleHiseSerCyStryrAlaLeuGluSerLeuProGluIleGlyValIysGlyLe 926
 Db 5987 TCTAAATTTCAATGTGTGCGCACTAGAGAGTCTCCCTGAGGAGGCTGGAAGTTT 6046
 QY 926 uIleSerLeuThrGlnLeuSerIleThrTyrrCySglnMetLeuGlnCySyleuProGluI 946
 Db 6047 ATCTTCACTCAGAGATTATTTGTTGAACACTGTACATGCTTAATAGTTTACAGAGGG 6106
 QY 946 yLeuGlnHiseLeuThrAlaLeuThrAsnLeuSerValGluPheCySproThrIleAlaI 966
 Db 6107 ATTGCACACCTTAACAACCTCAGACAAAGTTAAAAATTTGGGGAGTGCACAACTGATCA 6166
 QY 966 sArgCySglnIysGlyIleGlyGluAspTrpTyrrIysIleAlaHiseIleProArgValPh 986
 Db 6167 GCGGTGGAAGAGGATAGAGAAAGACTGCGACAAATTTCTCAATCTCTATGTGA 6226
 QY 986 eIleTyrr 988
 Db 6227 TATATAT 6233
 RESULT 13
 ID ADF17763 standard; DNA; 3971 BP.
 XX ADF17763;
 AC ADF17763;
 DT 12-FEB-2004 (first entry)
 XX DE S_bulbocastanum RGC3-b1b coding DNA containing an intronic sequence.
 XX KM gene; ds; RGC3-b1b; Rpl-b1b gene cluster; growth regulant;
 XX KW oomycete infection; introgression breeding; plant; late blight.
 XX OS Solanum bulbocastanum.
 XX OS
 XX Key location/Qualifiers
 FH 1. 3971
 FT CDS
 FT /tag= a
 FT /product= "RGC3-b1b protein"
 FT /note= "this coding sequence contains one intron"
 FT /transl_except= (pos: 1459..14560, aa: Gly)
 FT intron
 FT 428..1458
 FT /*tag= b
 FT /number= 1
 XX EP134979-A1.
 XX EN
 XX PD 13-AUG-2003.
 XX PR 08-FEB-2002; 2002EP-00075565.
 XX PR 08-FEB-2002; 2002EP-00075565.
 XX PR
 XX (KWE-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

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XX Van Der Vossen EAG, Allele UHM;
XX WPI: 2003-714439/68.
XX P-PSDB: ADF17766.
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes and tomatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX Example 5, SEQ ID NO 39; 86pp; English.
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-blb) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-blb, RGC1-blb, RGC3-blb and RGC4-blb, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polynucleotide sequence is the Solanum bulbocastanum RGC3-blb coding
XX DNA containing an intronic sequence in an exemplification of the
XX invention.
XX
XX Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 2 74e-300 Length: 3971
XX Score: 3606.50 Matches: 763
XX Percent Similarity: 63.02% Conservative: 77
XX Best Local Similarity: 57.24% Mismatches: 137
XX Query Match: 70.34% Indels: 357
XX DB: 10 Gaps: 9
XX
US-10-647-268-2 (1-988) x ADF17763 (1-3971)
OY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
DB 1 ATGGGTGAAGCTTTCATTCAAGTTGTGTGACCAATCTCATCTTCTCTCAAAAGGGAA 60
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGlyIleLeuGlnSerThrPheThrThr 40
DB 61 CTGTGATTCGCTTTCGTTTTCAGATGATGATTCAGAAAGCTTTCAGACATGTTTCTACA 120
OY 41 IleglnAlaValLeuGlnAspAlaGlnIleuIleuIleuAspIleAlaIleglnuIle 60
DB 121 ATCCAAAGCGCTCTGAGATGCTCTCAAGAGAGCACTCAAGCAAGCCCTTCAAAAAT 180
OY 61 TrpLeuGlnIleuLeuAsnAlaAlaAlaIleuIleuIleuAspIleLeuAspGluCysIle 80
DB 181 TGGTTCGCAAAAACCTAATGCTCTCATATGAAAGTCGATGATCATCTGGATGAATATAA 240
OY 81 ThrGluAlaProIleArgGlnIleuIleuAsnIleuIleuIleuIleuIleuIleuIle 100
DB 241 ACTAAGGCC--ACAAGATTCCTTGACATCTGAATATGGCCGTTATCATCCAAAGGTATAC 297
OY 101 ThrPheArgHisIleIleGlyIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 120
DB 298 CCTTTCCTGTCACAGAGTTGGGAAAGATGACCAAGTCATGAAAACCTGAATGCATTT 357
OY 121 AlaAlaGluArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIle 140
DB 358 GGTGAGGAACGAAGAATTTTCATTTGCAAGAAAGATTAAGAGACCAAGCTCTTACA 417
OY 141 ArgGlnThrGlyPhe----- 145
DB 418 CGGGAACAGGTAC-TCACTTAAATTAGTATTAACAATTAGTTATATTCATTGTTT 476

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OY 145 ----- 145
DB 477 GGGCAATGATCAATATTATGTAAAGTCAATATATCTACTGATGTAAGTAATGTTAA 536
OY 145 ----- 145
DB 537 ATATACCTTAGTTATATCTATTTAGTACGAACATATCTCTCCATATATCTTTGGAACAAT 596
OY 145 ----- 145
DB 597 ATTCCCTTAACGAATTAAGACAGTGAAAGTTCAGATTCAATTAATTCACCCCAATTT 656
OY 145 ----- 145
DB 657 TAAGATCTGATTTCTTTAGGAAACCACTCATCTCTCCGTTTGAATCTTAAAGAAACA 716
OY 145 ----- 145
DB 717 GCTCAGAAAAAGAGTTTCTCTGTTCTGTTTCTGTCGATTTGTCTTAATCCAAT 776
OY 145 ----- 145
DB 777 AACAAACATACAAATTAATATATATGTTCAAGATGAGGTAGTCTTTCTAGTACATG 836
OY 145 ----- 145
DB 837 AACTAGTGAATATTTGTTTAAAGAAAGAAAGAAATGATTAGCTGATTTCTTTCA 896
OY 145 ----- 145
DB 897 GAGTGAATATAGGGGATTAAGTTGAGCATATAGTTCATGCTTATTTCTTCTTA 956
OY 145 ----- 145
DB 957 AAGTAACAGTTTCAAAAGAAATGATATCAAGTACGGTAATGAAATTAATAGACAGTTC 1016
OY 145 ----- 145
DB 1017 TAACTACAAAATGATGATGAAATCTTAAATATCACTGACAAATATCATCTTAAATPAA 1076
OY 145 ----- 145
DB 1077 GCTACCAATTAATATCATGATACAGAGAAAGAAACCAAAAAATTAGGGGTAATTTT 1136
OY 145 ----- 145
DB 1137 GATTCTATGCTTATCATCATGCTTCCCATCAATCAAGAAATTTGTCCAAGTAT 1196
OY 145 ----- 145
DB 1197 AAACGGTCCGTATATTTGATTGAAAGTAAACAGAGATACATTTGACTTAAAGTA 1256
OY 145 ----- 145
DB 1257 TAACAATAGATATTTTGATCATTTTATGATCAAAATTCATGCTTTTGGGAGAAG 1316
OY 145 ----- 145
DB 1317 GAAGTTCAATGTTTTCATATGCTCTCATCTCATCCATATCTTTATTTGCAAAAC 1376
OY 145 ----- 145
DB 1377 CCTTCTATTTAACTATTTTTCGCCGACTCTATAGCTTGAATGTAACATATTTCTC 1436
OY 146 ----- 146
DB 1437 ATCTGACATTTGCTTGACACAGGTTCTGTGTTAACTGAACCAAGTTTATGGAAGGAC 1496
OY 157 LysGluIleuAspGluIleValIleIleuIleuIleuIleuIleuIleuIleuIleuIleu 176
DB 1497 AAAGAAAAGATGAGATGATGAAATCTTATTAACAATGTTAGTGAATGCCCAAAATCTC 1556
OY 177 ProValIleuProIleuGlyIleuGlyIleuGlyIleuGlyIleuIleuIleuIleuIleu 196

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1557 TCAGTCCCTCCCAATCTGTGATGGGGAGCTAGAGAAAGACAACCTCTTCCCAAAATGGTC 1616
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1617 TTCAATGATGAGAGAGTAAGTAGCGCTTCTTAAATCCCAAAATGGAATTTGGCTCTCGAAT 1676
217 AaPheAaAaGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeu 236
1677 GATTTGATGAGAGAGTAGTGTATTAAGCAATAGTATGATCTATTTGAAGGAAAGTCCCTC 1736
237 GlyGlyMetAaPheLeuAlaProLeuGlnLysLysLeuAaGAsPheLeuAaGlnLysLys 256
1737 AGTGACATGAGACTGGCTCCCACTTCAAAAGAGCTTCAAGAGTGTGATGAATAAGAAAAGA 1796
257 TyrLeuLeuValLeuAaPheValITrpAaGlnAaPgiNaAaPgiLysTrpAlaLysLeuArg 276
1797 TACTTCTTGTCTTGTGATGATGTTGGAATGAAATCAACATAGGTGGCTAATTTTAAAGA 1856
277 GlnValLeuLysValAlaAaSerGlyAaSerValLeuThrThrArgLeuGlnLys 296
1857 GCAGTCTTGAAAGTGGAGCAAGTGTGCTATTTGTTCTACTACTACTGCTTGTAAAG 1916
297 ValGlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAaLysSerGlnLysAaP 316
1917 GTTGATCAATTAATGGAACATGTCACATATGATGATGTCATATCTGCTCAGAGGAT 1976
317 CysTrpLeuLeuPheMetGlnArgAlaPheGlyIleGlnGluIleAaLysLeuAaLys 336
1977 TGTGTGTTTTGTGTTGATGAGCGTGCATTTGACACCAAGAAATTAATTCAAACCTT 2036
337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThr 356
2037 GTGGCAATCGGAAAGAGATGTGAAAATGAGTGGTGGCTCTTACCAAGCAAGCT 2096
357 LeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnITrpGluHisValArgAaPse 376
2097 CTGGAGGATATTTCCGCTTCAAGAGAGAAAGAAATGGAATGGAACATGTGAGACAGT 2156
377 GluIleTrpLysLeuProGlnGluGluSerIleLeuProAlaLeuArgLysSerTyr 396
2157 CCGATTTGGAAATTTCCCTCAAGATGAAGTTCTATTTGCTCCCTGAGCGCTTGAATAC 2216
397 HisHisLeuProLeuAaPheArgGlnCysPheThrTyrCysAlaValPheProLysAaP 416
2217 CATCATCTTCCACTTGATTTGACAAATGCTTTGTGATTTGCGGATATTCCTCAAGAGC 2276
417 ThrGluMetGluLysGlyAaLysLeuIleSerLeuITrpMetAlaHisGlyPheIleLeuSer 436
2277 ACCAAAATCGCAAAAGAAAATCTTATCGCTTTTGGATGGCAATGCTTTCTTTATCG 2336
437 LysGlyAaLysLeuGluLeuGlnAaValGlyAaGlnValITrpAaGlnLysLeuArg 456
2337 AAAAGAAATTTGGAGCTAGAGGATGATGAGTATGAAGTATGGAATGAATTAATTAATCTGAGG 2396
457 SerPhePheGlnGlnIleGluValLysSerGlyGlnIThrTyrPheLysPheHisAaPheLeu 476
2397 TCTTCTTCCCAAGAAATGGAATGATGATGTAATAAATCTTATTAAGATGATACCTC 2456
477 IleHisAaPheLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAaLysGlu 496
2457 ATCCATGATTTGGCTACATCTCTGTTTTCAGCAACACATCAAGCAAGCAATTTGCTGAA 2516
497 IleIleValGluAaLysTyrIleHisMetMetSerIleGlyPheThrLysValAaLysSer 516
2517 ATAAATGCTAATTAATGATGATATATGATGATGATGATGATGATGATGATGATGATGATGAT 2576
517 TyrSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAaLysSerAaPhe 536
2577 TACTCTCTTCACTCTTGGCAAAAGTTGTCTAATTAAGGCTCTTAATTAAGAAACTCG 2636
537 LysLeuLysGluLeuProSerSerIleGlyAaPheValHisLeuArgTyrLeuAaLysLeu 556
2637 AACCTAAATCAATTAACATCTTCCATGGAGATCTAGTACATTTAAGATTAAGTGAAGCTTG 2696
557 SerGlyAaLysThrSerIleArgSerLeuProAaGlnLeuCysLysLeuGlnAaLysLeuGln 576
2637 TCTGGCAATTTTGAATTCGTATTCCTTCCAAAGATTTATGACAGCTTCAAAATTTGCAAG 2756
577 ThrLeuAaPheLysIleGlyCysHisSerLeuCysLysLeuProLysGluThrSerLysLeu 596
2757 ACTCTTATCTACATTAATTAATGAGCTCTCTTCTGTTGGCAAAACAAACAAATGAACCTT 2816
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2817 GGTAATCTCCCAAACTTTTACTTGTATGATGCTGT---TCATTAAGCTCAACGACCAAGAG 2873
617 IleGlySerLeuThrCysLeuLysThrLeuSerAaGlyPheValAlaGlyIleGlnLysLys 636
2874 ATAGATTTGATGACATGCTTAAAGCTTAAAGTCTTAAGTCTTGTATTATGGC---AAGGAAA 2930
637 SerCysGlnLeuGlyLysLeuAaGlnAaLysLeuAaLysTyrGlySerIleGluIleThrHis 656
2931 GGTATCAACCTTGGTGAATTAATAAACTTAATCTTAATGCTCAATTCATCAACAAA 2990
657 LeuGluAaGlyValLysAaAaPheAaPheAaLysGluAlaAaLysSerAlaLysGluAa 676
2991 CTGACAGAGTGAAGAAAGATAGCGATGCAAAAGAGCTAATTTATCTGCTAATAAGCAAT 3050
677 LeuHisSerLeuSerMetLysITrpAaPheAaPgiLysITrpProArgIleTyrGluSerGlu 696
3051 CTGACCTTTTATGCTGATAGTTGGAGCTTGATGGAACATAGA---TATCATCA--- 3104
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3105 -----GAAGTTCTTGAAGCCCTCAACACACCTCAATCGAATTAATTAAGAAATCAAT 3158
717 GlyPheArgGlyIleArgLeuProAaPheTrpMetAaHisSerValLeuLysAaValAla 736
3159 GGCTTCGAGAGAAATCCGCTCCAGATTTGATGATCAATCACTGTTTGAATAATTTTGC 3218
737 SerIleGluIleIleSerCysLysAaCysSerCysLeuProProPheGlyGluLeuPro 756
3219 TCTATTAAGAAATTAAGAGTTGGAAGAACTGCTCATATCTTAACCCCTTGTGTAGCTGCT 3278
757 CysLeuLysSerLeuGlnLeuITrpArgIleSerAlaGluValGluTyrVal---AaPse 775
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776 GlyPheProIThrArgArgPheProSerLeuArgLysLeuAaLysLeuGluPheGly 795
3339 GTTCATCT---GGAAGGTTTCCATCTTGAAGAAACTGTTATATGGAACCTTATAGT 3392
796 AaLysLeuLysGlyLeuLeuLysLysGluGluGlnGlnCysProValLeuGlnGluIle 815
3393 AATCTAAAGAGATGCTGTAAGAAAGAGAGAAAGCAATTCCTGTGCTTGAAGAGATG 3452
816 GluIleLysCysCysProMetPheValIleProIThrLeuSerSerValLysLeuVal 835
3453 ACATTTTACTGTGCTTATGTTTCTTATTCGACCTTTCTTCTGTAAGCAATGAAA 3512
836 ValSerGlyAaPheLysSerAaPheAlaIleGlyPheSerSerIleSerAaLysLeuAaLys 855
3513 GTTATTTGGC-----ACAGATGCAACAGTTTGAAGTCCATATCTTAATCTTGAAGCTCTT 3566
856 ThrSerLeuGlnIleArgTyrAaLysGluAaPheAlaSerLeuProGlnGluMetPheLys 875
3567 ACTTCCCTTGAACATTAAGCAATTAAGCAATTAAGCTTCACTCCAGAAAGAGATGTTCAAA 3626
876 SerLeuAlaAaLysLeuLysTyrLeuAaLysLeuSerPheTyrPheAaLysLeuLysGluLeuPro 895
3627 ACCCTTGAATCTCAATTAATCTGATATCTTCTTCTTGAAGATCTCAAGAGATGCT 3686
896 ThrSerLeuAlaSerLeuAaLysLeuLysHisLeuGlnIleHisSerCysTyrAlaLeu 915
3687 ACCAGCTGGCTAGTCTCAATGCTTGAAGAGTCTCAATTAATTAATTTGTTAAGCAGCTA 3746
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OY 916 GluSerLeuProGluGluValIysGlyLeuIleSerLeuThrGlnLeuSerIleThr 935
DB 3747 GAGAGTCTCCAGAGAGAGGAGGTTTAACCTACACCGAATTTCTCTCACT 3806
OY 936 TyrCysGluMetLeuGlnCysLeuProGluGlyLeuGlnIleThrAlaLeuThrAsn 955
DB 3807 AACTGTATGATGCTAAATGTTTACCGAGAGGATTCGACGACCTTAACGAGCCCTCAACT 3866
OY 956 LeuSerValGluPheCysProThrIleuAlaIysArgCysGlyIleGlyGluAsp 975
DB 3867 TTTAACTAATCTCAATGCTCAATGATATTCAAGCGGTGTGAGAGAGGAATAGAGAAAGAC 3926
OY 976 TrpTyrIysIleAlaIleIleProArgValPheIleTyr 988
DB 3927 TGGCAGAAATGCTGCATTCATTCATTTGACTCTAAT 3965
RESULT 14
ADH51535
ID ADH51535 standard; DNA; 3971 BP.
XX
AC ADH51535;
XX
DT 25-MAR-2004 (first entry)
XX
DE S bulbocastanum RGC3-b1b gene SeqID52.
XX
KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato; gene;
KM de; RGC3-b1b.
XX
OS Solanum bulbocastanum.
XX
PN US2003221215-A1.
XX
PD 27-NOV-2003.
XX
PF 07-FEB-2003; 2003US-00360522.
XX
PR 07-FEB-2003; 2003US-00360522.
XX
PA (KMEK-) KMEK EN RESEARCHERDRUF AGRICO BV.
XX
PI Allefs JHM, Van Der Vossen EAG;
XX
WP; 2004-010903/01.
XX
PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX
PS Claim 6; SEQ ID NO 52; 98bp; English.
XX
CC This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of the S
CC bulbocastanum RGC3-b1b gene which is related to the invention.
XX
SQ Sequence 3971 BP; 1273 A; 700 C; 790 G; 1208 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2.74e-300 Length: 3971
Score: 3606.50 Matches: 763
Percent Similarity: 63.02% Conservative: 77
Best Local Similarity: 57.24% Mismatches: 137

Query Match: 70.34% Indels: 357
DB: 12 Gaps: 9
US-10-647-268-2 (1-988) x ADH51535 (1-3971)
OY 1 MetAglAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
DB 1 ATGGCTGAAGCTTTCATTCAGGTGTCTAGACATCTCACTTCTTCTTCTCAAGGGGAA 60
OY 21 LeuGlyLeuIleLeuGlyPheIysAspGluPheGlnIlyLeuGlnIleThrPheThrThr 40
DB 61 CTTGTATGCTTTTCGGTTTTCAGATGAGTTCCAAAGGCTTTCAAGCATTTTCTTCA 120
OY 41 IleGlnAlaValLeuGluAspAlaGlnIlyLeuGlnLeuIysAspIlyAlaIleGluAsn 60
DB 121 ATCCAGCCGCTCTGGAAGATGCTCAAGAGACATCAACGACGACGCTTGAAGAAAT 180
OY 61 TrpLeuGlnIlyLeuAsnAlaIleAlaIleTyrGluAlaAspAspIleLeuAspGluCysIys 80
DB 181 TGGTTGCAAAAACCTCAATGCTGTACATATGAACTGATGACATCTTGATGAATATATA 240
OY 81 ThrGluAlaProIleArgGlnIlyAsnIlyAsnIlyTyrGlyCysTyrHisProAsnValIle 100
DB 241 ACTAAGGCC--ACAGATTCCTGCAAGCTGAAATATGCGCTTATTCATCCAAAGTTATC 297
OY 101 ThrPheArgHisIlyIleGlyIlyArgMetIlyIleMetGlyIlySleuAspValIle 120
DB 298 CTTTCCGTCAACAGTTGGGAAAAGATGAGCAACAGATGAAAGAACTGAATGCATTT 357
OY 121 AlaAlaGluArgIleIlyPheHisLeuAspGluArgThrIleGluIleGlnValAlaThr 140
DB 358 GCTGAGGACGAAAGAAATTTTCATTTGCAAGAAAAGATTATAGAGACAAAGCTGTACA 417
OY 141 ArgGlnThrGlyPhe----- 145
DB 418 CGGAAACAGGTAC-TCATCTTAATTAAGTTACAACTTAAGTTATATTCATTTGTTTT 476
OY 145 ----- 145
DB 477 GGGCATGATCAATATTATGTAAGTCAAAATATACATGACTAGTGAATAATAGTTAA 536
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RESULT 15
ADP17764 ID ADP17764 standard; DNA; 3899 BP.
AC ADP17764;
DE 12-FEB-2004 (first entry)
DE s_bulbocastanum RGc4-b1b coding DNA.
XX gene; ds; RGc4-b1b; Rpi-b1b gene cluster; growth regulant;
XX oomycete infection; introgression breeding; plant; late blight.
XX Solanum bulbocastanum.
XX Key Location/Qualifiers
FT CDS 1..3899
FT /tag= b
FT /product= "RGc4-b1b protein"

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FT /note= "This sequence contains 3 introns and some
FT translation exceptions"
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FT /*tag= c
FT /number= 1
FT exon 511..542
FT /*tag= d
FT /number= 2
FT intron 543..618
FT /*tag= e
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FT exon 619..742
FT /*tag= f
FT /number= 3
FT intron 743..1365
FT /*tag= g
FT /number= 3
FT exon 1366..3899
FT /*tag= h
FT /number= 4

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EP1334979-A1.
13-AUG-2003.
08-FEB-2002; 2002EP-00075565.
08-FEB-2002; 2002EP-00075565.
(KWEE-) KWEEK EN RESEARCHBEDRIJF AGRICO BV.
Van Der Vossen ENG, Allefs JTHM;
WPI; 2003-714439/68.
P-PSDB; ADP17768.
New resistance gene conferring resistance against an oomycete pathogen,
useful for producing plants, especially potatoes and tomatoes, resistant
against oomycete pathogens such as Phytophthora infestans.
Example 5; SEQ ID NO 40; 86bp; English.
This invention relates to novel isolated polynucleotides that confer
resistance against late blight caused by the oomycete pathogen
Phytophthora infestans, which threatens both tomato and potato crops.
Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
and which cause disease resistance to bacteria, fungi, nematodes etc.
These R genes, namely Rpi-b1b, RGc1-b1b, RGc3-b1b and RGc4-b1b, can be
described as plant growth regulants. They are useful in providing
resistance to Phytophthora infestans, especially in Solanum tuberosum
(potato) plants to protect against oomycete infection or to demonstrate
disease susceptibility. Resistance can be conferred by transformation of
existing potato and tomato cultivars with the gene, a procedure that is
more straightforward and faster than conventional introgression breeding.
This polynucleotide sequence is the Solanum bulbocastanum RGc4-b1b coding
DNA containing an intronic sequence in an exemplification of the
invention.
Sequence 3899 BP; 1186 A; 678 C; 846 G; 1189 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.72e-282 Length: 3899
Score: 3400.00 Matches: 717
Percent Similarity: 62.94% Conservative: 105
Best Local Similarity: 54.90% Mismatches: 159
Query Match: 66.32% Indels: 326
DB: 10 Gaps: 10
US-10-647-268-2 (1-988) x ADP17764 (1-3899)

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Db 121 ATTCAAGCTGTGCTTCAAGATGCTCAGAGAGAACATTTGAAGAGACAAAGCATTTGAGAT 180
QY 61 TTrpLeuGlnLeuLeuAsnAlaAlaAlaTyrgluAlaAspAspIleLeuAspGluCysLeu 80
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QY 137 ----- 137
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QY 137 ----- 137
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 Job time : 1241 secs

GenCore version 5.1.6
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Run on: April 16, 2005, 23:37:44 / Search time 385 Seconds
(without alignments)
4199.069 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
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Scoring table: BLOSUM62
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1198	23.4	4946	3	US-08-930-996A-1
3	1028.5	20.1	4208	3	US-09-004-838-1
4	1008.5	19.7	4163	3	US-09-004-838-70
5	966.5	18.9	2353	3	US-09-004-838-2
6	715	13.9	1662	3	US-09-004-838-6
7	609.5	11.9	3997	3	US-08-947-823-2
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9	575.5	11.2	9870	4	US-09-245-928A-15
10	571.5	11.1	3982	4	US-08-947-823-4
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38	419	8.2	5134	3	US-09-301-085-157	Sequence 157, App
39	419	8.2	5134	5	PCT-US95-04589-157	Sequence 157, App
40	376.5	7.3	13149	3	US-09-004-838-87	Sequence 87, Appli
41	367.5	7.2	5829	3	US-09-004-838-109	Sequence 109, App
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43	367	7.2	3756	4	US-09-813-742A-2	Sequence 2, Appli
44	367	7.2	3760	1	US-08-261-663A-3	Sequence 3, Appli
45	367	7.2	3760	3	US-09-357-206A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-3
Sequence 3, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUHR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 3:


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RESULT 2
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: Sequence 1, Application US/08930996A
: Patent No. 6100449
: GENERAL INFORMATION:
: APPLICANT: FLUHR, Robert
: APPLICANT: ESHED, Yuval
: APPLICANT: ORI, Naomi
: APPLICANT: PARAN, Ilan
: APPLICANT: ZAMIR, Daniel
: TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
: TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
: TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROMDY AND NEIMARK
: STREET: 419 Seventh Street, N.W., Suite 300
: CITY: Washington
: STATE: D.C.

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COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 4946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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NAME/KEY: CDS
LOCATION: 299..3958
US-08-930-996A-1

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Qy 527 -----SerIleuArgValIleuAsnIleuSerAspIle 536
Db 2024 GTGTTCATTAACATATCTGCTTACATAAGATCTTGAGGGCACTATCTGTCTCATTAAC 2083
Qy 537 LysIleuIysGlnIleuProSerSerIleGly---AspIleuValHisIleuArgTyIleuAsn 555
Db 2084 CAGATGTAGGGTGTTCGCAATGACTGTTTATCAAAATTAAGCTCTCAGATTTTGGAC 2143
Qy 556 LeuSerGlyAsnThrSerIleArgSerIleuProAsnGlnIleuCyIysIleuGlnAsnIleu 575
Db 2144 CTCTCT---GAGACATTCATTAACAAAGTTGCGGATTCATTTTGTGTGTATTAATTA 2200
Qy 576 GlnThrIleuAspIleuHisGlyCyHisIleuSerIleuCyIysIleuProIysGlnThrSerIys 595
Db 2201 GAGACATCTTCCTCTCTCATCTGTGAATATCTTGAGAGCTTACGCTCGAATGAGAGAG 2260
Qy 596 LeuGlySerIleuArgAsnIleuIleuAspGlyCyTyIysGlyIleuThrCyMetProPro 615
Db 2261 TTGATTAATCTTGCGTCATCTTGACATTAAGCAACCTGGCGCTTGAG---ATCCACTA 2317
Qy 616 ArgIleGlySerIleuThrCyIleuIysThrIleu-----SerArgPheValIleGlyIle 633
Db 2318 CATCTGACGACAGTTGAAAAGCTCCCAAGTTGTGGGAGGACCAAGTTCTTGATAGTGT 2377
Qy 634 GlnIysIysSerIleuGlnIleuGlyIleuIleuArgAsnIleuIleuTyGlySerIleuIle 653
Db 2378 TGGAGAAATGAA---TATTTGGGTAAAGCACCC-----AACTTATATGATCTCTCA 2428
Qy 654 IleThrHisIleuGlnIleuArgValIleAsnAspMetAspAlaIysGlnIleuAsnIleuSerAla 673
Db 2429 ATTCTAGAGTTGAGAAATGTGTGTGATGAAAGGAAAGCTGTGAAGGCAAAATGAGGAG 2488
Qy 674 LysGlnIleuAsnHisSerIleuSerMetIysThrAspAspAspGlyIleuArgIleTyx 693
Db 2489 AAGGATCATGTGTTGACATTTATCTGAGTGAAGCTGAAGCAATTAAGCTGACATTC 2548
Qy 694 GluSerGlyIysValIleuGlnIleuIleuIleuIysProHisSerAsnIleuThrCyIleu 713
Db 2549 CAACACAGAAAGA---GACATATCTGATGAGCTACGCGCCCAATTAACATTAAGCAGATT 2605
Qy 714 ThrIleArgGlyPheArgGlyIleArgIleuProAspThrMetAsnHisSerValIleuIys 733
Db 2606 GAAATTCATGATATTAAGGAGCAAACTTTCCAACTGGGTAGCTGATCCTTTGTGT 2665
Qy 734 AsnValIleSerIleGlnIleIleSerCyIysAsnCySerCyIleuProProPheGly 753
Db 2666 AAGCTGGTGATTTGATCTTAAGAACTGCAAGGACTGTACTCTCTCCGACGACTAGGA 2725
Qy 754 GlnIleuProCyIleuIysSerIleuGlnIleuThrArgIysSerAlaGlnIleuIleuVal 773
Db 2726 CAATCTCCCTTTGTTGATTCCTTTCCAT---AGAGGATGCAATGGGATTAAGAGTGTG 2782
Qy 774 AspSerGlyPheProThrArg----- 780
Db 2783 ACAGAAAGATTCTATGCGAGATGTCTCCAAAAAGCTTTTAATCTCTGTGAGAGTT 2842
Qy 781 -----ArgArgPhePro 784
Db 2843 AGATTGGAAGATATGCTGAATGGAAGCAATGGCACACATAGAAATTTGAGAGATTCCT 2902
Qy 785 SerIleuArgIysIleuAsnIleuArg-----Gln 793
Db 2903 ACATCTTGAAATCTTTCATTAATAAATTTGCCCTGAGCTCAGTTGGAGATACCATTC 2962
Qy 794 PheGlyAsnIleuIysGlyIleu----- 800

Db 2963 TTTTCAGTTTAAAAAGGTAGATATATGATTTGTAAGTGTGTACTCTCTCTTTT 3022
Qy 801 -----LeuIysIys 803
Db 3023 AGCATCTGCACTACCTTGAAGAGAAATTAAGATATCTGTGTGCCAAAAATTAATTTG 3082
Qy 804 Gln-----GlyGln----- 806
Db 3083 GAGCGCGCAGTTGTGAGATTTGTGAGATTTGAGTGTGATTTGATTTGTGTGTA 3142
Qy 807 -----GlnIleuCyProValIleuGlnIleuGlnIleuIysCySer--- 820
Db 3143 GATGATATATCAGCTGAGTTTCTCCCAACAGACGTCATATGAGATATGAGAAATTTGCCAC 3202
Qy 821 -----PrometPheValIleProThr----- 827
Db 3203 AACGTACTAGTTTGTGATTTCTACTGCGACGTGAAGTCTCCATATTCGGAATTTGAA 3262
Qy 827 ----- 827
Db 3263 AAATCTCGATGCGATGTGAGAGAGCGGCCGAGCTGACGTCAATATTTGGGAGAT 3322
Qy 828 -----LeuSerSerValIysIysIleu----- 834
Db 3323 AAGAAAGCTCAAGTGTCTTCAGAACTCCTTCATCTCTCAAGAAAGCTCGACTGACTTAT 3382
Qy 834 ----- 834
Db 3383 TGTCAGAAATAGAGAAATTCGCTTCATTAACAAATATCGATATATGATATTC 3442
Qy 835 -----ValIleSerGlyAspIysSerAspAlaIleGlyPheSerSerIleSerAsnIleu 852
Db 3443 AAGAACTGTGTGAATGGCCGAAGAGAC-----TGGCATTTA 3478
Qy 853 MetAlaIleuThrSerIleuGlnIleuArgTyxAsnIysGlnIleu----- 866
Db 3479 CAGAGACTCAGAGATTATGATATCAATGATGAGAGTGAAGAAATTTGAACATTGG 3538
Qy 867 -----AlaSerIleuProGlnIleu 872
Db 3539 GAGTTGCCCTTCCTATTCAGAGACTATTCATATTCATTCGAAACATTAAGCAGCCAA 3598
Qy 873 MetPheIysSerIleuAlaAsnIleuIysTyIleu-----AsnIleSerPheTyx 888
Db 3599 CATCTCAAAAGCTCAGCTCTCTCAATTTCTACGTATTTGTGTGATTTATTCAGATT 3658
Qy 889 PheAsnIleuIysGlnIleuProThrSerIleuAlaSerIleuAsnAlaIleuIleuGln 908
Db 3659 CAGTCACAGGCCCACTT---TCTCTCTTTCTCAGCTCAGCTGCTTCAAACTCAACA 3715
Qy 909 IleHisSerCyTyIleuIleuGlnIleuSerIleuProGlnIleuIysValIysGlyIleuIleSer 928
Db 3716 ATCTGAAATTTTCTTAATCTTCATCTCACTACCTGAATCAGCAGCTGCCCTCC---TCC 3769
Qy 929 LeuThrGlnIleuSerIleuThrTyxGlnIleuMetIleuGlnIysIleuPro---GlnGlyIleu 947
Db 3770 CTCTCTCAGCTGATCATCTCCAAATGCTCTTAATCTCAATCTCCATTCCTCAATTAAGGAGTG 3829
Qy 948 GlnHisIleuThrAlaIleuThrAsnIleuSerValGlnIleuPheCyProThrIleuAlaIysArg 967
Db 3830 CCC-----TCTTCCCTCTCAGCTATTCATTTCCAAATGTCCATGTCTCAGCAGCTA 3883
Qy 968 CyGlnIysGlyIleGlyIleuAspTyIysIleuAlaHisIleProAspValPheIle 987
Db 3884 CTAGAAATTTGACAGGGGGAACTGACAGAAATTTGCTCATATCCCACTATCAGATC 3943

RESULT 3

US-09-004-838-1
; Sequence 1, Application US/0904838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michémore, Richard W.

APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Confering Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4208 base pairs
TYPE: nucleic acid
STRADENESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4208
OTHER INFORMATION: /note= "RLG1A"
US-09-004-838-1
Alignment Scores:
Pred. No.: 1.66e-102 Length: 4208
Score: 1028.50 Matches: 321
Percent Similarity: 47.49% Conservative: 181
Best Local Similarity: 30.37% Mismatches: 389
Query Match: 20.06% Indels: 169
DB: 3 Gaps: 29
US-10-647-268-2 (1-988) x US-09-004-838-1 (1-4208)
QY 1 MetAlaGlu-----AlaPheLeuGlnValIleuLeuAspAsnIleuThrCysPhe 16
DB 1099 ATGGCTGAATGCTCTTCTTCTGCTCTTCTTGACACGCGTCTTGAAAGAGTGCACATTTGAA 1158
QY 17 IlegnglyGluLeuGlyLeuIleuGlyPheLysAspGluPheGluLysLeuGlnSer 36
DB 1159 GCCTTGAAGAAGATGCTGCTCCAAAGAAATTGATCGACCTTAAGCAATTTGAAGAGG 1218
QY 37 ThrPheThrIleGlnAlaValLeuGluAspAlaGlnIleuLysGlnIleuLysAspLys 56
DB 1219 ACATTAGACCAATCCAGATCTGCTTAACGATGCTTCCACAGAGGAAGTAACATAATGA 1278
QY 57 AlaIleGluAsnTrpLeuGlnLysLeuAsnAlaAlaIleuGlnAlaAspAlleu 76
DB 1279 GCGGTTAAAGATGGCTGAATGATCTCCCAACATTTGCTTAAGACATGACGACCTACTT 1338
QY 77 AspGluCysLysThrGluAlaProIleuArgGlnLysLysAsnLysTyGlyCysTyHis 96
DB 1339 GATGATTTTGCAACTGAAGCTGTCACMGCTGAGTTGACGAGAGGAGGTGAGACCTCTCC 1398

QY 97 ProAsnVal-----IleThrPheArgHisLysIle 106
DB 1399 AGTATGTATAGAAAACCTAATCCCAAGTGTGTGACAAAGTTCTCCACAAAGTATAGATG 1458
QY 107 GlyLysArgWetLysLysIleMetGluLysLeuAspValIleAlaIleGluArgIleLys 126
DB 1459 CATGCCAAGTTAGATGATTTGCCACAGGTTTCAAGAACCTGTAGAGGCCAAATTAAT 1518
QY 127 PheHisLeuAspGluWetArgThrIleGluArgGlnValAlaThrArgGlnThrGlyPheVal 146
DB 1519 CTGTGTTAAGTGTATACATATGAAAGCCAAATTTGAAAGCTATGAGCGCTCTTG 1578
QY 147 LeuAsnGluProGlnValTyGlyArgAspLysGluLysAspGluIleValLysIleLeu 166
DB 1579 GTATATAAAGCCGTCGTGCGACGTGAAGATGATTAAGAAAATTCGTGAGAAAGCTG 1638
QY 167 Ile-----AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
DB 1639 TTGGGGATTAAGATGATCAGGAGTCAAAACTTCAGCATCGTCCCATATGTTGTATG 1698
QY 185 GlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlu 204
DB 1699 GGTTGAGTTGTTAAACACCTAGCTAGACTTTTGTATATGAAAGAAAGTAAAGAT 1758
QY 205 HisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGluLysArgLeuIle 224
DB 1759 CACTTCAACCTCAGCGCTGGGTTTGTCTTGATGATGATGATGATGATGATGATGATG 1818
QY 225 LysGluIleValGluSerIleGluGluLysSerLeuGlyLysMetAspLeuAlaProLeu 244
DB 1819 AGAGTTATTTATATCATCTGATCGGGGAAAGAGAGTTTGAAAGCTTAATCTCTCT 1878
QY 245 GlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyLeuLeuValIleAspAspVal 264
DB 1879 CAAAGAGCTTTAAAGAGAACTTAAGAACAGCATATTTCTAATAGTTTGAGATGATG 1938
QY 265 TrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysValGlyAlaSer 284
DB 1939 TGCTGTAAGCTATGATGATGAGAGAAATAGTGGGCCCATCTTGGGGGTCTCTCT 1998
QY 285 GlyAlaSerValLeuThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeu 304
DB 1999 GGAAGTAGAATTAACATGACAACTCGAGAGGCAATTCACAGAAAGCTGGGCTTTTCT 2058
QY 305 GlnProTyGlnLysSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetGlnArg 324
DB 2059 CATCAAGACCTCTGGAGGCTTATTCACAGATGATGCTTGTCTTGTGCTTCACACAC 2118
QY 325 AlaPheGlyHisGlnGlu---GluIleAsnLeuAsnLeuValAlaIleGlyLysGluIle 343
DB 2119 GCATTGTGTATCAAACTTTGATTCATCCACATCAAGGCCACATGAGAACTGTCTT 2178
QY 344 ValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPhe 363
DB 2179 GTGAAGAATGTATGCTTACCTTGTAGCTTAAACAACCTGGAAGGTTATTAAGACA 2228
QY 364 LysArgGluGluArgGlnTrpGluHisValArgAspSerGluIleTrpLysLeuProGln 383
DB 2229 AAAACAGACGAGAAACATGGAAGAGCTGTGATGATGATGATGATGATGATGATG 2298
QY 384 GluIleSerSerIleLeuProAlaLeuArgLeuSerTyHisHisLeuProLeuAspLeu 403
DB 2299 AGCGAT---GAGATTTGTCGCGCTCTTGAAGTAAAGCTAATGATGATGATGATG 2355
QY 404 ArgGlnCysPheThrTyGlyAlaValPheProLysAspThrGluMetGlyLysAsn 423
DB 2356 AAGCTRTTATTGTGATATGCTCTTGTCTTCCAAAGCATATGATGATGATGATGATG 2415
QY 424 LeuIleSerLeuTrpMetAlaHisGlyPheIle---LeuSerLysGlyAsnLeuGluLeu 442
DB 2416 TTGATTTCTATTGTGATGACGAAGGTTTGTGACCAACCAACATATTAACATGCAAG 2475

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Binhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-07810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 4163 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..4163
OTHER INFORMATION: /note= "RLG1-E169"
US-09-004-838-70

Alignment Scores:
Pred. No.: 2,686-100 Length: 4163
Score: 1008.50 Matches: 311
Percent Similarity: 46.52% Conservative: 177
Best Local Similarity: 29.65% Mismatches: 395
Query Match: 19.67% Indels: 166
Gaps: 27

US-10-647-268-2 (1-988) x US-09-004-838-70 (1-4163)

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DB 1099 ATGGCTGAATTCGTTCTTCTGCTCTTCTTGACAGCGTGTTGAAAGCTGGCATTTGAA 1158
QY 17 ILeGlnGlyLeuLeuGlyLeuLeuPheLeuAspGlnPheGlnLeuLeuInser 36
DB 1159 GCCTTGAAAGAAATGTTGCTCCCAAAAGAAATTGAATCTGACCTTAAGAAATTGAAGAG 1218
QY 37 ThrPheThrThrIleGlnAlaValLeuGlnAspAlaGlnLeuLeuAspLeu 56
DB 1219 ACATTAGACCAATCCAGATCTGCTTAACATGCTTCCAGAGAGAACTAATGATGAA 1278
QY 57 AlaIleGlnAsnTrpLeuGlnLeuLeuAsnAlaAlaIleGlnAlaAspAspIleLeu 76
DB 1279 GCCGTTAAAGATGCTGATGATGATCTCCAAACATTTGGCTTATGACATGACGACCTACTT 1338
QY 77 AspGlnCysLeuThrGlnAlaPheProIleArgGlnLeuLeuAsnLeuLeuGlyCysThrHis 96
DB 1339 GATGATTTTGGCACTGAAGCTCTTCAACGCTGAGTTGACCGAGAGGCTGAGCCCTCC 1398
QY 97 ProAsnVal-----IleThrPheArgHisLeu 106
DB 1399 AGTAGGTGAAGAACTAATCCCAAGTTGTCACAAAGTTTCTCAAAAGTAAATAGAGATG 1458
QY 107 GlyLeuAsnMetLeuLeuIleMetGlnLeuLeuAspValIleAlaAlaGlnArgIleLeu 126
DB 1459 CATGCCAAGTTAGATGATTTCCACACAGGTTACAGAACTGATGAGGCAAAAATATAT 1518
QY 127 PheHisLeuAspGlnArgThrIleGlnArgGlnValAlaThrArgGlnThrGlyPheVal 146
DB 1519 CTGTGTTTAAGTGTATTAACATATATAAAGCCAAAATTTGAAAGGTATGAGCGCTTTTG 1578
QY 147 LeuAsnGlnProGlnValIleArgAspLeuLeuGlnLeuAspGlnIleValLeuLeu 166
DB 1579 GTAGATGAAGCGGACACTGCTGCGAGCTGAAGATGATTAAGAAAATTTGCTGGAAGAGCTG 1638
QY 167 Ile-----AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
DB 1639 TTGGCGGATTAAGATGAATCAGGAGATCAAAAATTTCAGCATCTGCTCCCATAGTTGTTATG 1698

QY 185 GlyLeuLeuGlyLeuThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGln 204
DB 1699 GTGGAGTTGGTAAACAACACTCTAGACTTGTATGATGAAAGAAAGTGAAGAT 1758
QY 205 HisPheHisProLeuIleTrpIleCysValSerGlnAspPheAsnGlnLeuArgLeuLeu 224
DB 1759 CACTTTCGAACCTAGAGGCTTGGGTTGTCTCATAGATGTCAGTGTCCCAATATTAAGC 1818
QY 225 LysGlnIleValGlnSerIleGlnGlyLeuSerLeuGlyMetAspLeuAlaProLeu 244
DB 1819 AGACTTATTTATCAATCTGTACCTGGGAAAGAGAGATTGAAAGCTTAATCTGCTT 1878
QY 245 GlnLeuLeuLeuAspLeuLeuAsnGlyLeuLeuValLeuValLeuAspAspVal 264
DB 1879 CAAGAGCTCTTAAGAGAACTTAGAACCAAGCATTTCTTAATAGTTTGTGATGATGTG 1938
QY 265 TrpAsnGlnAspGlnAspLeuTrpAlaLeuLeuArgGlnValIleLeuValAlaSer 284
DB 1939 TGGTCTGAAGCTATGATGATTTGGAGAAATTAAGTGGCCCATTCCTTGGCGGGCTCTC 1998
QY 285 GlyAlaSerValLeuThrThrThrArgLeuGlnLeuValGlySerIleMetGlyThrLeu 304
DB 1999 GGAAGTGAATTAATCATGACAACTCGAAGAGCAATTCCTCAGAAAGCTGGCTTTCT 2058
QY 305 GlnProTrpGlnLeuSerAsnLeuSerGlnGlnAspCysTrpLeuLeuPheMetGlnArg 324
DB 2059 CATCAAGACCTCTGAGAGGCTCTATCAAGATGATGCTTGTGTTGCTCAACAC 2118
QY 325 AlaPheGlyHisGlnGlu--GlnIleAsnLeuAsnLeuValAlaIleGlyLeuGlnLeu 343
DB 2119 GCATTGTGTACCAAACTTTGATTCACATCAACACTAGGCCACATGGAGCACTGTTT 2178
QY 344 ValLeuLeuLeuCysGlyGlyValProLeuAlaAlaLeuThrLeuGlyGlyIleLeuArgPhe 363
DB 2179 GTGAAGAAATGTAGTGGCTTACCTTAGCTTAAGACACTTGAAGGTTTAAAGACA 2238
QY 364 LysArgGlnGlnArgGlnTrpGlnIleValArgAspSerGlnIleTrpLeuLeuProGln 383
DB 2239 AAAACAGACAGAAACATGAGAGAGCTGTGATAGTGAATGAGGTTGAGAAAG 2298
QY 384 GlnGlnLeuSerIleLeuProAlaLeuArgLeuSerGlyHisIlePheProLeuAspLeu 403
DB 2299 AGCGAT--GAGATGTTGCTCGGCTCTTAGACTAAGCTACAAATGATCTTTCGCKCTTTG 2355
QY 404 ArgGlnCysPheThrTrpCysAlaValPheProLysAspThrGlnMetGlnLeuGlyAsn 423
DB 2356 AAGCTRTTGTGATATATGCTCTTGTTCCTCAAGACATAATGATTTGACAAAGAGAG 2415
QY 424 LeuIleSerLeuTrpMetAlaHisGlyPheIle--LeuSerLysGlyAsnLeuGlnLeu 442
DB 2416 TTGATTTATTTGGATGAGTGCAGAGAGGTTTTTGACCAACCAACTATYMAACAAGTCAAG 2475
QY 443 GlnAsnValGlyAsnGlnValTrpAsnGlnLeuTrpLeuArgSerPhePheGlnGlnIle 462
DB 2476 CAAGCTTGGGTCTTAATATTTTAAGAGTTRTGTCAAACTKCTTTTTCATA----- 2529
QY 463 GlnValLysSerGlyGlnThrTrpPheLysMetHisAspLeuIleHisAspLeuAlaThr 482
DB 2530 CATGCTCTTAATRCAAACTGTGTTGTGATGATGACCTTAATGAATGATTTGGCTACA 2589
QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIle-----ArgGln 496
DB 2590 TTTGTGCTGAGAAATTTTTCAGAGTTGACATAGATGAGAGAAAGAAATTTAGAGATG 2649
QY 497 IleIleValGlnAsnTrpIleHisMet----- 505
DB 2650 SAATCTTGGARAGACACGACATATGTCATTTGATGTGAGATATCATATAGTTTACAA 2709
QY 506 -----MetSerIleGly 509
DB 2710 ARGTTGAGCCATTAGAGAGCTTAAAAATTTGAGAACATTTTATGACATGTCTGTTGGG 2769


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; LOCATION: 1..2353
; OTHER INFORMATION: /note= "RLGIB"
US-09-004-838-2

Alignment Scores:
Pred. No.: 4,38e-96 Length: 2353
Score: 966.50 Matches: 242
Percent Similarity: 53.52% Conservative: 131
Best Local Similarity: 34.72% Mismatch: 265
Query Match: 18.85% Indels: 59
DB: 3 Gaps: 12

US-10-647-268-2 (1-988) x US-09-004-838-2 (1-2353)

OY 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspLeuThrCysPheIleGlnGlu 20
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 289 CTTGGTTCGCGCTCTTTGCGGTCTTTGAAAAGCTTCTTGAAGCCTTGAAGG 348
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 21 LeuGlyLeuIleLeuGlyPheLeuAspGluPheGluLeuGlnSerThrPheThr 40
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 349 GTTGGCTCTCCAAAGTAATGACAAAGAGCTCGAAATTAAGTCAATGATCAAT 408
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 41 ILeGlnAlaValLeuGlnAspAlaGlnLysGlnLeuLysAspLysAlaIleGln 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 409 ATAAAGCTCTGCTCAATGATGCTTCTCAGAAAGAAATAGTAAGAGAGCTTTAA 468
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 TrpLeuGlnLysLeuAsnAlaAlaIleTyrglyAlaAspAlaIleLeuAspGlu 80
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 469 TGGTGAATGCTCTTCAACATTTGCTTACGACATAGATCTTGGCGAATTTGCA 528
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 81 ThrGluAlaProIleArgGlnLysLysAsnLysTyrgly----- 93
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 529 ACCAAAGCTATCCATCTGTAAGTCTCTGAGGAATCGGGCCACCATCAACAAGT 588
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 94 -----CysTyHisProAsnValIleThrPheArgHisLysIleGlyLys 108
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 589 AAGTTAATTCATCTTGTCTCTAGTTGTCAAGTACT-----AAGATCGGCAAC 639
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 109 ArgMetLysLysIleMetGlnLysLeuAspValIleAlaAlaGluArgIleLys 128
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 640 AAGATACATTAATATTACCAAGAGTTACAGAACTATTAGAAAGAAATTAATTT 699
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 129 LeuAspGluArgThrIleGluArgGlnValAlaThrArgGlnThrGlyPheVal 148
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 700 TTATGTGAATTTGGTGAAGCGGAAGAACTTCGAATTAAGAAATCAGAACCTTT 759
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 149 GluPro--GlnValTyrglyArgAspLysGlnLysAspGluIleValLysIle 167
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OY 760 GATCCATCTAGATATTGTGACGACAGATGATTAAGAAAGCGTGTCTCAAGCT 819
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 168 AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGly 187
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 820 GAACCATGTGAT-----AGAAACTTTAGCATCTTGCNATAGTGGATGGGTTA 873
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 188 GlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHis 207
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 874 GATTAAGACCATTTAGTGAAGACTTTGTATGATTAATTAAGCAAGTAAAGACT 933
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 208 ProLysIleTrpIleCysValSerGlnAspPheAsnGlnLysArgLeuIleLys 227
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 934 CTCAAGGCGGTGGTGTGTCTTGATGATGATTTGATCTTCGATTAAGCAAAAC 993
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 228 ValGlnSerIleGlnGlnLysSerLeuGlyMetAspLeuAlaProLeuGlnLys 247
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 994 TTCGATCGATGAGAGGAGGAAACCAAGATTAAAGATTAAATCTGCTTCAAGT 1053
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 248 LeuArgAspLeuLeuAsnGlyLysLysTyrglyLeuLeuValLeuAspAspVal 267
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1054 TTAAAGCAAAATCTCAAGAAAGCATTTCTGTGTTCTTGATGATGATGAGCGAG 1113
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 268 AspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysValGlyAlaSerGly 287
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1114 AGCTATCTGATTTGGAAATCTTGAAGGTTCATTTCTAGCAGAGCACAGGAAGTAA 1173

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OY 288 ValLeuThrThrThrArgLeuGlnLysValGlySerIleMetGlyThrLeuGlnPro 307
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1174 GTATCATCTACACACCCGCAAGTCTGCTGTGTAACCAATGGGTCATGATCAACAT 1233
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 308 GluLeuSerAsnLeuSerGlnGlnAspCysTrpLeuLeuPheMetGlnAlaPheGly 327
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1234 CAATTTGTCTGATTTGTCAATGACAAATGCTTATCTTATTTGTCAACGCGATTTGGT 1293
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 328 ---HisGlnGlnGlnIleAsnLeuAsnLeuValAlaIleGlyLysGlnIleValLys 346
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1294 GTAAATGCTTTGATTCACATCCGATCTTAACACATGGGTGAAGGATTTGTTAA 1353
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 347 CysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPheLysArg 366
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1354 TGTGATGTTTCCCATTTGGCTTTGATTTGACACTTGGAGGTTATTAGAGCAAAAG 1413
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 367 GluArgGlnTrpGlnHisValArgAspSerGlnIleTrpLysLeuProGlnGln 386
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1414 GAGGAAGAAATGGAAGAACTATTGAATATGAGATATGAGGTTAGAAAGAGAT--- 1470
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 387 SerIleLeuProAlaLeuArgLeuSerTyHisIleAspProLeuAspLeuArg 406
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1471 GAGATTATTCGGYTCTTACGCTAAGCTATATGATCTTCTGCTCTTTGAAGCAT 1530
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 407 PheThrTyrglyAlaValPheProLysAspThrGluMetGlyLysAsnLeuIleSer 426
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1531 TTTGCATATTCCTCTCTTGTCCCAAGACATATGTTCAACAAGAAAGTATTTTA 1590
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 427 LeuTrpMetAlaHisGlyPheIleLeuSerLysGly---AsnLeuGlnLeuGln 445
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1591 TTATGATATGGCAGAAAGGTTTTCACAAATGAATAAACAAGTCAAGAAAGCGCTTA 1650
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 446 GlyAsnGlnValTrpAsnGlnLeuTyrglyLeuArgSerPhePheGlnGlnIle 465
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 466 SerGlnGlnThrTyrglyPheLysMetHisAspLeuIleHisAspLeuAlaThr 485
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OY 1705 GATGACAAATGCTGTTTGTGGTGCACGACTTGAATGACTTGGCCACATCTGTGCT 1764
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 486 SerAlaSerThrSerSerSerAsnIle-----ArgGlnIleIleValGlnAs 503
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1765 GGAATTAATTTTAAAGATTAGACATTGAATGAAGAAAGGCTTTGAAAAATACC 1824
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 504 HisMet----- 505
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1825 CATATGTCATTTGTTGTGAGATTAATGATGTTTCAAAAGTTCCGAACCTTAAAG 1884
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 506 -----MetSerIleGlyPheThrLysValIleSerSer 516
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1885 GCTAAAAAATTGAGAACTTTCTTAGCAATGCTGTGGAGATGAATAAAGTTGACA 1944
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 517 TyrSerLeuSerHis-----LeuGlnLysPheValSerLeuVal 530
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 1945 TTTTATCTTATTAATAAGTCTTGAATGACTTACCTACGAAATTAACCATTTGA 2004
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 531 LeuAsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuVal 550
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2005 CTAAAGTTTGAATTTCTTAGATCAAGAGGTAAGTCAAAATTAATTAAGCAATTT 2064
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 551 LeuArgTyrglyLeuAsnLeuSerGlyAsnThrSerIleArgSerIleProAsnGln 570
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OY 2065 TTGGCGATCTTAATTTATCA---CACACGAGTATCACACATTTAACGAAAAAGT 2121
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 571 LysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeu 590
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2122 AATCTTTTAAACCTTAAACAACTTATGCTTTGTGGCTGTGTTTATTAACCAAGT 2181
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 591 LysGlnThrSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrgly 610
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 2182 AACCACTTCTTAAGCTTTGAATTAATTAACGATTTGACATTTAGCAATCTCCGG 2241

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Qy 611 ThrCysMetProPheArgIleGlySerIleuThrCysIleuLysThrLeuSerArgPheVal 630
Db 2242 AAGAAGATGCTCTCGGCGATTGTAATGAAGAACTTACACACCTCTCCAGCTCAT 2301
Qy 631 ValGlyIleGlnLysLysSerCysGlnIleuGlyGluLeuArgAsnLeuAsn 647
Db 2302 ATGGAGGTGAATAATGACTAAAGAGCTTAAGAACTTAACAATACTTCAT 2352

RESULT 6
US-09-004-838-6
Sequence 6, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmere, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US -08/781,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Elmhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1662 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..1662
OTHER INFORMATION: /note= "RLGIF"
US-09-004-838-6

Alignment Scores:
Pred. No.: 1.7e-68 Length: 1662
Score: 715.00 Matches: 165
Percent Similarity: 57.14% Conservative: 103
Best Local Similarity: 35.18% Mismatches: 183
Query Match: 13.95% Indels: 19
Gaps: 7

US-10-647-268-2 (1-988) x US-09-004-838-6 (1-1662)
Qy 30 GluphegIuLysLeuGlnSerThrPheThrTrlIleGlnAlaValLeuGluAspAlaGln 49
Db 128 GAGCTCAAGAACTGTAAGAGGCTTAATTCAGATCAAGATCTGTCCTTAAGATGCTCT 187
Qy 50 LysIysGlnLeuLysAspLysAlaIleGlnLubnTrpLeuGlnLysLeuAsnAlaIala 69

Db 188 GAGAAAGAAATAGATGATGAAGCTGTAAAGAAATGGCTGAATGCTTCAACATTTGCT 247
Qy 70 TyrGluAlaAspArgIleLeuAspGluCysLysThrGluAlaProIleArgGlnLysLys 89
Db 248 TACGACATGAGCGACTTACTTATGATTTGGCAACCGAACTATGATCGTGAAGTGC 307
Qy 90 AsnLysTyrGlyCysTyrHisProAsnVal----- 99
Db 308 CACGATCTGAGGCTC-CACGACCTGTGAAGAAAGATATCCCACTTGTGCACAGAT 366
Qy 100 IleThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGluLysLeuAspVal 119
Db 367 TTCCTACTTAAGTACATGATCGTACCAAGTATATATATATACATCAAGTTCACAGAA 426
Qy 120 IleAlaIleGluArgIleLysPheHisLeuAspGluArgThrTrlIleGluArgGluValAla 139
Db 427 CTGGTAGAGGAAAAGATATCTGGCTTAAGTGAAGGTGAAGCCCAAAACATACC 486
Qy 140 ThrArg-----GlnThrGlyPheValLeuAsnGluProGlnValTyrGlyArgAspLys 157
Db 487 AACGAGATTAAGACCTCTTGTGA---GATGATCTACATTTATGTCGTGAAGGT 543
Qy 158 GluLysAspGluIleValLysIleLeuLysAsnAsnValSerAsnAlaGlnThrLeuPro 177
Db 544 GATAAGGATGATGCTTCATACGCTGCTGAGAGATGACCAACGATGATGAACCTTTAGC 603
Qy 178 ValLeuProIleLeuGlyMetGlyGlyLeuGlyLysThrTrlLeuAlaGlnMetValPhe 197
Db 604 ATCTGCCAATATGTTGATGATGGTGGTGGTGAAGACGACTTACGCTTACGCTTTGAT 663
Qy 198 AsnAspGlnArgValIleGluHisPheHisProLysIleTrpIleCysValSerGluAsp 217
Db 664 GACGAGATGCAAGAGAGATCACTTGCAACTCAAGCGTGGTGTGTTGCTTGAATAG 723
Qy 218 PheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGluLysSerLeuGly 237
Db 724 TTGTATATCTCAATATATAGCAAGATTAATCTTCAATGATGATGATGATGATGATGAT 783
Qy 238 GlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyr 257
Db 784 TTTAAGACTTAATATCTCTTCAAGTACGCTGTAAGAAAGATTTCAAGAAAGATTT 843
Qy 258 LeuLeuValLeuAspAspValTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGln 277
Db 844 CTWTTGTTGTCGATGATGTTTGAAGTGAAGCATACAGATGGAAATTTCTGACAGCT 903
Qy 278 ValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGluVal 297
Db 904 CCATTTCTTGCAAGGGGCAACGAAAGTATATCATGACGACCCGGAAGTGTCTGTTG 963
Qy 298 GlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnLysAspCys 317
Db 964 CTACCAAACTCGGTTCAATCAACCTTACCACTTCTGTTTGTTCACATGAATATGCT 1023
Qy 318 TrpLeuPheMetGlnArgAlaPheGlyHisGlnGlu---GluIleAsnLeuAsnLeu 336
Db 1024 YTGCTTTATTTCTGACAGATGATTTGGGTGAAGATATCACTTCATCAACCAACTT 1083
Qy 337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaLysThr 356
Db 1084 AAACACACAGGATGAAGATGTTGAAGAAATGTACGCGTTTACCATTTGCTTATATCA 1143
Qy 357 LeuGlyLysIleLeuAspPheLysArgGluGluArgGlnTrpGluHisValArgAspSer 376
Db 1144 CTGGGAGRTTGTGARGACAAAGAAAGATGAGAAAGTGAAGAGTGTGAATATGT 1203
Qy 377 GluIleTrpLysLeuProGlnGluGlnSerSerIleLeuProAlaLeuArgLysSerTyr 396
Db 1204 GAATATGCGGCTGAGAAAGAGAT---GAGATTGTCCGCTTAAACTAAGCTAC 1260
Qy 397 HisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAsp 416

Db 1261 AATGATCTCTGCTCTTTGAAGAAGTTGTCATCTGCTCTTCCCAAAAGAC 1320
Qy 417 ThrgluMetGluYsglyAsnLeuIleSerLeuTrpMetAlaHisglyPheIle--Leu 435
Db 1221 TATGTTGTCATTAAGAGAGAGATGTTGTTGTCATGACAGAAAGGTTTTCACACCA 1380
Qy 436 SerlysglyAsnLeuIleGluIleGlnValGlyAsnGluValTrpAsnGluLeuTyrLeu 455
Db 1381 TCAACCAACAGCAAGTCBAGTGAACGCTTGCGHCTGAAGTTTGGATGAATGTTGTCA 1440
Qy 456 ArgSerPhePheGlnGluIleGluValIysSerGlyGlnThrTyrPheIleMetHisAsp 475
Db 1441 AGATCATTTTTCAA-----CATGCCCTGATGCCAATGATGTTTGTATGATGATC 1494
Qy 476 LeuIleHisAspLeuAlaThrSerLeu 484
Db 1495 CTGATGATGACTTGCGHACATCTGTT 1521

RESULT 7
US-08-947-823-2
; Sequence 2, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kalooshian, Isgonchi
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Molligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Confering
; TITLE OF INVENTION: Pest Resistance in Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 85..3852 /note= "Copy 1 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
; US-08-947-823-2

Alignment Scores:
Pred. No.: 3 91e-56 Length: 3997
Score: 609.50 Matches: 257
Percent Similarity: 41.64% Conservative: 144
Best Local Similarity: 26.69% Mismatches: 383
Query Match: 11.89% Indels: 179
DB: 3 Gaps: 37

US-10-647-268-2 (1-988) x US-08-947-823-2 (1-3997)

Qy 5 PheLeuGlnValIleuAspAsnLeuThrCysPheIleGlnGluLeuGlyLeuIle 24
Db 1252 TTTCATGATCTTCTACACATACACTTAATGATTTGTAATTCATTAATTCATTT 1311
Qy 25 LeuGlyPheIleAspGluPheGluIleGlnValSerThrPheThrThrIleGlnAlaVal 44
Db 1312 GCTTTGATTAAGAAAGAAATCGAGCTGTGAAGCAAGCACTGAAATTCATTAATTCATTC 1371
Qy 45 LeuGluAspAlaGlnIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 64
Db 1372 TTTCATGATCTTCTACACATACACTTAATGATTTGTAATTCATTAATTCATTT 1419
Qy 65 LeuAsnAlaAlaIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 84
Db 1420 CTAGAT---GTGGCTTATGAGGCAAAAGATGCTATGATTCGA--- 1458
Qy 85 IleArgGlnIleIleAsnIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 99
Db 1459 ATTAATTTGTCAGAGTAAT---GGTCTTACATCTTATTTTTCATCTCCATTCATTC 1512
Qy 100 IleThrPheArgHisIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIleGlyIle 119
Db 1513 ATA-----AAGAATCACTTAATTCAAAGAAAGATCTCTGCT 1551
Qy 120 -----IleAlaIleGluArg-----IleIlePheHisIleuAspGluArgThr 133
Db 1552 TTAGATGAGAACATTTCCCAAGAGACAGGCTTAATCTGTGTAATCTCCCAAGAACCA 1611
Qy 134 IleGluArgGlnValAlaThrArgGlnThrGlyPheValIleuAsnGluProGlnValTyr 153
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Qy 154 GlyArgAspIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 173
Db 1651 GCTTTGAGAGAGAAACAACTTGATCTAGAAAGCTC-----ACCAGGATGCTG 1701
Qy 174 GlnThrLeuProValIleuProIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 193
Db 1702 GCAGATCTAGATGTCATTTTCATCTGATGCGGCGGATTCAGGTAAGTAATCTACTTTGGCA 1761
Qy 194 GlnMetValPheAsnAspGlnArgValIleGluIlePheHisProIleTyrIleCys 213
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Db 1822 GTTCACCAAGGATGTGATGAGAAAGAGTTGTAATCAATTTTCACGTAAGTAAGTGC 1861
Qy 224 LysSerLeuGlyGlyMetAspLeuAlaProLeuGlnIleIleGluIleGluIleGluIleGluIle 253
Db 1862 TCAGATTCAAATTTGAGTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1941
Qy 254 GlyIleIleGlyIleLeuValIleuAspAspValIleGluIleGluIleGluIleGluIleGluIle 273
Db 1942 GGAAGAGATATCTTATTTGCTTGAATGAGCTGCG-----GATTACTAATCAATGAGAT 1995
Qy 274 LysLeuArgGlnValIleuValIleGlyAlaSerGlyAlaSerValIleuThrThrThrArg 293
Db 1996 GAGTTAACAAGACCTTTCTGTAATCTTAAGAAAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2055
Qy 294 LeuGluIleValIleGlySerIleMetGlyThrLeu-----GlnProTyrGluLeuSerAsn 311

Db 2056 ---GAAAGGAGTGGCTTTGGATGAGAAAGCTGAACTGATCCCTTGGACCTTGATG 2112
Qy LeuSerGlnGluAProCysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlu 331
Db 2113 CTAAGACCAAGATGAAAGTTGGAACCTATTAGAGAAAGGGCATTTGGGAAT---GAGAGT 2169
Qy 332 IleAsnLeuAsnLeuValAlaIleGlyLysGluIleValLysLysCysGlyGlyValPro 351
Db 2170 TGCCCTGATGAACATTAGATGTCGGTAAAGAAATAGCCGAAATATTGTAAGGGCTTCT 2229
Qy 352 LeuAlaIleLysThrLeuGlyGlyIleLeuArgPheLysArgGlnGluArgGln---Trp 370
Db 2230 TTGGTGGCTGATCTGATGCTGAGTCAATGCTGGAGGAGAAAGAAAGAGCTGTGG 2289
Qy 371 GluHisValArgAspSerGluIleTrpLysLeuProGlnGlnGlnGlnSerSerIleLeuPro 390
Db 2290 CTTGAAGTTCAAGATGATTGAGTCTTTTATTGAAACAGTGAAGTGAAGTGAAGTGA 2349
Qy 391 AlaLeuArgLeuSerTrpHisIleLeuProLeuAspLeuArgGlnCysPheThrTrpCys 410
Db 2350 GTTATAGAAATTAAGTATGACCATTTACCACTCAAGCCATGCTTGCTGTATTTT 2409
Qy 411 AlaValPheProLysAspThrGlnMetGlnLysGlyAsnLeuIleSerLeuTrpMetLys 430
Db 2410 GCAAGTTTCCGAAAGACACTTCAATCTATGAGTGAATGTTTATTTCGGTCT 2469
Qy 431 HisGlyPheIleLeuSerLysGlyAsnLeuGlnLeuValGlyAsnGlnValTrp 450
Db 2470 GAAGATTTGGGAAAGACGAGATGAACAGTATGAAAGAGTGTGAAGTTTATGTG 2529
Qy 451 AsnGlnLeuTrpLeuArgSerPhe-----PheGlnGlnIleGlnValLysSerGly 467
Db 2530 GATGATTTAATTTACAGTACGCTGTGATTTGTTTCATGAGATGCTTATGACTGAT 2589
Qy 468 GlnThrTrpPheLysMetHisAspLeuIleHisAsp----- 479
Db 2590 -----TTCCAAATTCATGATCTTGTCATGATGCTTTTGATGATAAAGCAAGAAAG 2640
Qy 480 -----LeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIle 497
Db 2641 GAAATTTGTTGATCAATAGATCAAGTCTCATGATTTGTCCTCGTCATTAAT 2700
Qy 498 IleVal-----GluAsnTrpIleHisMetMetSerIleGlyPheThrLysVal 513
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Qy 514 ValSerSerTrpSerLeuSerHisLeuGlnLysPheValSerLeuArgValLeuAsnLeu 533
Db 2761 AAGAAAGGCAATCTGCTGTAACACCTC-----TATCTTGTGAGGATTAATGGA--- 2808
Qy 534 SerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTrp 553
Db 2809 -----GACCAGCTGATGACAGTGTCTGTGATGCACTTCCACTTAAGACAC 2853
Qy 554 LeuAsn-----LeuSerGlyAsnThrSerIle-----ArgSerLeu 565
Db 2854 TTGAGGCTTCTTAGAGTGTGGAACCTGATACGCTTTTATCAGTGAAGATTTCTTG 2913
Qy 566 ProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSer 585
Db 2914 CTGATGAAATATGATGATGATTAATCATTTGAGTACTATTCATTCATGAC-----ACACAA 2967
Qy 586 LeuCysCysLeuProLysGlnThrSerLysLeuGlnSerLeuAspAsnLeuLeuAsp 605
Db 2968 GTTAAATATCTGCTTCTTCTTCTTCAACCTCTGGAATCTGAAGAGCTGTGTGCT 3027
Qy 606 GlyCysTrpGlyLeuThrCysMetProProArgIleGlySerLeuThrCysLeuLysThr 625
Db 3028 ACCAACAAGATCAATCTGTACTATACCGAAGATTTTGATCTTGTAAATTTGAGAGT 3087
Qy 626 LeuSerArgPheValValGlyIleGlnLysLysSerCysGlnLeuGlyGlnLeuArgAsn 645
Db 3088 CTGTCTC-----GTGATGCTGTGTCTTCTC----- 3111

Qy 646 LeuAsnLeuTrpGlySerIleGlnIleThrHisLeuGlnArgValLysAsnAspMetAsp 665
Db 3112 -----TTTGATGATGAT 3123
Qy 666 AlaLysGlnAlaAsnLeuSerAlaLys-----GluAsnLeuHisSerLeuSer 681
Db 3124 GCAGATGATCAATATTTGATGACAGAGACAAAGTTTGAAGAACTTGAGAAATTTAAAG 3183
Qy 682 MetLysTrpAspAspAspGluArgProArgIleTrpGlnSerGlnLysValGlnValLeu 701
Db 3184 -----GACSTGTGATTTCTTCTTTCGAAAGATTAACAAAG 3216
Qy 702 GluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIle 721
Db 3217 AATATTTTCAAAAGATTTCCCAATCTTCAGTGTCTTCA-----TTT 3258
Qy 722 ArgLeuProAspTrpMetAsnHisSerValLeuLysAsnValSerIleGlnIleIle 741
Db 3259 GAACTCAAGAGTCAATGAGATTAATCAACAGCAACATTCG----- 3300
Qy 742 SerCysLysAsnCysSerCysLeuProPheGlnGlnLeuProCysLysLysSerLeu 761
Db 3301 -----TTCTCGAATTTGATTTCTTAAGTGAACATA 3330
Qy 762 Glu-----LeuTrpArgGlySerAlaGlnValGlnTrpValAspSerGlyPhe----- 777
Db 3331 GAAACACTCTCTGTAGGTTTAAAGTTTAAAGCAACAAACGATAGTGGTCTCTGTAGCG 3390
Qy 778 -----ProThrArgArgArgPheProSer-----LeuArgLysLeuAsnIleArgGln 793
Db 3391 ACAATCGGCCCGTGGATTTTCACTTCCCTTCAAAATTTGAATACTGTGCTCGTGA 3450
Qy 794 PheGlyAsnLeuLysGlyLeuLeuLysGlyLeuLysGlnGlnGlnCysProValLeuGln 813
Db 3451 TTTCGGCTGACATCCGATTCATCACTATCAACATAGCG-----AAGTGGCCCAACCTGAA 3504
Qy 814 GluIleGlnIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLys 833
Db 3505 GAGTTG-----TTCCTTATCAT 3522
Qy 834 LeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMet 853
Db 3523 ACAATCATCCATGAGAGAAATGAGACATGGGAGGAGACACCTTGAAGATTCGAAA 3582
Qy 854 AlaLeuThrSerLeuGlnIleArgTrpAsnLysGlnAspAlaSerLeuProGlnGlnMet 873
Db 3583 TTTTGAACCTTCAATCAAGTTAGTATTTCCAAAGTGGAGGCTTGA-----GAGGAATCC 3636
Qy 874 PheLysSerLeuAlaAsnLeuLysTrpLeuAsnIleSerPheTrpPheAsnLeuLysGln 893
Db 3637 TTC-----CCCATCTTGAAGAAATTAACATGGGGAGATGCTAAGCTAGAGAG 3687
Qy 894 LeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGlnIleHisSerCysTrp 913
Db 3688 ATTCACCTTGGTTTGGAGATATTATTCATTTGAAATCTATCAAAATTTGAAAGAGTCT 3747
Qy 914 AlaLeuGln 916
Db 3748 CAACCTGAA 3756

RESULT 8
US-08-947-823-1
Sequence 1, Application US/08947823
Patent No. 6114605
GENERAL INFORMATION:
APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isagouni
APPLICANT: Yachobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Pest Resistance in Plants

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1

Alignment Scores:
Pred. No.: 3,666-54 Length: 51952
Score: 609.50 Matches: 257
Percent Similarity: 41.64% Conservative: 144
Best Local Similarity: 26.68% Mismatches: 383
Query Match: 11.89% Indels: 179
DB: 3 Gaps: 37

US-10-647-268-2 (1-988) x US-08-947-823-1 (1-51952)
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DB 46344 TTCATGACATCTTCTACATCACTTAATAATGATTGTTAGATTCTTAATGCTTATTCAATT 46403
QY 25 LeugllyPheleuAspGluPheGluLysleuGlnserlthPheThrThr11leGlnAlaVal 44
DB 46404 GCTTGTGATTAAGGAAGAAATCGAGCTGCGAAGCAAGACCTGAATTCATTAAGATCATTC 46463
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QY 65 LeuAsnAlaAla11ATyTGTuAlaAspAsp11leuAspGluCyLysThrGluAlaPro 84
DB 46512 CTAGAT---GTGCTTATAGGCAAAAGATGTCATAGATTCA----- 46550
QY 85 11eAspGlnLysleuAsnLysTyTgLyCyTyYH18-----ProAsnVal 99
DB 46551 ATTATGTTGTCAGATTAAT-----GCTCTTACATCTTATTGTCACCTTCCCATTAAC 46604
QY 100 11eThrPheArgHisLys11leGlyLysArgMetLysLys11leMetGluLysLeuAspVal 119
DB 46605 ATA-----AAGAGATCAAACTTATCAAGAAAGAGATCTCTGCT 46643

QY 120 -----11leAla1aGluArg-----11leYsPheHisLeuAspGluArgThr 133
DB 46644 TTAGATGAGAAACATTCOCAGACAGAGCTATGCTGTGAACCTCTCCCAAGAAACCA 46703
QY 134 11leGluArgGlnValAla11ThrArgGlnThrGlyPheValLeuGlnGluProGlnValTyT 153
DB 46704 GTTGAGAGAAAGTCATTGACA-----ACTGATTAATAACTGTGA 46742
QY 154 GlYArgAspLysGluLysAspGlu11leValLys11leuL1eAsnValSerAsnAla 173
DB 46743 GGTTTTGAAGAGAAACAACTTGATTCCTTAAGAAAGTC-----ACCAAGTGAATCG 46793
QY 174 GlnThrLeuProValLeuPro11leuGlyMetGlyLysleuGlyLysThrThrLeuAla 193
DB 46794 GCAGATCTTACATGATTCATTCGATCGATGATCCGGGTTCAAGGTAAACTCTATTGGCA 46853
QY 194 GlnMetValPheAsnAspGlnArgVal11leGlnHisPheHisProLys11eTPr11eCy 213
DB 46854 TACAAAGTATACATATGATTAAGTCAGTTTCTAGCCGTTTGCACCTTCGTGCATGGTCACG 46913
QY 214 ValSerGluAspPheAsnGluLysArgLeu11leYsGlu11leValGluSer11leGluGln 233
DB 46914 GTGACCAAGAGATGATGAGAAAGATGTTGAAATTCATTTTCAGTCAAGTATGAGAC 46973
QY 234 LysSerLeuGlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuAsn 253
DB 46974 TCAGATTCAAATAATGAGTGAAGATATGATGTTGCTGATTAATTCGAAACAACTGTTT 47033
QY 254 GlYLysLysTyTleuLeuVal11leuAspAspVal1TThAsnGluAspGlnAspLysTPrAla 273
DB 47034 GGAAAGAGATATCTTAATGTTCTTATGATGACGCTGG-----GATCTACTACATGGGAT 47087
QY 274 LysLeuArgGlnValLeuLysValGlyAlaSerGlyLysAspValLeuThrThrArg 293
DB 47088 GAGTTTAACAAACCTTTTCTCGAATCTAAGAAAGAGTGAATTTTGAACAACCTCGG 47147
QY 294 LeuGluLysValGlySer11leMetGlyThrLeu-----GlnProTyGluLeuSerAsn 311
DB 47148 ---GAAAAGAAAGGCTTTCATGGAACCTGAACCTGATCTCTTCCTTCGATTG 47204
QY 312 LeuSerGlnGluAspCySTPrLeuLeuPheMetGlnArgAlaPheGlnLys11leGlnGlu 331
DB 47205 CTAAAGACCAAGTGAAGATGGAACCTTATGAGAAAGAGGATTTGGGAAT--GAAGAT 47261
QY 332 11eAsnLeuAsnValAla11leGlyLysGlu11leValLysLysCyGlyGlyValPro 351
DB 47262 TGCCCTGATGAACCTTAATGATGCTGTAAGAAATTAACCGAAATTTGAAAGGCTTCCT 47321
QY 352 LeuAlaAlaLysThrLeuGlyLys11leuArgPheLysArgGluGluArgGln--TPr 370
DB 47322 TTGGTGGCTGATCGATTTGCTGGAGTCATTCGAGAGGAAAGAAAGAGATGTGTGG 47381
QY 371 GlnHisValArgAspSerGlu11eTPrLysLeuProGlnGlnGluSer11leuPro 390
DB 47382 CTGAAGTCAAGATGATTTGAGTTCTTTATTTTGAACAGTAAAGTGAAGTATGAAA 47441
QY 391 AlaLeuArgLeuSerTyYH1811leuProLeuAspLysArgGlnCyPheThrTyTys 410
DB 47442 GTTATGAATTAATGATTAACATTTACATCAATCAACCTCAAGCATGCTGCTGATTTT 47501
QY 411 AlaValPheProLysAspThrGlnMetGluLysGlyAsnLeu11eSerLeuTPrMetAla 430
DB 47502 GCAAGTTTTCGAGAGACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 47561
QY 431 HisGlyPhe11eLeuSerLysGlyAsnLeuGlnGlnGlnValGlyAsnGluValTPr 450
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QY 451 AsnGluLeuTyTleuArgSerPhe-----PheGlnGlu11leGluValLysSerGly 467
DB 47622 GATGATTTTAATTAACAGTACGTTGATATTGTTTCAATGAGATAGGTTATGACTGAT 47681
QY 468 GlnThrTyTPrPheLysMetHisAspLeu11eHisAsp----- 479


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Oy 84 Proilearglnlysllysasnlyserlyglsystrynhis-----Proasn 98
Db 4715 ---ATTATGTTGTCAGATTAAT-----GGTCTTACATCTTAATTTCTCACTCCCAT 4765
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Db 4766 ACCATA-----AAGAAGATCAAACTTAATAAGAAAGAGATCTCT 4804
Oy 119 Val-----llealalaglyarg-----llelysphenileuasp6lyarg 132
Db 4805 GCTTAGATGAGAAACATTTCCCAAGACAGAGGTCAATCTGTGCAACTGCCCAAGAA 4864
Oy 133 ThrilleguatrglnvalalaThrargglnthrglyphevalleuasn6lyproglval 152
Db 4865 CCAGTTGAGAGAAAGTCATGACA-----ACTGATMAAATAATT 4903
Oy 153 Tyrglylsargasrlyslglnlylsarg6lyllevallyslleleuulleuasp6lyser 172
Db 4904 GTAGGTTTTGAGAGAGACAAACTTGATTAAGTAAAGCTC-----ACCAAGTGA 4954
Oy 173 Ala6lynthleuprovalleuasp6lyleu6lymetglsygllyleu6lylsrThrleu 192
Db 4955 CCCCAGATTTAGATGATGATTCATCCATCCAGGTATCCGGGTTCAGGTAAACATCTTG 5014
Oy 193 Ala6lymetvalpheuasp6lynar6lyalle6lyhnsphenlsprolyslletrple 212
Db 5015 GCATCAAAAGTATACATGATTAAGTCAGTTTCTAGACATTTTGACCTTGTCAGGTGTC 5074
Oy 213 Cysvalser6lyasrphasn6lylsarg6lyleu6lyleu6lyleu6lyleu6lyleu 232
Db 5075 ACGGTGATGACAGATGATGACACAGAAAGTTGGTGAATACATTTTCACTGCAAGTTAGT 5134
Oy 233 Glnlysserleu6lyglymetasrleu6lylaProleu6lysllysleu6lyasrphleu 252
Db 5135 GGCTCAGATTCAAATTTGAGTGAAGAAATATGATGTTGCTGCAATTAATTCGGGAAACA 5194
Oy 253 Asnglylsylslyrleu6lyvalleu6lyasr6lyval17rpa6nglnasr6lyasrlystr 272
Db 5195 TTTGAAAAGAGTATCTTAATGTTGATGATGATGTTGG-----GATTACTACTACAT 5248
Oy 273 Ala6lyleu6lyglnvalleu6lyslval6lylaser6lyvalaser6lyleu6lythr 292
Db 5249 GATGAGTTGACAAAGCTTTTCTGAAAGTAAAGAAAGAGTAAATTTTGAACACT 5308
Oy 293 Argleu6lylyleu6lyserilemetglsythrleu-----GlnPro6lyrglnleu 310
Db 5309 CGA---GAAAAGAAAGTGGCTTTGCAATGGAAGCTGAACACTGATCCTTGAACCTTGA 5365
Oy 311 Asnleu6lyser6lyasr6lystrleu6lyphen6lymet6lynar6lylaPhe6lyhns6ly 330
Db 5366 TTGCTAAAGACAGAAAGTTGGGAACTTTTGAAGAAAGAAAGCACTTTGGTAAAT---GAG 5422
Oy 331 Glnulleu6lyasrleu6lyvalala6lylyslglnulleu6lylysls6lyglnval 350
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Oy 351 Proleu6lyala6lyThrleu6lylyleu6lylsarg6lyphelysarg6lyglnargln 369
Db 5483 CTTTGTGCTGCTGATGATGATGCTGAGTCAATTCCTGGGAGGAAAGAAAGAAAGAGTGG 5542
Oy 370 TTPGlnhlsvalasr6lyser6lyul6lytr6lylsleu6lypro6lygln6lyser6lyleu 389
Db 5543 TGGCTTGAAGTCAAAAGTATTGAGTTGAGTTTATTTATTAACAGTGAAGTGAAGTGAAG 5602
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Oy 410 Cysala6lyphePro6lyasr6lythr6lymet6lylyslasrleu6lyleu6lytr6lymet 429

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Oy 450 Trp6nglnleu6lyleu6lyasr6lyphe-----Phe6lyglnulle6lyval6lyser 466
Db 5783 ATGATGATTTAATTTCCAGTACCTGTTGATTAATTTGTTCAATGAGATA-----GGT 5833
Oy 467 Gln6lynth6lyr6lyleu6lymet6lyla6lyrleu6lyleu6lyasrleu6lyla 481
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Oy 482 ---Thrs6lyser6lye-----Ser6lyaser6lyser6lyser6lyleu6lygln 496
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Db 6059 -----ATTAATGAGACCACTGATGACAGTGTGTTGATGATGATGATGAT 6106
Oy 552 Arg6lyleu6lyleu6lyser6lyasr6lynth6lyser6lyleu6lyarg----- 563
Db 6107 AGACACTTGAAGCTTAATTAAGTGTGAGCTGGAACCTCTTTAATCATGTGATGAT 6166
Oy 564 Serleu6lypro6nglnleu6lysls6lyleu6lyasrleu6lynth6lyleu6lyasr6ly 583
Db 6167 TCTTTGCTGAATGAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 6220
Oy 584 His6lyser6lysls6lyleu6lyleu6lyThr6lyser6lyleu6lyser6lyleu6lyasr 603
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Oy 624 Lys6lythrleu6lyasr6lypheval6lyl6lyl6lyl6lylysls6lyser6lyglnleu 643
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Oy 644 Arg6lyasrleu6lyleu6lyser6lyleu6lyleu6lyThr6lyleu6lyasr6ly 663
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Oy 664 Met6lyala6lysls6lyleu6lyasr6lyleu6lyleu6lyleu6lyleu6lyleu6ly 679
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Oy 680 leu6lymet6lystr6lyasr6lyasr6lyasr6lyleu6lyleu6lyleu6lyleu6ly 699
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Oy 700 Val6lyleu6lyala6lyPro6lyleu6lyser6lyasrleu6lyThr6lyleu6lyleu6ly 719
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Oy 720 Gln6lyleu6lyleu6lyPro6lytr6lymet6lyasr6lyleu6lyleu6lyasr6lyleu 739
Db 6515 ---TTTGAATCAAGAGTCACTGATTAATTAACAGAGCAACATGCG----- 6559
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Qy 777 PheProThrArgArg-----ArgPheProSerLeuArgLysLeuAsnIleArg 792
Db 6644 GTTGGACAAATCCGCCCTGGGATTTTTCACCTCCCTCA----- 6682
Qy 793 GluPheGlyAsnLeuLysGlyLeuLeuLysGluGluGluCysProValLeu 812
Db 6683 -----AATTGAAAGAACTGTG-----TTG 6703
Qy 813 GluGluIleGluIleLysCysAspMetPheValIleProThrLeuSerValLys 832
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Qy 833 LysLeu-----ValValSerGlyAspLysSerAspAlaIleGlyPheSer 847
Db 6764 AATTGTCCCTTATGATACATCATCCAGGAGAGAAATGACATGCGGAGAGAAAC 6823
Qy 848 SerIleSerAsnLeuMetAlaLeuThrSerLeuGluIleArgTyrAsnLysGluAspAla 867
Db 6824 ACTTTGAGAAATCTCAAAATTTTGAACCTGCGTCTACTGACTCTTCCAAAGTGGAGGTT 6883
Qy 868 SerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSerPhe 887
Db 6884 GGA-----GAGCAATCCTTCCCAATCTTGAGAAATTTAAAGTCCAGAAATGCTG--- 6934
Qy 888 TyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysIleLeu 907
Db 6935 -----AAGCTTGAGAGATTCACCTAGTTTGGAGATATTATTCATTGAAATTTATC 6988
Qy 908 GluIleHisSerCysTyrAlaLeuGlu 916
Db 6989 AAAATTGAAAGATCTCAACTTGAA 7015

RESULT 10
US-08-947-823-4
; Sequence 4, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Williamson, Kalsohian, Isouhli
; APPLICANT: Yaghoobi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Confering
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/947,823
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/18802
; FILING DATE: 09-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,191
; FILING DATE: 10-OCT-1996
; ATTORNEY/AGENT INFORMATION:

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; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-070210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 87..3860
; OTHER INFORMATION: /note= "Copy 2 cDNA for M1 nematode
; OTHER INFORMATION: resistance gene of tomato"
; US-08-947-823-4

Alignment Scores:
Pred. No.: 6,28e-52 Length: 3982
Score: 571.50 Matches: 255
Percent Similarity: 41.44% Conservative: 147
Best Local Similarity: 26.29% Mismatches: 378
Query Match: 11.15% Indels: 191
DB: 3 Gaps: 40

US-10-647-268-2 (1-988) x US-08-947-823-4 (1-3982)
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Db 1314 TCTTGATTAAGGAAGAAATCGAGTGTGTCAGACAGAACTGAATTCATTAGATCATTC 1373
Qy 45 LeuGluAspAlaGluLysLysGluLeu---LysAspLysAlaIleGluAsnTrpLeuGln 63
Db 1374 TTGGGGAGTGTGCTGAGCAAGATTTGATTAAGAT---ATCTGGGACAGCT 1421
Qy 64 LysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLysThrGluAla 83
Db 1422 GTTCTAGAT---GTGCTTATGAGCGCAAGATCTCATAGTTCA----- 1463
Qy 84 ProIleArgLysLysLysAsnLysTyrGlyCysTyrHis-----ProAsn 98
Db 1464 ---ATTATTGTTGCGAGTAAT---GGTCTTACATCTTATTTCTCACTTCCCATTT 1514
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Db 1515 ACCATA-----AAGAAATCAAACCTTATCAAGAAAGAGATCTCT 1553
Qy 119 Val-----IleAlaAlaGluArg-----IleLysPheHisLysAspGluArg 132
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Qy 133 ThrIleGluArgGluValAlaThrArgGlnThrGlyPheValLeuAsnGluProGluVal 152
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Qy 173 AlaGlnThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLysThrThrLeu 192
Db 1704 CCGCAGATTTAGATGATCATTTTCATACCGGTATGCGGTTGACGTTAAACTACTTGG 1763
Qy 193 AlaGlnMetValPheAsnAspGlnArgValIleGluHisPheHisProLysIleTrpIle 212
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Db 3684 -----AGCTTGAGAGATTCACCTAGTTTGGAGATATTATTCATTGAATTTAT 3736
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Db 3737 CAAAATGTGAAGAGTCTCAACTTGAA 3764

RESULT 11
US-09-360-186-2
Sequence 2, Application US/09360186
Patent No. 6262343
GENERAL INFORMATION:
APPLICANT: Staekawicz, et al.
TITLE OF INVENTION: B2 Resistance Gene
FILE REFERENCE: 50687
CURRENT APPLICATION NUMBER: US/09/360,186
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: 60/093,957
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3099
TYPE: DNA
ORGANISM: Capsicum annuum
FEATURE:
NAME/KEY: CDS
LOCATION: (93)..(2810)
US-09-360-186-2

Alignment Scores:
Pred. No.: 3,97e-50 Length: 3099
Score: 553.50 Matches: 245
Percent Similarity: 38.93% Conservative: 170
Best Local Similarity: 22.98% Mismatches: 376
Query Match: 10.80% Indels: 275
Gaps: 40

US-10-647-268-2 (1-988) x US-09-360-186-2 (1-3099)

Qy 4 AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyLeuGlyLeu 23
Db 111 GCTTCTTATGAGAACATAGAAATCTCTTGAACATTCATTCGCCGATGCAATCTCTA 170
Qy 24 IleLeuGlyPheIlyAspGluPheGlnIlyLeuGlnSerThrPheThrIleGlnIle 43
Db 171 TCCTGTGATCACAGAGAACTTTCGCTCTTCTGAAAAATTATGTTCCCTGGAAGTA 230
Qy 44 ValLeuGluAspAlaGlnIlyLeuS-----GlnLeuIlyAspIlyAlaIleGlu 59
Db 231 TTGTGCAAGAACTTTGAGAAAAACAATGTTTTGGGAAATGACGATTTTGAAGTAG 290
Qy 60 AsnTrpLeuGlnIlyLeuAsnAlaIleAlaIlyTrpGlu-----AlaAspAsp 74
Db 291 ---GTAGAGAAAGTTGCAAGTCTGATATACAAATTCACAGTAAGTAAGACT 347
Qy 75 IleLeuAspGluCysIlyThrGlnAlaProIleAspGlnIlyIlyAsnIlyTrpGlyCys 94
Db 348 GTACTGGGAGAAATTAAGC-----CAGAAAAAAAAGCG----- 383
Qy 95 TyrHisProAsnValIleThrPheArgHisIlySerIleGlyIlyArgMetIlySerIleMet 114
Db 384 -----CGTCGAAGTTTCTGCAAGCTTCACACAACTACAC 419
Qy 115 GluIlyIleAspValIleAlaIleAlaGlnIlyArgIleIlyPheHisIlyLeuAspGluArgThrIle 134
Db 420 GAGGACATGATCATATCTGGAAGAGTCGACAAAGATCCAAAGATTAAGAAAAACAAGTA 479
Qy 135 GluArgGlnValAlaIleThrArgGlnThrGlyPheValIleAspGlu----- 149
Db 480 TCAGAGATCATTTGTTTCATGATTTTCAAGTTCAACAAAGATATTTTGAAGTTAAG 539
Qy 150 ProGlnValIlyTrpGlyArgAspIlyGluIlyAspGluIleValIleIleuIleAsn 169

Db 540 AACATATGTTGACGATGATCAAGAAAGAGTTGTAGAGATCTGATAGAAAGC 599
Qy 170 ValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMetGlyIleuGlyIly 189
Db 600 TACTCTGGGAGACC-----AAAGTCATCCCGATGTGCGGATGGGAGATAGGTA 653
Qy 190 ThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProIly 209
Db 654 ACAACCTTAGCAAAAGAAAGTTTACATATGATCAATTCATTCATGCCCTTTGATGTTGAT 713
Qy 210 IleTrpIleCysValSerGluAspPheAsnGluIlyAspArgIleIlySerGluIleValGlu 229
Db 714 GCTGGGCTACCATATCTCAACACACACAAAAAGAAATTTGCTGGGCTTCTGAT 773
Qy 230 SerIle-----GluGlnIlySerIleuGlyIlyMetAspLeuAlaPro--- 243
Db 774 TCACCAATCAAAATGATGACAGGGTTAAGATGTGTGAAGCAGAGCTTACGACATG 833
Qy 244 LeuGlnIlyIlyLeuArgAspLeuLeuAsnGlyIlyIlySerIlyLeuValIleuAspAsp 263
Db 834 TTACGAAAAGTTTAAG-----AGAAAGCTTACTTATGTCTTGGATGAT 881
Qy 264 ValTrpAsnGluAspGlnAspIlyTrpAlaIlyLeuArgGlnValIleuIlyVal---Gly 282
Db 882 ATCTGAGAT-----TGTGAAGTGGGATGGCGTGAGACGATGCTTCCAACTGAAGAC 935
Qy 283 AlaSerGlyAlaSerValIleuThrThrThrArgLeuGlnIlyIlySerIleMetGly 302
Db 936 AATCAGGAGCTCAAAATCTGTGATGACCCGTATGATGAAGATCTTGTATGCTTGT 995
Qy 303 ThrLeuGln---ProTyrGluLeuSerAsnLeuSerGlnIlyAspCysTrpLeuIlyPhe 321
Db 996 GTAGAGATTTTCTTTCGGATGATGACCTTCATGATCAAGATGACAGTCTTTTC 1055
Qy 322 MetGlnArgAlaPheGlyHisGlnGlnIleAsnLeuAsnValAlaIleGlyIly 341
Db 1056 AAAAGTCAGCATTTTCA---AGTGAAGCATTACCATATGATGATTCGACAGCTTGGAAAG 1112
Qy 342 GluIleValIlyIlyCysGlyIlyValProLeuAlaAlaIlySerThrLeuGlyIlyLeu 361
Db 1113 CAAATCGCAATGATGATGACAGGGTTACCACTATTCGTGTTGACAGGGCTTCTC 1172
Qy 362 ArgPheIlyAspGluGlnIlyArgIleTrpGluHisIlyValArg-----AspSerGluIle 378
Db 1173 AAATCTAAAGGACAAATGAAAGATTCGAAAATGTTGCTTAAGATGTCAGTCTTC 1232
Qy 379 TrpIlyIleuProGlnIlyGlnIlySerSerIleuProAlaIleuArgIlySerThrHis 398
Db 1233 ACAATGATCTGTGTAACGATGTTCA-----CGTGTCTTGGGTTGATTAAGATCAC 1286
Qy 399 LeuProLeuAspLeuArgGlnCysPheThrTrpCysAlaValPheProIlyAspThrIly 418
Db 1287 TTGCAAGCGCATTAATAACAATGTTCTTCATTTCCGAAATTTTCCGAAAGACATGAT 1346
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Db 1347 ATTCAGTGAAGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
Qy 439 AsnLeuGluLeuGlnAsnValGlyAsnGluValTrpAsnGluLeuTrpLeuArgSerPhe 458
Db 1407 GATTGGAAGAGAG-----GTTGAGAAAGTGT 1433
Qy 459 PheGlnGluIle----- 462
Db 1434 TTGCAAGAGCTTGTGATAGTCTAGTCTCTGTCGACAGAGAGATCGAGATGAACA 1493
Qy 463 GluValIlySerSerGlyGlnThrTrpPheIlyMetHisAspLeuIleHisAspLeuAlaThr 482
Db 1494 AAAATTCATCA-----TGTAAAGTTCAATCTTAATATAGACTGTGC--- 1538
Qy 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTrp 502

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Db 1539 -----GAGAGAGAAATTCAAAGGAGAGACATT 1565
Qy 503 ILehiSmetSerIleGlyPhe----- 510
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Db 1626 TATAAATGACCCCTTAAGCGGTGACGTGATGAAATTAATTAATTCCTTACGT 1685
Qy 510 ----- 510
Db 1686 CTTATAGGCGCTTTACCCCTTAATGCTGATGAGATCATGACACACAAAT 1745
Qy 511 -----ThlySValValSerSerIleu----- 519
Db 1746 CTTTGAACGAAACCATTCGTGTTCTTTTCATCTTGAGCCTTAATTAATGTTCTC 1805
Qy 520 ---SerHisLeuGlnLysPheValSerIleuArgValLeuAsnLeuSerAspIleuLeu 538
Db 1806 AAATGAGAGGTTCATTTCAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1865
Qy 539 LysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu----- 556
Db 1866 GATGGTTCCCTCGAGAGATCTAGCCTCATCTGTGAGGTACCTATCATTTGTTTCAAC 1925
Qy 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysGlyLeuGlnAsnLeuGln 576
Db 1926 TATGGGAATTCGATGTA-----CCTCCGAAATTTGAGGTATGAGATTCGACG 1976
Qy 577 ThrLeuAspLeuHisGlyCysHisSer---LeuCysCysLeuProLysGlnThrSerLys 595
Db 1977 ACATTCATTTGTTCAACGCTTCGATCAGATATTAATTAATTTTTCGAGAAATTTGGAA 2036
Qy 596 LeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProPro 615
Db 2037 CTAAATGCAATTAAGGATCTTAATCTGACCCAGATTTTATTCGACAGATTGCCAAGTGA 2096
Qy 616 ArgIleGly-----SerLeuThrCysLeuLysThrLeuSer----- 627
Db 2097 TCTGTGTCAGAAAGGACATTTGATTTTCAAACTTAACAACTTAATTTCTTGTCT 2156
Qy 628 -----ArgPheValValGlyIleGlnLysLeuSerCysGlnLeuGly 641
Db 2157 CCACGTTGTCACAGAGAGGTATTAATGAGGATTCAGAAATGCAAA---AAATTAAGA 2213
Qy 642 GlnLeuArgAsnLeuAsnLeuTyrGlySerIleGlnIleThrHisLeuGlnLysValLys 661
Db 2214 ATCAGTGGAAATAGGATGACTATAAAGTTTTCGGGACTCGGCTCCCAAC----- 2267
Qy 662 AsnAspMetAspAlaLysGlnLysLeuSerAlaLysGlnAsnLeuHisSerLeuSer 681
Db 2268 -----AATCTTGTCTATCTGCACGAACTTGAATTAATTAAGT 2303
Qy 682 Met---LysTyrAspAspAspArgLysProArgIleTyrGlnSerGlnLysValGlnVal 700
Db 2304 CTTATATCTGTGATTAATAGCCTTTGCGAGATGATTTCAAGTSCAAAAGCTTTTCCA 2363
Qy 701 LeuGlnAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
Db 2364 GCAGAGCTCAGAGAGTTGAAGTTGGAAGAACTTAATCTAAGC----- 2405
Qy 721 IleArgLeuProAspTyrMetAsnHisSerValLeuLysAsnValValSerIleGlnIle 740
Db 2406 -----TGGTCATACCTTGACATCATAGCTGAGTGGCTTAAGGTG 2450
Qy 741 IleSerCysLysAsnCysSerCys-----LeuProProPhe 752
Db 2451 CTGAGACCTAGTATGACGCTTGTGTGAGGAGATGCGATCCATTTGTATAGGATTT 2510
Qy 753 GlnGlnLeuProCysLeu-----LysSerLeuGlnLeuTyrArgIleSerAla 768
Db 2511 AATCGATTGAGGCTTTGCTAATTAATTAATTAATTTCTCAAGTTCTGAAAGCC----- 2564

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Qy 769 GlnValGlnTyrValAspSerGlyPheProThrArgArgRgpProSerLeuArgLys 788
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Qy 789 LeuAsnIleArgGlnPheGlyAsnLeuLysGlyLeuLeuLysLysGlnGlnGln 808
Db 2595 CTCATGATTGAAAGTTGCCAAAAATTTGAAA-----GAG 2627
Qy 809 CysProVal-----LeuGlnGlnIleGlnIleLysCysCysPro 821
Db 2628 ATACCCATTGAGTTTGACATATACACACACTACAGCTGATTAAGAGAGTGTCT 2687
Qy 822 MetPheValIleProThrLeuSerSerValLysLysLeuValValSerGlyAspLysSer 841
Db 2688 CCCAACTTGCGGGAATCTGCTGCACGAAATTCAGAAA-----GAACAA 2729
Qy 842 AspAlaIleGlyPheSer-----SerIleSerAsnLeuMetAlaLeuThrSer 857
Db 2730 GAAAGACCTCGGAAACAAACCTGTGATGTTGTTCTCAATCCATTTGAAGAGAGTGTAT 2789
Qy 858 LeuGlnIleArgTyrAsnLysGlnAspAlaSerLeuProGlnGlnMet----- 873
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Qy 874 -----PheLysSerLeuAlaAsn 879
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Qy 880 LeuLysTyrLeuAsnIleSerPhe-----TyrPheAsnLeuLysGlnLeuPro 895
Db 2910 TTCAGAGAGATGATGATATCTTTGTTGTGTTGATACATATTTTGAGTTTACTGATTCCT 2969
Qy 896 ThrSerLeuAlaSerLeu 901
Db 2970 TCTTCCCTTCTCTTTTA 2987

RESULT 12
US-09-864-680A-2
; Sequence 2, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, Brian J
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B62 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 2
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)..(2810)
; OTHER INFORMATION:
US-09-864-680A-2

Alignment Scores:
Pred. No.: 3,976-50
Score: 553.50
Percent Similarity: 38.93%
Best Local Similarity: 22.98%
Query Match: 10.80%
DB: 4
Matches: 245
Conservative: 170
Mismatch: 376
Indels: 275
Gaps: 40

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US-10-647-268-2 (1-988) x US-09-864-680A-2 (1-3099)

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111 GCTTCTCTTAAGAAACAATAGAAATCTCTTGAACATTCATTCGCCATGCAATCTTA 170
24 IleuGlnPheLeuAspGlnPheGlnIleuLeuGlnSerThrPheThrIleGlnAla 43
171 TCCTGTGATCACAGAAAGAACTTGGCGCTCTTCGTGAAAAAGTAGTCCCTGGAAATA 230
44 ValIleuGlnAspAlaGlnIleuLeuS-----GlnIleuLeuAspAlaIleu 59
231 TTGTGCAAGAACTTTGCAAAAAACAATGTTTGGGAAATGACCGAATTTGAAGTAAAG 290
60 AsnTrpLeuGlnIleuLeuAsnAlaAlaIleuGln-----AlaAspAsp 74
291 ---GTAAGAGAAAGTTGCAAGTGTCTGTAATACAAATTCACATGACGTAACAGAACT 347
75 IleuLeuAspGlnCysLeuThrGlnIleuAspTrpIleArgGlnIleuLeuAsnIleuLeu 94
348 GTACTGGGAGAAATTAAGC-----CAGAAAAAAAGGCG----- 383
95 TyrHisProAsnValIleThrPheArgHisLeuIleGlyIleuLeuAsnIleuLeu 114
384 -----CGTCAAGGTTTCGTCAAGGCTGCAACAGTACAAAGTACCA 419
115 GluIleuLeuAspValIleAlaIleuGlnArgIleuLeuPheHisIleuAspGlnIleuThrIle 134
420 GAGGACATGAGATCATATCTGAAAGAGTGCACAAAGATTCACAAATTAAGAAACAGATA 479
135 GluIleuGlnValAlaThrArgGlnIleuGlnIleuPheValIleuAsnGln----- 149
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170 ValSerAsnAlaGlnIleuLeuProValIleuProIleuGlnIleuMetGlnIleuGlnIleu 189
600 TACTCTGGGGAACCC-----AAAGTCATCCCGAGTGTGGGAGTGGGAGTAAAGTAA 653
190 ThrThrIleuAlaGlnIleuMetValPheAsnAspGlnIleuValIleuGlnIleuPheHis 209
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210 IleTrpIleCysValSerGlnAspPheAsnGlnIleuValIleuLeuIleuValIleuGln 229
714 GCCTGGGCTACCATATCTCAACAGCACAACAAAGAAATTTTGGCTGGCTTCGAT 773
230 SerIle-----GlnIleuLeuSerIleuGlnIleuMetAspLeuAlaPro--- 243
774 TCCCAACATCAAAATGATGACAGGCTTAAGATGATGTGTAAGCAGACGCTGACAGACATG 833
244 LeuGlnIleuLeuAspLeuAspLeuLeuAsnGlnIleuValIleuLeuValIleuAspAsp 263
834 TTACAGAAAGATTTAAAG-----AGAAAGAGCTACTTAATGTCTTGGATGAT 881
264 ValTrpAsnGlnIleuAspLeuTrpAlaIleuLeuArgGlnValIleuLeuValIleu 282
882 ATCTGAGAT-----TGTGAAGTGTGGGATGCGCTGAGACGATCTTCCAACTGAAGAC 935
283 AlaSerGlnAlaSerValIleuThrThrArgLeuGlnIleuValIleuGlnIleuMetGln 302
936 AATCAGAGGAGTCAAAATCTGTGATCAACCGTAAATGATGAAAGCTTGTATGCTGCT 995
303 ThrIleuGln---ProGlnIleuSerAsnIleuSerGlnIleuAspCysTrpIleuLeuPhe 321
996 GTAGAGAAATTTTCTTGGCGATGAGCTTCATGATCAAGATGAGAGTGGAGCTTTTC 1055
322 MetGlnIleuArgIleuGlnIleuGlnIleuLeuAsnIleuValAlaIleuGlnIleu 341
1056 AAAAGTCAGACATTTTCA---AGTGAAGCATTAACATGATGATGAGTTCGAGACTGTTGAAAG 1112

342 GluIleuValIleuLeuCysGlnIleuValIleuProIleuAlaAlaIleuThrIleuGlnIleu 361
1113 CAATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1172
362 ArgPheLeuAspGlnIleuGlnIleuTrpGlnHisValArg-----AspSerGlnIle 378
1173 AAATCTAAAGAGCAATAGAAAGATTTGGAACCTGTCTGTAAGATGTCACATCTTCCTC 1232
379 TrpIleuLeuProGlnIleuGlnIleuSerIleuProAlaIleuAspLeuSerThrHis 398
1233 ACAATGATCTGATGAAACGATGTTCA-----CGTGTCTTGGGATGATGATGATGATG 1286
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1287 TTGACAAAGCATCTTAAACATGCTCTTCGATTTCCGAATTTTCCAGAAAGACATGAT 1346
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1347 ATTCACAGTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1406
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1407 GATTGGAAAGGAG-----GTTGAGAAAGTGT 1433
459 PheGlnIleu----- 462
1434 TTGCAAGAGCTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1493
463 GluValIleuSerGlnIleuThrTrpPheLeuMetHisAspLeuIleuHisAspLeuAlaThr 482
1494 AAATTTGATCA-----TGTAGGTCATGATCTTAATATATGACCTGTGC--- 1538
483 SerIleuPheSerAlaSerThrSerSerSerAsnIleuArgGlnIleuIleuValIleuGlnIleu 502
1539 -----GTGAGAAAGTTCAAAGGAGAAACATT 1565
503 IleHisMetSerIleuGlnPhe----- 510
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510 ----- 510
1626 TATAAATGACGCCCTTAAGCGCGTACGTGATGAATTAATTAATTCCTATGCT 1685
510 ----- 510
1686 CTTATAGGCTCTTCTTACCCCTGTAATCGTACATGAGATCATGACAAACAAT 1745
511 -----ThrIleValIleuSerSerIleu----- 519
1746 CTTTGAAGACAAACCATCTGTGTTCTCTTTGATCTTGAAGCTTTATATATGTTCTC 1805
520 ---SerHisIleuGlnIleuPheValSerIleuArgValIleuAsnIleuSerAspIleuLeu 538
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539 LeuGlnIleuProSerSerIleuGlnAspLeuValHisIleuArgIleuLeuAsnIleu----- 556
1866 GATGTTTCCCTCAGAGATACATGAGCTCATGCTGTTGAGTACATATCTTCAGC 1925
557 SerGlnIleuThrSerIleuArgSerIleuProAsnIleuCysIleuGlnIleuAsnIleuGln 576
1926 TATGAGATTTCCATGTA-----CTTCAGAAATTTGCAAGATTTGAGAACTTCGAG 1976
577 ThrIleuAspLeuHisGlnIleuCysHisSer---LeuCysCysIleuProGlnIleuSerIleu 595
1977 ACATTCATTTGTTCAAGGTTTCATGATGATATATATATTTTGTGAGAAATTTGGGAA 2036
596 LeuGlnIleuArgIleuAsnIleuLeuAspGlnIleuValIleuThrCysMetProPro 615
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QY 616 Arg116Iegly-----Ser1euThrcysleuThrsleuSer----- 627
Db 2097 TCTGTGTGACAAAGAGAGGACTTGATTTTCAAACTTACAACTATTTCTTACTGTCT 2156
QY 628 -----ArgPheValValGly11IeglnIlySlySerCySglnIleuGly 641
Db 2157 CCAGCTGTGTGACAGAGAGAGGATTTATTTAGGGGATTCAGAAATGTCAAA--AAATTAGA 2213
QY 642 GluLeuArgAsnLeuAsnLeuThrcyGlySer11IeglnIleThrcySleuGlnArgValIys 661
Db 2214 ATCAGTGGAATAAGAGTACCTATTAATAAGTTTCGGAGCTTGCGGCTTCCCAAC----- 2267
QY 662 AsnAspMetAspAlaIalysGlnIalAsnLeuSerAlaIysGlnAsnLeuHisSerleuSer 681
Db 2268 -----AsnCTTGTCTATCTGCAAGCACTTGAAATATTTAGCT 2303
QY 682 Met---LysTrpAspAspAspGlnArgProArg11IeYrgIuSerGlnIlyValGlnVal 700
Db 2304 CTTATATCTGTGATTATATAGCTTTTGGCAGATCATTTCAAGTGCAAAAGCTTTTCCA 2363
QY 701 LeuGlnIalAlaLeuLysProHisSerAsnLeuThrcySleuThrcy11IeArgGlyPheArgGly 720
Db 2364 GCACGCTCAAGAGAGTTGAGTTGAGAAAGAACTTATCTTACG----- 2405
QY 721 IleArgLeuProAspTrpMetAsnHisSerValIleuLysAsnValIalSer11IeglnIle 740
Db 2406 -----TGGTCATCTTGGACATCATAGCTGAGTTGCCCTTACAGGTG 2450
QY 741 IleSerCySlySAsnCySserCyS-----LeuProProPhe 752
Db 2451 CTGAAGCTGATGATGACGCTGTGTGTGAGAGAAATGCAATTCGAATTTATGGAGATT 2510
QY 753 GlyIleuLeuProCySLeu-----LysSerLeuGlnIleuThrcyGlySerAla 768
Db 2511 AATCATTTGAAGCTTTTCTATTAATATAGTTTCTCAAGTTCTGGAAGCC----- 2564
QY 769 GluValGlnIyValIalAspSerGlyPheProThrArgArgPheProSerleuArgLys 788
Db 2565 -----ACAAATGACAAATTTCTGTCTCTTACAGGC 2594
QY 789 LeuAsnIleArgGlnPheGlyAsnLeuLysGlyLeuLysGlyGlnGln 808
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Db 2688 CCCAAACTTGGGAGATCTGCTGCACGAATTCAGAAA-----GACAA 2729
QY 842 AspAlaIleGlyPheSer-----Ser11IeSerAsnLeuMetAlaLeuThrcy 857
Db 2720 GAAAGACTTCGAAACAAACCTGTGATGTTGCTATCTCAATCCATTTGAAGAGAGTGAT 2789
QY 858 LeuGlnIleArgTrpAsnLysGlnAspAlaSerLeuProGlnGlnMet----- 873
Db 2790 TCTGATTCAGAGAACATTAGAAAGAGATCTCAAGCGCAGAGAGATTGAATCTTGGGAT 2849
QY 874 -----PheLysSerLeuAlaAsn 879
Db 2850 TTCAATTTGGCCCTCTATACAAAATACACATTAATATCGGTTTCAACAGCATGTGAC 2909
QY 880 LeuLysTrpLeuAsnIleSerPhe-----TyrPheAsnLeuLysGlnLeuPro 895
Db 2910 TTCCAAGAGATGTGATATCTTTTGTGTGTAAACATATTTGAGTTTGTACTGATTCCT 2969
QY 896 ThrSerLeuAlaSerLeu 901
Db 2970 TCTTCCCTTCTCTTTTAA 2987

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US-09-360-186-4
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Stakavicz, et al.
; TITLE OF INVENTION: Bsz Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capesicum annum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2718)
US-09-360-186-4

Alignment Scores:
Pred. No.: 6.77e-50 Length: 2718
Score: 550.50 Matches: 226
Percent Similarity: 39.27% Conservative: 151
Best Local Similarity: 23.54% Mismatches: 340
Query Match: 10.74% Indels: 243
DB: Gaps: 36

US-10-647-268-2 (1-988) x US-09-360-186-4 (1-2718)
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QY 24 IleLeuGlnPheLysAspGlnPheGlnLysLeuGlnIleThrcyPheThrcy11IeGlnAla 43
Db 79 TCTGTGTATCACAGAGAAACCTTGGCCTCTGTGTAAAGAAAGTTAGTTCCCTGAAAGTA 138
QY 44 ValLeuGlnAspAlaGlnLysLys-----GlnLeuLysAspLysAla11Iegln 59
Db 139 TTGTGCAAGAACTTTGAGAAACAAATGTTTGGCGAAATGACGCAATTTGAAAGTAGAG 198
QY 60 AsnTrpLeuGlnLysLeuAsnAlaAlaLysGln-----AlaAspAsp 74
Db 199 ---GTAAGAGAAAGTTGCAAGTGTCTGATATACAAATTCAGTACAGACTAACAGAACT 255
QY 75 IleLeuAspGlnCySlySLeuThrcyGlnAlaProIleArgGlnLysAsnLysTrpGlyCyS 94
Db 256 GTACTGGGAGAAATTAAGC-----CAGAAAAAAGGCG----- 291
QY 95 TyrHisProAsnValIleThrcyPheArgHisLysIleGlyLysArgMetLysLeu11IeMet 114
Db 292 -----CGTGAAGCTTTCGTCATCAAGCCTGCACAAAGTAGCA 327
QY 115 GluLysLeuAspValIleAlaGlnArg11IeLysPheHisLysAspGlnArgThrcy11Ie 134
Db 328 GAGACATCATGATCATATGTGAAAGAGTCGACAAAGATCCAAAGATTAAGAAAAACAAGTA 387
QY 135 GluArgGlnValAlaThrArgGlnThrcyPheValLeuAsnGln----- 149
Db 388 TCAAGAGAAATCATTTGTTCAATTTTCAAGTTTCAACAAACGATATTGTAAGGTTAAG 447
QY 150 ProGlnValTyrGlyArgAspLysGlnLysAspGlnIleValIysIleLeu11IeAsnAsn 169
Db 448 AACATATATGTTGAGCGTATGATCAAGAAACAGTTTGAAGATCTGATGAGAGC 507
QY 170 ValSerAsnAlaGlnThrcyProIleLeuProIleLeuGlnIyMetGlyLysGlyLys 189
Db 508 TACTCTGGGGAAGCC-----AAAGTCATCCGATTTGCGGATGCGAGCATAGATAA 561
QY 190 ThrThrcyLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProLys 209

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Db 562 ACAACCTTAGCAAAAGAGATTACATGATGATCAATCAATTCAGCCGTTTGATGATTCAT 621
Qy 210 ILethrIleCyValSerGluAspPheAsnGluValSerGluIleValGlu 229
Db 622 GCGTGGGCTACCATTCATCTCAACAGACACAAAGAAATTTCTCGGCGCTTCGAT 681
Qy 230 SerIle-----GluGluIleSerLeuGluGlyMetAspLeuAlaPro--- 243
Db 682 TCCCAATCAAAATAGATGACAGCGTTAAAGATGATGCTGAAGACAGACTGACAGACTG 741
Qy 244 LeuGluIleValSerGluAspLeuLeuAsnGluIleValSerGluIleValSerGlu 263
Db 742 TTACAGAAAGATTAAAG-----AGAAAGAGCTACTTAATGCTTGGATGAT 789
Qy 264 ValTrpAsnGluAspGluAspLeuTrpAlaValSerGluIleValSerGluIleVal 282
Db 790 ATCTGGAGT-----TGTAAGTGTGGAGTGGCGGAGACAGATGCTTCAACGTGAAGAC 843
Qy 283 AlaSerGlyAlaSerValLeuThrThrArgLeuGluValGlySerIleMetGly 302
Db 844 AATGACAGGAGTCCGAATCTGTGATCCCGTAATGATGAAGTACGTTGATGCTGCT 903
Qy 303 ThrLeuGlu---ProTyrGluLeuSerAsnLeuSerGluAspCysTrpLeuLeuPhe 321
Db 904 GTAGAGAAATTTCTTTCGCGATGAGCTTCATGATCAAGATGAGATGGAGCTTTTC 963
Qy 322 MetGluArgAlaPheGluIleGluGluIleAsnLeuAsnLeuValAlaIleGlyVal 341
Db 964 AAAAGTCAGACTTTTCA--AGTGAAGCATTTACCATATGAGTTCCAGACTGTGGAAG 1020
Qy 342 GluIleValIleValSerGlyValProLeuAlaAlaValSerLeuGluGlyIleLeu 361
Db 1021 CAATTCGAGATGATGATGACGGGTACCTAATACTATTCGCGGTTCGACGGCTTTC 1080
Qy 362 ArgPheValArgGluGluArgGluIleTrpGluIleValArg-----AspSerGluIle 378
Db 1081 AAATCTAAAGAGCAATGAGATGAGAACTGTGCTAAAGATGATCAATTCGCTC 1140
Qy 379 TrpIleValProGluGluIleGluSerSerIleLeuProAlaLeuArgLeuSerTyrHis 398
Db 1141 ACAAAATGATCTGTGAACGATGTTCA-----CGTGTGCTGTGGTTCAGTTACGATCAC 1194
Qy 399 LeuProLeuAspLeuArgGluIleCysPheThrTyrCysAlaValPheProIleAspThrGlu 418
Db 1195 TTGCAAGCCATCTAAACATGCTTCTGCAATTCGGAATTTTCCAGAGACAGTGAT 1254
Qy 419 MetGluIleValSerLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerIleGly 438
Db 1255 ATTCAGAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
Qy 439 AsnLeuGluIleGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhe 458
Db 1315 GATTGGAAAGGAGG-----GTTGAAGAGTGT 1341
Qy 459 PheGluGluIle----- 462
Db 1342 TTGCAAGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1401
Qy 463 GluValIleSerGlyGluIleThrTrpPheIleMetHisAspLeuIleHisAspLeuAlaThr 482
Db 1402 AAATTTGATCA-----TGTAAGTTCATGATCTAATATATGACTCTGTC--- 1446
Qy 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyr 502
Db 1447 -----GTGAGAGAAATTCAAGCGAGAAACATT 1473
Qy 503 IleHisMetSerIleGlyPhe----- 510
Db 1474 TTATTCATGAACGACATTTCTTGTGACGTATCATATCCAGATGTTCAATCTCTGATG 1533
Qy 510 ----- 510

Db 1534 TATAAATGCAGCCCTTAAAGCGGTGACGTGTGATGAATTAATTAATTTGCTCCATAGCT 1593
Qy 510 ----- 510
Db 1594 CTTTATAGGGCTCTTTTACCCCTGTAAATGCTCAGTTGAGAGATCATGACAAACAAT 1653
Qy 511 -----ThrIleValIleSerTyrSerLeu----- 519
Db 1654 CTTTGAAGAACCCATTCCTTTCTTTCCTTTTCATCTGTGAGCCTTAATATATGTTCTC 1713
Qy 520 ---SerHisLeuGluIlePheValSerLeuArgValLeuAsnLeuSerAspIleLeuLeu 538
Db 1714 AAATCAGAGGTGTTCATTTCAATTAATCTCAAGCTGTGAGCTGAGACACAGACAGATT 1773
Qy 539 LysGluIleProSerSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeu----- 556
Db 1774 GATGCTTCCCTCGAGAGATCTAAGCTCTACGTGTGAGGTCCTTATCTTCATCTTCAGC 1833
Qy 557 SerGlyAsnThrSerIleArgSerLeuProAsnGluIleCysValSerGluAsnLeuGlu 576
Db 1834 TATGGAATTTGCATGTA-----CTCCAGAAATTTGCAGTTATGGAATCTGAG 1884
Qy 577 ThrLeuAspLeuHisGlyCysHisSer--LeuCysCysLeuProIleGluIleThrSerIle 595
Db 1885 ACATTCATTTGTTCAACGGTTTCAGATCAATATTAATTTTGTGCTGAGAAATTTGGGA 1944
Qy 596 LeuGluIleSerLeuArgAsnLeuLeuAspLeuIleCysTrpGlyLeuThrCysMetProPro 615
Db 1945 CTAAATGCAATTAAGCACTTAATACTGCCAGATTTTATTTGCTCCAGATGCGCAAGTGA 2004
Qy 616 ArgIleGly-----SerLeuThrCysLeuIleThrLeuSer----- 627
Db 2005 TCTGTGACAAAGAGAGGACTGATTTTCAAACTTACAACTAATTTCTTACTTGTCT 2064
Qy 628 -----ArgPheValValGlyIleGluIleValSerCysGluLeuGly 641
Db 2065 CCAGCTTTGTCACGAGAGAGTATTAATGAGGATTCAGAAATGTCAAA--AAATTTGGA 2121
Qy 642 GluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHisLeuGluArgValIle 661
Db 2122 ATCAGTGAATTAAGATGATCAATTAAGATTTTCGGAATCTCGGCGCTCCCAAC----- 2175
Qy 662 AsnAspMetAspAlaValSerGluAlaAsnLeuSerAlaValSerGluAsnLeuHisSerLeuSer 681
Db 2176 -----AATCTGTCTATCTGACAGCAACTTGAATATGAGT 2211
Qy 682 Met---LysTrpAspAspAspGluArgProArgIleTyrGluSerGluValGluVal 700
Db 2212 CTTATATCTGTGATTTATGACCTTTTCCAGATGATCTTCAAGTGCAGAAAGCTTTTCCA 2271
Qy 701 LeuGluAlaLeuIleProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
Db 2272 GCAACGCTCAAGAAAGTTGAAGTTGAGAAAGCTTATGTAAC----- 2313
Qy 721 IleArgLeuProAspTrpMetAsnHisSerValLeuValSerIleGluIle 740
Db 2314 -----TGTATACTTGGACATCATACCTAGTTGCTTAACCTTGAAGTG 2358
Qy 741 IleSerCysValSerCysSerCys-----LeuProProPhe 752
Db 2359 CTGAAGCTGATGATGACGCTGTGTGTGAAGATGACATCCAAATTTGATGAGATTT 2418
Qy 753 GlyGluLeuProCysLeu-----LysSerLeuGluLeuTrpArgGlySerAla 768
Db 2419 AATGATTTGAAGCTTTGCTAATTAATATAGTTTCTCAAGTTCTGAAAGCC----- 2472
Qy 769 GluValGluIleValAspSerGlyPheProThrArgArgPheProSerLeuArgGly 788
Db 2473 -----ACAAATGACAAATTTCTGTCTTGAAGCC 2502
Qy 789 LeuAsnIleArgGluPheGluAsnLeuValGlyLeuLeuValSerGluGluGluGlu 808
Db 2503 CTCATGATTAAGATTCAGAAATTTGAAA-----GAG 2535

QY 809 CysProVal-----LeuGluValIleGluIleLysCysCysPro 821
Db 2536 ATACCATTGATTGTCAGATATACACACTACGCTGATGATTGAAGAGTTCCT 2595

RESULT 14
US-09-864-680A-4
Sequence 4, Application US/09864680A
Patent No. 6762285
GENERAL INFORMATION:
APPLICANT: Staskawicz, Brian J
APPLICANT: Dahlbeck, Douglas
APPLICANT: Tai, Thomas H
TITLE OF INVENTION: B2 RESISTANCE GENE
FILE REFERENCE: 42250/234021 (5830-4A)
CURRENT APPLICATION NUMBER: US/09/864,680A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/360,186
PRIOR FILING DATE: 1999-07-23
PRIOR APPLICATION NUMBER: US 60/093,957
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2718
TYPE: DNA
ORGANISM: Capsicum annuum
US-09-864-680A-4

Alignment Scores:
Pred. No.: 6,77e-50 Length: 2718
Score: 550.50 Matches: 226
Percent Similarity: 39.27% Conservative: 151
Best Local Similarity: 23.54% Mismatches: 340
Query Match: 10.74% Indels: 243
Gaps: 36

US-10-647-268-2 (1-988) x US-09-864-680A-4 (1-2718)

QY 4 AlaPheLeuGlnValIleuLeuAspAsnLeuThrCysPheIleGlnGlyLeuGlyLeu 23
Db 19 GCTTCTCTTATGAGAACATATGATCTCTTGAACATTCATCCGATGCAATCTCTA 78
QY 24 IleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThrIleGlnAla 43
Db 79 TCCTGTGATCAGAGAGAACATTTGCCCTCTTCGGAAGAAAGTTAGTTCCTGGAAGA 138
QY 44 ValLeuGluAspAlaGlnLysLys-----GlnLeuLysAspLysAlaIleGlu 59
Db 139 TTGTTCAGAGACTTTGAGAAAACAATGTTTTGGGAAATGACGAGATTTGAGATGAG 198
QY 60 AsnTrpLeuGlnLysLeuAsnAlaAlaIleLysGlu-----AlaAspAsp 74
Db 139 ---GTAAAGAAAGTTGCAAGTCTGCTGTAATACACAAATTCAACTGAGACTAAACGAACT 255
QY 75 IleLeuAspGluCysLysThrGlnAlaProIleArgGlnLysLysAsnLysTyrgLys 94
Db 256 GTACTGGGAGAAATTAAGC-----CAGAAAATAAGCG----- 291
QY 95 TyrHisProAsnValIleThrPheArgHisLysIleGlyLysArgMetLysLysIleMet 114
Db 292 -----CGTCGAGAGTTTCGCAAAAGCTTCGCAACAGTAGCA 327
QY 115 GluLysLeuAspValIleAlaIleGluArgLysPheHisLeuAspGluArgThrIle 134
Db 328 GAGGAGCATGATCATATCTGGAAGAGTGCACAAAATCCAAAGATTAAGAAAACAAGTA 387
QY 135 GluArgGlnValAlaIleThrArgGlnThrGlyPheValLeuAsnGlu----- 149
Db 388 TCAGAGAAATCATGCTGATGATTTTTCAGAGTTCAACAACGATATTTTGAAGTTAG 447
QY 150 ProGlnValTyrGlyArgAspLysGluLysAspGluIleValLysIleLeuIleAsnAsn 169

Db 448 AACAAATGTTGACGTGATGATCAAGGAAACAGTTGTTAGAGATCTGACTAAGAC 507
QY 170 ValSerAsnAlaGlnThrLeuProValIleuGlnIleMetGlyLysLeuGlyLys 189
Db 508 TACTCTGGGAGAACCC-----AAGTCATCCCAATGTCTGGAGTTGGAGGACATAGGTAA 561
QY 190 ThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHisProLys 209
Db 562 ACAACCTTACCAAAAGAAAGTTTACATGATGATGATCAATCTTATGCGCTTTGATGTTCA 621
QY 210 IleTrpIleCysValSerGluAspPheAsnGlnLysArgLeuIleLysGluIleValGlu 229
Db 622 GCCTGGCTACCAATCTCAATCTCAACAGCACAAAGAAATTTTGCTGGCCCTTTCAT 681
QY 230 SerIle-----GluGluLysSerLeuGlyLysMetAspLeuAlaPro--- 243
Db 682 TCCCAATCAAAATGATGATGACAGGTTTAATGATTTGTGAAGACAGCTAGACAGCATG 741
QY 244 LeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrgLeuLeuValIleAspAsp 263
Db 742 TTACAGAAAAGTTTAAAG-----AGAAAGAGTACTTAATATGTCTTGATGAT 789
QY 264 ValTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValIleLysVal---Gly 282
Db 790 ATCTGAGT-----TGTGAAGTGTGGATGGCGTGAGACAGTCTTCCAACTGAAGAC 843
QY 283 AlaSerGlyAlaSerValIleuThrThrArgLeuGlnLysValGlySerIleMetGly 302
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QY 303 ThrLeuGln---ProTyrGluLeuSerAsnLeuSerGlnLysAspCysTrpLeuLeuPhe 322
Db 904 GTAGAGAAATTTTCTTGGCGATGAGCTTCATGATGAAGATGAGAGTGGAGCTTTTC 963
QY 322 MetGlnArgAlaPheGlnHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLys 341
Db 964 AAAAGTCAGCATTTTCA---AGTAAAGCATTACCATATGATTCGAGACTGTGGAAG 1020
QY 342 GluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyLysLeu 361
Db 1021 CAATTCGAGATGATGATGACGAGGTTACACTAATCTATGTCGTGGTGCAGGCTTCTC 1080
QY 362 ArgPheLysArgGluGluArgGlnTrpGlnHisValArg-----AspSerGluIle 378
Db 1081 AAATCTAAAGAAAGAAATGAGAGATTTGAAAACCTTGCTAAAGATGTCMAATGCTC 1140
QY 379 TrpLysLeuProGlnGluGlnSerSerIleuProAlaLeuArgLeuSerTyrHis 398
Db 1141 ACAAAATGATCTGATGAAACATGTTCA-----CGTGTCTGGGTGAGTTAGATGATCAC 1194
QY 399 LeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGlu 418
Db 1195 TTGACAGCGATCTTAAACAATGCTTCTGATTCGGAATTTTCCAGAAAGACAGTAT 1254
QY 419 MetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGly 438
Db 1255 ATTCAGTGAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
QY 439 AsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhe 458
Db 1315 GATTTGGAGAGAGC-----GTTGAGAAAGTGT 1341
QY 459 PheGlnGluIle----- 462
Db 1342 TTGCAAGAGCTTTCGATGATGATGATGATCTCTGTCAGCAAGAGAGTGCAGATGAGAA 1401
QY 463 GluValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThr 482
Db 1402 AAAATTTAGATCA-----TGTAAAGTCTAGTCTTAATATGATGATGATGATGATGAT 1446
QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyr 502
Db 1447 -----GTGAGAGAAAGTTCAAAAGGAGAAACATT 1473

QY 503 ILeHsMeSeSerIleGlyPhe----- 510
DB 1474 TTTATCATGAAAGCATTTGTTGACGATCATATCCAGATGTTCAATCTGTATG 1533
QY 510 ----- 510
DB 1534 TATAAATGACGCCCTTAAAGCGCTGATGTAATTAATTATGTCCTATGAT 1593
QY 510 ----- 510
DB 1594 CTTTATAGGCTCTTCTTAACCCCTTAATGCTCATGTTGAGATCATGACAACAT 1653
QY 511 -----ThlyeValValSerSerTySerLeu----- 519
DB 1654 CTTTGAAGACGATTCCTGTTTCTTCTTCACTTGAAGCCTTATATATGTTCTC 1713
QY 520 ---SerHsLeuGlnLysPheValSerLeuArgValLeuLeuSerAspIleLysLeu 538
DB 1714 AAATCGAGGTTGTTCAATTCTCAAAAGCTTGAGCTGACACAGACAGATT 1773
QY 539 LysGlnLeuProSerSerIleGlyAspLeuValHsLeuArgTyLeuLeuLeu----- 556
DB 1774 GATGTTCCCTCCGAGATTAAGCTTCATCTGTTGAGGTACTTATCATTTGTTCA 1833
QY 557 SerGlyAenThrSerIleArgSerLeuProAenGlnLeuCyLysLeuGlnAenLeuGln 576
DB 1834 TATGGAAATTCGATGTA-----CTCCAGAAATTTGACAGTTATGCAATTCGAG 1884
QY 577 ThrLeuAenLeuHsGlyCyHsHisSer---LeuCyCyLeuProLysGlnThrSerLys 595
DB 1885 ACATTCATGTTCAACGCTTCCATCGATTAATTAATTTTGGCAGAAATTTGGGAA 1944
QY 596 LeuGlySerLeuAenLeuLeuLeuLeuArgLysTyGlyLeuThrCyMetProPro 615
DB 1945 CTAATGCATTAAGGATCTTAAGTTCGAGATTTTGGCCAGATTTGCCAGATTTGCCA 2004
QY 616 ArgIleGly-----SerLeuThrCyLeuLysThrLeuSer----- 627
DB 2005 TCTGTGTCAAAGAGGACCTGATTTTTCAAACTTTCACAACTATTTCTTACTGTCT 2064
QY 628 -----ArgPheValValGlyIleGlnLysLysSerCyGlnLeuGly 641
DB 2065 CCAGCTTTGTCACGAGAGGATTTATGAGGATTCAGAAATGTCAAA---AAATTAGA 2121
QY 642 GlnLeuAenAenLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 661
DB 2122 ATCAGTGAATTAAGGATGACTTAAAGTTTTCGGAATCTGGGCTTCCCAAC----- 2175
QY 662 AenAenMetAenAlaLysGlnLeuLeuSerAlaLysGlnAenLeuHsSerLeuSer 681
DB 2176 -----NATCTTGTCTATCTGCAGCAACTTGAATATTGAGT 2211
QY 682 Met---LysTPAAspAspLysArgProArgIleTyGlnSerGlnLysValGlnVal 700
DB 2212 CTTATATCTGTGATTATAGCCTTTTGCAGATGATCATTTCAAGTGAAGAGCTTTTCA 2271
QY 701 LeuGlnAlaLeuLysProHsSerAenLeuThrCyLysLeuThrIleArgGlyPheArgGly 720
DB 2272 GCAACGCTCAAGAAAGTTGAAGTGAAGAAAGAACTTATCTTAAGC----- 2313
QY 721 IleArgLeuProAenThrMetAenHsSerValLeuLysAenValValSerIleGlnLeu 740
DB 2314 -----TGGTCACTACTTGGACATCATAGCTGAAGTGGCTTAACCTTGAGGTG 2358
QY 741 IleSerCyLysAenCySerCyS-----LeuProProPhe 752
DB 2359 CTGAAGCTGATGATGACGCTTGTGTGATGAAGATGCAATTCATTTAGGAGATT 2418
QY 753 GlnLysLeuProCyLysLeu-----LysSerLeuGlnLeuThrArgGlySerAla 768
DB 2419 AATGATTTGAAGCTTTGCTAATTAATATATGTTTCTCAAGTCTGGAAGGCC----- 2472

QY 769 GlnValGlnTyValAspSerGlyPheProThrArgArgArgPheProSerLeuArgLys 788
DB 2473 -----ACAATGACAAATTTCTGCTGTCAGAGCC 2502
QY 789 LeuAenIleArgGlnPheGlyAenLeuLysGlyLeuLeuLysGlnGln 808
DB 2503 CTCATGATTGAAGTTCGCAAAATTTGAAA-----GAG 2535
QY 809 CysProVal-----LeuGlnGlnIleGlnIleLysCySerPro 821
DB 2536 ATACCATTTGAGTTTGCAGATATACACACTTACAGCTGATTGATTGAAGAGTGTCT 2595

RESULT 15
US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staekawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT FILING DATE: US/09/360,186
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capricorn annuum
US-09-360-186-1

Alignment Scores:

Pred. No.:	5,186-48	Length:	31491
Score:	550.50	Matches:	226
Percent Similarity:	39.27%	Conservative:	151
Best Local Similarity:	23.54%	Mismatches:	340
Query Match:	10.74%	Indels:	243
DB:	3	Gaps:	36

US-10-647-268-2 (1-988) x US-09-360-186-1 (1-31491)

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QY 24 IleLeuGlyPheLysAspGlnPheGlnLysLeuGlnSerThrPheThrIleGlnAla 43
DB 1558 TCTGTGATCACAGAAAGAACTTGGCTCTTGTGAAAAGTTAGTTCCTGGAAGTA 1617
QY 44 ValLeuGlnAspAlaGlnLysLys-----GlnLeuLysAspLysAlaIleGln 59
DB 1618 TTTGTCAAGAACTTTGAGAAAACAAATGTTTGGGGAATGAGCATTTTGAAGTGAAG 1677
QY 60 AenThrPheGlnLysLeuAenAlaAlaIleTyGln-----AlaAspAsp 74
DB 1678 ---GTAAGAGAGTTCGAAGGCTGCTGATATACAACTTCACTGAGACTTAACGAACT 1734
QY 75 IleLeuAspGlnCyLysTyThrGlnAlaProIleArgGlnLysAenLysTyGlyCyS 94
DB 1735 GTACTGGAGAAATTAAGC-----CAGAAAAAAAAGGCG----- 1770
QY 95 TyThrProAenValIleThrPheArgHsLysIleGlyLysAspMetLysLysIleMet 114
DB 1771 -----CTGCAAGGTTTGTGTCAAACCTGCAACAGTGA 1806
QY 115 GlnLysLeuAspValIleAlaAlaGlnArgIleTySphHsLysAenArgGlnArgThrIle 134
DB 1807 GAGACATGATCTATCTCTGGAAGAGTCCGACAAAGATCAAGTTAAAGAAAAAGTA 1866
QY 135 GlnArgGlnValAlaThrArgGlnThrGlyPheValLeuAenGln----- 149
DB 1867 TCAAAGAAATCATGTTGATGATTTTCAAGTTCAACAAACGATATTTGAAGTTAAG 1926

[illegible]

QY 483 SerLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnThr 502
 Db 2926 -----GTGAGAGAAAGTTCAAAAGGAAACATT 2952
 QY 503 IleHisMetSerIleGlyPhe----- 510
 Db 2963 TTTATCATGAACGACATTGTTCTTGAGGTATCATATCCAAATGTTCAATCTGTGATG 3012
 QY 510 ----- 510
 Db 3013 TATAAAATGCAGCCTTTAAGCGCGTGACTGTGATGAAATTAATTAATTGTCCATTGTT 3072
 QY 510 ----- 510
 Db 3073 CTTATATAGGCTCTTTTACCCCTGTAAATCGTACGTGAGAGATCATGACAAACAAT 3132
 QY 511 -----ThrValValSerSerThrSerLeu----- 519
 Db 3133 CTTTGAAGAACCAACCATTCCTGTTTCTCTTTTCATCTTACGTAGCCTTATATATATGTTCTC 3192
 QY 520 ---SerHisLeuGlnIlyPheValSerLeuArgValLeuAsnLeuSerAspIleLeuLeu 538
 Db 3193 AAATCGAGGTTGTTCATTTTCAAAATTACTCAAACTCTTGAGCTGAGACACAGACAGATT 3252
 QY 539 LysGlnLeuProSerSerIleGlyAspLeuValHisLeuArgThrLeuAsnLeu----- 556
 Db 3253 GATGGTTTCCCTCGAGAGATCTAAGCTCATCTGTTGAGTACTATCATGTTGTTCCAGC 3312
 QY 557 SerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysIlySerGluAsnLeuGln 576
 Db 3313 TATGGAAATTTTCAGATGA-----CTTCCAAAAATTTGCACGATTGAGAACTTGACAG 3363
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 Db 3364 ACATTTCATTGTTCAACGGTTTCCAGTACAGATATATATATTTTGTGTAGAGAAATTTGGGAA 3423
 QY 596 LeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysThrGlyLeuThrCysMetProPro 615
 Db 3424 CTAAAGCAATTAAAGCATCTTAACTGGCCAGATTTATTTGCCAGATTCGCCAAAGTGA 3483
 QY 616 ArgIleGly-----SerLeuThrCysLeuLysThrLeuSer----- 627
 Db 3484 TCTGTTGCAAAAGAGGACCTTGAGATTTTCCAACTTCAAACTTATTTCTTACTTGTC 3543
 QY 628 -----ArgPheValAlaGlyIleGlnIlySerCysGlnLeuGly 641
 Db 3544 CCAAGTTGTGCACGAGAGAGGATTATTTAGGGATTTCCAGATGTCAAA--AAATTGGA 3600
 QY 642 GluLeuArgAsnLeuAsnLeuThrGlySerIleGluIleThrHisLeuGluArgValLys 661
 Db 3601 ATCACTGGAAATTAAGAGATGACTATTAAGTTTGGGACTGTGGGCTTCCCAAC----- 3654
 QY 662 AsnAspMetAspAlaIlyGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSer 681
 Db 3655 -----AATCTGTGATCTGCAGCAACTGAATATTAGAT 3690
 QY 682 Met---LysTrpAspAspAspGluArgProArgIleThrGluSerGluLysValGluVal 700
 Db 3691 CTTATATCTGTGATTATATAGCCTTTTGGCACTGATCATTTCAAGTGCAAAAGCTTTTCCA 3750
 QY 701 LeuGluAlaLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGly 720
 Db 3751 GCACAGCTCAAGAAAGTTGAAGTTGAAAAGACTTATCTTAAC----- 3792
 QY 721 IleArgLeuProAspTrpMetAsnHisSerValLeuLysAsnValValSerIleGluIle 740
 Db 3793 -----TGTGCATACTTGACATCATAGCTGAAGTGCCTTAACCTTGAGGTG 3837
 QY 741 HisSerCysLysAsnCysSerCys-----LeuProProPhe 752
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Db      3898 AATCGATTGAAGCTTTGCTAATTAATAATAGTTTCTTCAGTCTGGAAGCC----- 3951
Qy      769 GluValGluTyValAspSerGlyPheProThrArgArgPheProSerLeuArgLys 788
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Qy      789 LeuAenIleArgGluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGln 808
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Search completed: April 17, 2005, 04:53:27
Job time : 568 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame.plus.p2n model

Run on: April 17, 2005, 03:01:49 ; Search time 1176 Seconds

(without alignments)
5096.863 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
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Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomum62
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Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	5028.5	98.1	3595	18	US-10-647-268-3
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4	4475	87.3	3347	18	US-10-647-268-5
5	3766.5	73.5	2913	17	US-10-360-522-48
6	3648	71.2	3260	17	US-10-360-522-51
7	3638.5	71.0	3592	17	US-10-360-522-49
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9	3606.5	70.3	3971	17	US-10-360-522-52
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ALIGNMENTS

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Sequence 1, Application US/10647268
Publication No. US20040237137A1
GENERAL INFORMATION:
APPLICANT: Oosumi et al., Teruko
TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
FILE REFERENCE: 0155_02
CURRENT APPLICATION NUMBER: US/10/647, 268
PRIOR FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: 60/407, 100
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 3193
TYPE: DNA
ORGANISM: Solanum bulbocastanum
FEATURE:
NAME/KEY: CDS

LOCATION: (52) .. (3018)
US-10-647-268-1

Alignment Scores:
Pred. No.: 0
Score: 5127.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 3193
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Mismatch: 0
Indels: 0
Gaps: 0

US-10-647-268-2 (1-988) x US-10-647-268-1 (1-3193)

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DB 112 CTGGATTGATTCTTGGTTTAAAGATGAGTTCCGAAAAGCTTCAAGCAGCGTTTACTACA 171
OY 41 IlegAlaValLeuGlnAspAlaGlnLeuGlnLeuGlnLeuGlnLeuGlnLeuGln 60
DB 172 ATCCAAAGCTGTCTGAAGATGCTCAGAAAGCAATGGAAGCAGCAAGCAATGCAAAAT 231
OY 61 ThrLeuGlnLeuLeuAspAlaAlaAlaTyrGlnAlaAspAspIleLeuAspGluCysLeu 80
DB 232 TGGTTGCAAGAACTCAATGCTGCTGATATGAGCTGATGACATCTTGACCAATGTAA 291
OY 81 ThrGluAlaProIleArgGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
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OY 141 ArgGlnThrGlyPheValLeuAspGlnProGlnValTyrGlyArgAspLeuGlnLeuAsp 160
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OY 281 ValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlnLeuValGlySerIle 300
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; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
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US-10-647-268-3

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Query Match: 98.08% Indels: 138
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DB: 18

US-10-647-268-2 (1-988) x US-10-647-268-3 (1-3595)

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Oy 41 11leGlnAlaValLeuGluAspAlaGlnYsGlnLeuYsAspYsAlaIleGluAsn 60
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163 LlysIleLeuIleAsnAsnValSerAsnIleGlnThrLeuProValLeuProIleLeuG 183
957 GAAATATCCGTGATTAACAATGTAGCAATGCCCAACACTTCCAGTCCCTCCCAATCTTGG 1016
183 yMetGlyGlyLeuGlyLysThrThrLeuValGlnMetValPheAsnAspGluArgValI 203
1017 TATGGGGGACTAGAGAAAGACACTCTTGGCCAAATGGCTTCATGATCAGAGATTA 1076
203 eGluHisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGluLysArgLe 223
1077 TGAGCATTTCCATCCCAAAATATGATTTGTGCTCGAAGATTTTAAATGACAGAGGTT 1136
223 uIleLysGluIleValGluSerIleGluGluLysSerLeuGlyGlyMetAspLeuAlaPr 243
1137 GATTAAGGAAATTTGATGATCTATTGAGAAAGACACTTGGTGCATGAGCTTGGCTCC 1196
243 oLeuGluLysLysLeuArgAspLeuLeuAsnGlyLysLysTyrLeuLeuValLeuAspAs 263
1197 ACTTCAAAAGAGCTTCGGACTGCTGTGATGAGAAAAAATTTTCTGCTCTTGATGA 1256
263 pValTrpAsnGluAspGluAspLysTrpAlaLysLeuArgGlnValLeuLysValGlyAl 283
1257 TCTTTGGATGAAGATCAAGATTAAGTGGCTAAAGATTAAACAAGCTTGAAGTGGAGC 1316
283 aSerGlyAlaSerValLeuThrThrThrArgLeuGluLysValGlySerIleMetGlyTh 303
1317 AAGTGCCTCTCTGTTCTTAACACTACTGCTTGAAGAGTTGATCAATATATGGGAAC 1376
303 rLeuGluProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMetG 323
1377 ATTGCAACCATTAATGATTTGTCAAAATTTGTCTCAAGAGATTTGGTTGTTTCTTCA 1436
323 nArgAlaPheGlyHisGlnGluGluIleAsnLeuAsnLeuValAlaIleGlyLysGluI 343
1437 AGCTGATTTGGGCAACAAGAAATTAATCTTAATCTTGGGCTATCGGAAGAGAGAT 1496
343 eValLysLysCysGlyGlyValProLeuAlaAlaLysThrLeuGlyGlyIleLeuArgPh 363
1497 TGTGAAAAATATGGGTGTGTGCTTACACGCTTAACCTTGGAGGTATTTTGGGCTT 1556
363 eLysArgGluGluArgGluTrpGluHisValArgAspSerGluIleTrpLysLeuProG 383
1557 TTAGAGAGAAAGAAAGACAGTGGAGACATGTGAGAGATAGTGAATTTGGACTCA 1616
383 nGluGluSerSerIleLeuProAlaLeuArgLeuSerTyrHisHisLeuProLeuAspLe 403
1617 AGAAGAAAGTTCTATCTGCTGCTCCCTGAGACTTAATACCATCACTTCCACTTGATT 1676
403 uArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMetGluLysGlyAs 423
1677 GAGACAAATGCTTTAATATTGTGAGATATTTCCAAAGAGATACGAAATGAGAAAGGAAA 1736

423 nLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGlyAsnLeuGluLeuG 443
1737 TCTTAATCTCTCTCGATGAGCAATGGTTTATTTATTCAGAAAGAAACTTGGAGCTAGA 1796
443 uAsnValGlyAsnGluValTrpAsnGluLeuTyrLeuArgSerPhePheGlnGluIleG 463
1797 GAATGTAGTAAAGAAATGAAATGAAATGAATTAATTAAGGCTTCTTCCAGAGATTGA 1856
463 uValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeuAlaThrSe 483
1857 AGTTAAATCTGTCAAACTTATTTCAAGATGCAATGATCTCATTCATGATCGGCAATC 1916
483 rLeuPheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrI 503
1917 TCTATTTCCGCAAGACATCAAGCAACATATCCGAGAAATATTTAGAAATTTACAT 1976
503 eHisMetMetSerIleGlyPheThrLysValValSerSerTyrSerLeuSerHisLeuG 523
1977 ACATATGATGTCCTAGTGTTCACCTAAAGTGATCTTACTCTCTTCCACTTCCA 2036
523 nLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLysGlnLeuProSe 543
2037 GAAGTTTGTCTGTTGAGGCTTATCTTAAGTGAATATAAATTAAAGCAGTTAACGCTC 2096
2097 TTCCATTTGAGATCTAGTACATTAAGATCTTAACCTTGTCTGCAATCTAGTATTTGC 2156
543 rSerIleGlyAspLeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThrSerIleAr 563
563 gSerLeuProAsnGlnLeuCysLysLeuGluAsnLeuGlnThrLeuAspLeuHisGlyCy 583
2157 TAGCTTCCAAACCAAGTATGACAGCTTCAAAATCTGCAGACTTTGATCTACATGGCTG 2216
583 sHisSerLeuCysCysLeuProLysGluTrpSerLysLeuGlySerLeuArgAsnLeuLe 603
2217 TCATTTACTTTGTTGTTGCCAAAGAAACAAGCAAACTTGTGTGCTTCCAAATCTTTT 2276
603 uLeuAspGlyCysTyrGlyLeuThrCysMetProProArgIleLeuLeuSerLeuThrCys 623
2277 ACTGATGTTGTCATGATGATGACTTGTATGCCCAAGAGATGAGATCTTGAACATGGCT 2336
623 uLysThrLeuSerArgPheValValGlyIleGluLysLysSerCysGlnLeuGlyGluLe 643
2337 TTAGACTTAAAGTAAATTTGTGTGGGAAATTCAGAAAGAAAGTTGTCACTTGGTGAAT 2396
643 uArgAsnLeuAsnLeuTyrGlySerIleGluIleThrHisLeuGluLysArgValLysAsnAs 663
2397 ACGAAACCTGATCTATGCTATGCTCAATGGAATCAGCATCTTGAAGAGAGAAAGAGA 2456
663 pMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLy 683
2457 TATGATCCAAAGAAAGCAATTAATTCGAAAGAAATCTGCATTTCTTAAGCATGAA 2516
683 sTrpAspAspAspGluArgProArgIleTyrGluSerGluLysValGluValLeuGluAl 703
2517 ATGGATGACATGAACTCCACGTAATATGATCAGAAAAAGTTGAAGTGAAGCTTGAAGC 2576
703 aLeuLysProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyIleArgLe 723
2577 TCTCAACACCACTCATCTGACTTGTTAACAATCAGGGGCTTCAAGAGAAATCCGCT 2636
723 uProAspTrpMetAsnHisSerValLeuLysAsnValValSerIleGluIleIleSerCy 743
2637 CCCAGACTGATGATCACTAGTTTAAAAAGTTGTCTCTATGAAATCAATCAGTTG 2696
743 sLysAsnCysSerCysLeuProProPheGlyGluLeuProCysLeuLysSerLeuGluLe 763
2697 CAAAATCTGCTCATCTTAACACCTTTGTGTGAGCTGCTTGTCAAAAAGCTAGAGTT 2756
763 uTrpArgGlySerAlaGluValGluTyrValAspSerGlyPheProThrArgArgArgPh 783
2757 ATGAGAGGGGTCTCGGAGAGTGAATGATTGATTCTGATTCCTCAAGAGAGAGGTT 2816
783 eProSerLeuArgLysLeuAsnIleArgGluPheLysAsnLeuLysGlyLeuLeuLysLy 803

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Db      2817 TCCATCTCTGAGAAAACCTAATATACGCAATTGATATCATCGAAGATTGCTGAAAAA 2876
Qy      803  egluglvglugluglucyprovalleuglugluleglluleyrcyvsprometph 823
Db      2877 GGAGGAGAGAGAGCATGCCCTGCTCTTGAGAGATAGAGATTAATGTTGCTCATGTT 2936
Qy      823  eValleProThrLeuSerSerVallyleValleValSerGlyAspLysSerAspAl 843
Db      2937 TGTATTCACACCTTCTTCTGTCAGAAATGGTAGTATGGGACACAGTCAAGTCC 2996
Qy      843  ailegilypheserSerlleSerAenleuMecAlaLeuThrSerleuglulleayrtyras 863
Db      2997 AATAGGTTTCAGTTCCATATCTAATCTCATGCTCTTACTTCCCTCAAAATCGCTATRA 3056
Qy      863  nlygluAspAlaSerleuProgluGluMecPheLysSerleuAlaAenleuLysTyle 883
Db      3057 CAAGAGAAATGCTTCTACTCCAGAGAGATGTTCAAAAGCCTTGCAAAATCTCAATACCT 3116
Qy      883  uAsnilleSerPheTyrcPheAenleuLysGluLeuProThrSerleuAlaSerleuAsnAl 903
Db      3117 GAATATCTCTTTTATCTTCAATCTTAAGAGCTGCTTACAGCTGCTAGTCTCAATCC 3176
Qy      903  aleuLysHleuGluilleHleuSerCyseTyrcAlaLeuGluSerleuProgluGluGly 923
Db      3177 TTGGAAGCATCTGGAATTCATAGTTGTTATGCACTAGAGAGTCCCGAGAGAGTGT 3236
Qy      923  llyglilyleuLleSerleuThrGluLeuSerlleThrTyrcyGluMecleuGluGly 943
Db      3237 GAAAGGTTTATTTCTACTCACACAGTTTATCCATTAACATGTAAGTAAGCTACATGTTT 3296
Qy      943  uProgluGlyleuGluHleuThrAlaLeuThrAenleuSerVallylePheCyseProth 963
Db      3297 ACCGAGGAGATTCGACGACCTTACAGCCCTTCAAAATTTATCAGTTGAGTTTGTCCAA 3356
Qy      963  rleuAlaLysArgCyseGluLysGlylleGlyGluAspTyrTyrcAlaHleuAlaHleu 983
Db      3357 ACTGGCCAGAGCGGTGTGAGAGAGAAATAGAGAGACGTGTAACAATAATGCTCAATCC 3416
Qy      983  carGValPheIleTyrc 988
Db      3417 TCGTGTGTTTATTTAT 3432

RESULT 3
US-10-647-268-9
; Sequence 9, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647,268
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 5028
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(553)
; OTHER INFORMATION: Potato Ubi3 promoter
; FEATURE:
; NAME/KEY: gene
; LOCATION: (973)..(4566)
; OTHER INFORMATION: Solanum bulbocastanum genomic Sbu11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1029)..(1459)
; FEATURE:

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; NAME/KEY: Intron
; LOCATION: (1460)..(1871)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1872)..(4404)
US-10-647-268-9

Alignment Scores:
Pred. No.: 0
Score: 5028.50
Percent Similarity: 87.66%
Best Local Similarity: 87.66%
Query Match: 98.08%
DB: 18

US-10-647-268-2 (1-988) x US-10-647-268-9 (1-5028)

Qy      1  MetAlaGluAlaPheLeuGluValleuLeuAspAenleuThrCysePheIleGluGlyGlu 20
Db      1029 ATGCGTGAAGCTTCTTCAAGTTCTGTAGACAATCTGACTGTTCATCCAAAGGGGAA 1088
Qy      21  LeuGlyLeuIleLeuGlyPheLysAspGluPheGlyLysleuGlnserThrPheThrThr 40
Db      1089 CTGGATTTGATCTTGTGTTTAAGAGATGATTCAAAAGCTTCAAAGCAGCTTATCAACA 1148
Qy      41  lleGlnAlaValleuGluAspAlaGlnLysLysGlnleuLysAspLysAlaileGluAsn 60
Db      1149 ATCCAGCTGCTGTGAGAGATGCTCAGAGAGACATTTGAAGACACAGCAATAGAAAAT 1208
Qy      61  TrrleuGlnLysleuAsnAlaAlaAlaTyrcAlaAspAspIleleuAspGluCyseLys 80
Db      1209 TGGTTGAGAAATCTCAATGCTGCTGCATATGAGGCTGATGACATCTTGACGAATGTAA 1268
Qy      81  ThrGluAlaProlleArgGlnLysLysLysTyrcTyrcThrLysProAsnValle 100
Db      1269 ACTAGGACCAATTAAGCAGAGAGAAACAAATATGGGTCTTATCATCAAAAGCTTATC 1328
Qy      101  ThrPheArgHleuLysIleGlyLysArgMetLysLyslleMetGluLysleuAspValle 120
Db      1329 ACTTTGCTCAAGATTTGGGAAAAGATGAAAAGATTAAGGAAACTAGATTAAT 1388
Qy      121  AlaAlaGluArgIleLysPheHleuAspGluArgThrIleGluArgGlnValAlaThr 140
Db      1389 GCAGCGGAGCAATTAAGTTTCATTGGATGAAGACTATAGAGACAGAGTTGCTTACA 1448
Qy      141  ArgGlnThr----- 143
Db      1449 CGCCAAACAGGTGCTCATCTAGATATTTTCTGAAAAACAGCTTATATCATCAAAATT 1508
Qy      143  ----- 143
Db      1509 CATGTGTGTTTGGGAATTCGTAAATCTTAATGTTGCTCAAGCTTAAGTAGTAAGT 1568
Qy      143  ----- 143
Db      1569 GGATCCAGCTTTGATTTATTAATCTATAGCTAAATCTGTTAGTGAAGTTTAAACAT 1628
Qy      143  ----- 143
Db      1629 ATATTAACCTCAGATTAATTCATAGCTTACTATAGATTAAGATAGAGCCCAAGCTTAA 1688
Qy      143  ----- 143
Db      1689 ATGACAGATTAAGCCAGAGTGTTTTACCTTATTAATTAACAATGATATAATATGTA 1748
Qy      143  ----- 143
Db      1749 ATTCAAAAAGTGATTTTATTAATTAATTAATTTGCTGCTTCAAGCTTATCATTT 1808
Qy      143  ----- 143
Db      1809 GTCTTTTACTGTGCAAAATTTCTACTTGTATTTTGTGTAAGTCTTACGAGCTTGAGCC 1868

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144 -GlyPheValLeuAsnGluProGlnValTyrGlyArgAspLysGluLysAspGluLeuVal 163
1869 AGGTTTGTCTTGAATGAAACCAAGTTTATGAAAGACAAAGAAAGGACGAGATAGT 1928
163 llylIleuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuG1 183
1929 GAAATTCCTGATTAACAATGTTAGCAATGCCAAACCTTCACAGTCCCTCCCAATACCTGG 1988
183 yMeG1yG1LeuG1yLysThrThrLeuAlaGlnMeValPheAsnAspGlnArgValI1 203
1989 TATGGGGGCACTAGAAAGACGACTCTGGCCCAATGGCTTCATGATGATCAGAGATAT 2048
203 eGlnIhisPheHisProLysI1eTrpIleGysValSerGluAspPheAsnGluLysArgLe 223
2049 TGAGCATTTCCATCCCAAAATATGSAATTTGTCTCGAAGATTTTAAATGAGAAAGGTT 2108
223 uI1eLysGluIleValG1uSerI1eG1uLysSerLeuG1yG1yMeAspLeuAlaPr 243
2109 GATTAAGGAAATTTGATGAAATCTAATTGAAAGAAAGTCACCTGGTGCAATGACTGGCTCC 2168
243 oLeuGluLysLysLeuArgAspLeuLeuAsnG1yLysLysTyrLeuLeuValLeuAspAs 263
2169 ACTTCAAAAGAAAGCTTCGGGACTTGCTGATGAAAGAAATATTTGCTGCTTAGATGA 2228
263 PValTrpAsnGluAspGluAspLysTrpAlaLysLeuArgGlnValLeuLysValG1yAl 283
2229 TGTTTGGAATGAAAGATCAAGATTAAGTGGGCTTAAGTTAAACAAGCTTGAAGCTTGGAGC 2288
283 aSerG1yAlaSerValLeuThrThrThrArgLeuGluLysValG1ySerI1eMeG1yTh 303
2289 AAGTGGCGGTTCTGTTCTTAACACACTACGCTTGAAGAAAGTTGGATCAATATATGGGAC 2348
303 rLeuGlnProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMeG1 323
2349 ATTGCAACCATATGAAATGTCTCAAAATTTGTCTCAAGAAAGATTTGTGTTGTTATGCA 2408
323 nArgAlaPheGluYH1sGlnGluGluI1eAsnLeuAsnLeuValAlaI1eG1yLysGluI1 343
2409 AGGTGATTTGGGACCCAAAGAAAGAAATTAATCTTAATCTTGGCTATCCGAAAGAGAT 2468
343 eValI1yLysCysG1yG1yValProLeuAlaAlaLysThrLeuG1yG1yI1eLeuArgPh 363
2469 TGTGAAAGAAATGTGGTGGTGGCTCTAGACACTAAACCTTGGAGGATTTTCCGCTT 2528
363 eLysArgGluGluArgGlnTrpGluI1h1sValArgAspSerGluI1eTrpLysLeuProG1 383
2529 TTAAGAGAGAAAGAACAGATGGGAAACATGTGAGAGATGAGATTTGAAAATGGCTCA 2588
383 nGluGluSerSerI1eLeuProAlaLeuArgLeuSerTyrH1sH1sLeuProLeuAspLe 403
2589 AAGAAAGAAATTTCTATTTCTGCTGCTGCTGAGACTTAAGTTACATCACCTTCCACTGATT 2648
403 uArgGlnCysPheThrTyrCysAlaValPheProLysAspThrGluMeGluLysG1yAs 423
2649 GAGACAAATGCTTATTAATTTGAGATATTCCTCAAGGATACCGAAATGAAAAGGGAAA 2708
423 nLeuI1eSerLeuTrpMetAlaH1sG1yPheI1eLeuSerLysG1yAsnLeuGluLeuG1 443
2709 TCTAACTCTCTCTGGATGGACATGCTTTTATTTATGAAAGGAAACTTGGAGCTAGA 2768
443 uAsnValG1yAsnGluValTrpAsnGluLeuTyrLeuArgSerPhePheGlnGluI1eG1 463
2769 GAATGATAGTAAATGAAATGAAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 2828
463 uValI1ySerG1yGlnThrTyrPheLysMeCh1sAspLeuI1eH1sAspLeuAlaThrSe 483
2829 AGTTAAATCTGGCAAACTTAATTTCAAGATGACATGATTCATTCATTCATTCATTCATTC 2888
483 rLeuPheSerAlaSerThrSerSerSerSerSerSerSerSerSerSerSerSerSerSer 503
2889 TCTAATTTTGGGACAGACATCAAGGACAGATATCCAGAAATTAATTAATTAATTAATTAAT 2948
503 eHisMetMetSerI1eG1yPheThrLysValI1eSerSerTyrSerLeuSerH1sLeuG1 523

2949 ACATATGATGTCATGCTGTTCACTAAAGTGATATCTTCTTACCTCTTCCCACTTGCA 3008
523 nLysPheValSerLeuArgValLeuAsnLeuSerAspI1eLysLeuLysG1nLeuProSe 543
3009 GAAGTTTGTCTGTGAGGGTGTCTTAATCTAAGTGAATTAATTAATTAATTAATTAATTAAT 3068
543 rSerI1eG1yAspLeuValH1sLeuArgTyrLeuAsnLeuSerG1yAsnThrSerI1eAr 563
3069 TTCAATGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3128
563 gSerLeuProAsnGluLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuH1sG1yCy 583
3129 TAGCTTCCAAACCAAGTTATGCAAGCTTCAAAATCTGCAAGCTTGTATCTACAGGCTG 3188
583 eHisSerLeuCysLeuProLysGluThrSerTyrLeuG1ySerLeuArgAsnLeuLe 603
3189 TCATTCATCTTGTGTGTGTCGCAAAAGAAACAAAGCAACTTGGATGTTGACATCTTT 3248
603 uLeuAspG1yCysTyrG1yLeuThrCysMetProProArgI1eG1ySerLeuThrCysLe 623
3249 ACTGATGGTTCATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 3308
623 uLysThrLeuSerArgPheValValG1yI1eGlnLysLysSerCysGlnLeuG1yGluLe 643
3309 TAAAGCTCTAAGTATGATTTGGTGGGAATTCAGAAAGAAAGTTGTCAACTGTGTAAT 3368
643 uArgAsnLeuAsnLeuTyrG1ySerI1eGluI1eThH1sLeuGluArgValLysAsnAs 663
3369 ACGAAACCTGAATCTTAATGCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3428
3429 TATGATGCAAAAGAAAGCAATTTATCTGCAAAAGAAATCTGCAATCTTAAACCAATGA 3488
663 pMeAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuH1sSerLeuSerMeLys 683
683 sTrpAspAspAspGluArgProArgI1eTyrGluSerGluLysValGluValLeuGluAl 703
3489 ATGGAGTACCATGATAGCGTCAAGATATATGAAATGAAAGATTAAGTGTGTTAGAGC 3548
703 aLeuLysProH1sSerAsnLeuThrCysLeuThrI1eArgG1yPheArgG1yI1eArgLe 723
3549 TCTCAACCACTCCCATCTGATCTGTTTAACATCAGGGGCTTCAGAGAAATCCGCT 3608
723 uProAspTrpMetAsnH1sSerValLeuLysAsnValI1eSerI1eGluI1eI1eSerCy 743
3609 CCAAGACTGATGATCACTCAGATTTGAAAGAAATGTTGTCTCTATTTGAATCAATCAGTTG 3668
743 eLysAsnCysSerCysLeuProProPheGluGluLeuProCysLeuLysSerLeuGluLe 763
3669 CAAGAACTGCTCATGCTTAACACCTTGTGTAGCTGCTGTCTTAAGAACTTAAGTT 3728
763 uTrpArgLysSerAlaGluValGluTyrValAspSerG1yPheProThrArgArgArgPh 783
3729 ATGAGGGGGGCTCGGGAAGTGAATGTTGATTCGTGATTCCTCAAGAAAGAGGTT 3788
783 eProSerLeuArgLysLeuAsnI1eArgGluPheG1yAsnLeuLysG1yLeuLeuLysLys 803
3789 TCCATCTCTGAGAAACCTTAATTAATTAATGCGGAATTTGATTAATGAAAGGATTCGAAADA 3848
803 eGluGluGluGluGlnCysProValLeuGluGluI1eGluI1eLysCysCysProMetPh 823
3849 GGAAGAGAAAGACATCCCTGCTTGAAGATTAAGATTAATTAATTAATTAATTAATTAAT 3908
823 eValI1eProThrLeuSerSerValLysLysLeuValI1eSerG1yAspLysSerAspAl 843
3909 TGTATTTCACACCTTTCTTCTGTCAGAAATTTGTAGTGGGCAAGTCAAGATGC 3968
843 aI1eG1yPheSerSerI1eSerAsnLeuMeCh1sLeuThrSerLeuGlnI1eArgTyrAs 863
3969 AATAGTTTCAAGTTCCATATCAATCTCATGTCTTCTTCCCTCCCAATTCGCTATTA 4028
863 nLysGluAspAlaSerLeuProGluGluMetPheLysSerLeuAlaAsnLeuLysTyrLe 883

Db 4029 CAAGAAGATCTTCACTCCAGGAAGAGATGTTCAAAAGCCCTTGCAATCTCAATACTT 4088
Qy uAsnIIeSerPheTYrPheAmnLeuLYeGluLeuProThrSerLeuAlaSerLeuAsnAl 903
Db 4089 GAATATCTCTTTTATCTTCAATCTTTAAAGAGCTGCTTACAGCTGGCTAGTCTCAATGC 4148
Qy 903 aLeuLYeHISLeuGluIleHISerCYeTYrAlaLeuGluSerLeuProGluGluLYa 923
Db 4149 TTTGAAGCATCTGAAATTTCAATGTTTATGCACTAGAGAGTCTCCCGAGGAAGGTGT 4208
Qy 923 lLYeGluLYeLeuIleSerLeuThrGlnLeuSerIleThrTYrCYeGluMeLeuGlnCYeLe 943
Db 4209 GAAAGGTTTAAATTTCACTCACACAGTTTATCCATTAACATCTGTGAATGCTACATGTTT 4268
Qy 943 uProGluGluLYeGlnHISLeuThrAlaLeuThrasLeuSerValGluPheCYeProTh 963
Db 4269 ACCGAGGAGATTGACGACCTTACAGCCCTCACAATTTATCAGTTGAGTTTGCCAAC 4328
Qy 963 rLeuAlaLYeArGYeCYeGluLYeGluLYeGluLYeGluLYeGluLYeGluLYeGluLYe 983
Db 4329 ACTGGCCAAAGCGGTGTGAAGAGGAATAGAGAAAGATGTRACAAATTTGCTCACATTCC 4388
Qy 983 cArGValPheIleTYr 988
Db 4389 TCGTGCTTTATTTAT 4404

RESULT 4

US-10-647-268-5
; Sequence 5, Application US/10647268
; Publication No. US20040237137A1
; GENERAL INFORMATION:
; APPLICANT: Oosumi et al., Teruko
; TITLE OF INVENTION: Solanum Bulbocastanum Late Blight Resistance Gene and Use Thereof
; FILE REFERENCE: 0155.02
; CURRENT APPLICATION NUMBER: US/10/647, 268
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(509)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (510)..(788)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (789)..(3344)
US-10-647-268-5

Alignment Scores:

Prod. No.: 0 Length: 3347
Score: 4475.00 Matches: 883
Percent Similarity: 83.94% Conservative: 37
Best Local Similarity: 80.57% Mismatches: 66
Query Match: 87.28% Indels: 110
Gaps: 2

US-10-647-268-2 (1-988) x US-10-647-268-5 (1-3347)

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Qy 21 LeuGluLYeLeuIleLeuGluLYePheLYeAspGluPheGluLYeLeuGlnSerThrPheThr 40
Db 117 GTTGATTTGATTTCTTGGTTTAAAGATGATGTTGCAAAAGCTTCAAAAGCATTTTACTACA 176

Qy 41 lIeGlnAlaValLeuGluAspAlaGlnLYeLYeGlnLeuLYeAspLYeAlaIleGluAsn 60
Db 177 ATCCAAAGCTGTGTAGAAAGATGCTCAGAAAGAAATTAAGAGCAACAGGCATATGAAAT 236
Qy 61 TrPLeuGlnLYeLeuAsnAlaAlaLYeGluAlaAspAlaIleLeuAspGluCYeLYe 80
Db 237 TGGTTGCAGAAACCAATGCTGTATATGAACTGACATCTGGAGCAAGTA 296
Qy 81 ThrGluAlaProIleArGYeGlnLYeLYeAsnLYeTYrGluCYeTYrHISProAsnValIle 100
Db 297 ACTAGGACCAATTAAGACAGAAAGAACAAATATGGGTGTTTATCATCCAAACGTTATC 356
Qy 101 ThrPheArGYeLYeLYeLYeArGYeLYeLYeArGYeLYeLYeArGYeLYeLYeArGYeLYe 120
Db 357 GCTTTCGCTCAAGATTTGGGAAAAGATGAAAAGATTATGAGAAACTGATGTAATT 416
Qy 121 AlaAlaGluAlaGluLYeLYePheHISLeuAspGluArGYeIleGluArGYeGlnValAlaThr 140
Db 417 GCACCGGAACGAATTAAGTTTCATTTGGCTGAAAGCACTACAGAGACAAAGTTGTCTACA 476
Qy 141 ArgGlnThr 143
Db 477 CGCCAAACAGGTGCTCATCTTAATATTTTCTAAAAAACAGCTTATATCATGAATT 536
Qy 143 143
Db 537 CATGTGTGTTGGATTTTCTAATCTAATATGTTGTCTCAAGTCAAGTAAAGTGC 596
Qy 143 143
Db 597 ATCCAGATTGGAT 656
Qy 143 143
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Db 717 GTGCATATGCTGCTGCTTCTCAAGCTTATCATTTGCTTTATGTGCAAAATTCCTC 776
Qy 144 144
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Qy 192 LeuAlaGlnMetValPheAsnAspGlnArGYeValIleGluHISpHeHISProLYeIleTrp 211
Db 957 CTTGCCCAAAATGCTTCAATGATCTCAGAGATTAATGACATTTCCCTCCCAAAATATGG 1016
Qy 212 lIeCYeValSerGluAspPheAsnGlnLYeArGYeLeuLYeGluLYeGluLYeGluLYeGluLYe 231
Db 1017 ATTTGTCTCTCGAAGATTTTAAAGAAAGGTTTAAAGAAATTTGTAATCTATA 1076
Qy 232 GluGluLYeSerLeuGluLYeLYeMetAspLeuAlaProLeuGlnLYeLYeLeuArGYeAspLeu 251
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Qy 252 LeuAsnGluLYeLYeTYrLeuLeuValLeuAspAspValTrpAsnGluAspGlnAspLYe 271
Db 1137 CTGAATGAAAAAATATTTGCTTGTCTTAGATATATTTGGATGAAGATCAAGATAG 1196
Qy 272 TrpAlaLYeLeuArGYeGlnValLeuLYeValGluAlaSerGluAlaSerValLeuThrThr 291
Db 1197 TGGCTTAAGTTTACGAAGGTTTGAAGGTTTGAAGCAAGTGTGCTTCTATCTTACCACT 1256
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Qy 312 LeuSerGlnGluAspCysLeuLeuPheMetGlnArgAlaPheGlyHisGlnGlu 331
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Qy 332 IleAsnLeuAsnLeuValAlaIleGlyLeuValIleValIleValCysGlyGlyValPro 351
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Qy 532 AsnLeuSerAspIleLysLeuLysGlnLeuProSerSerIleGlyAspLeuValHisIleu 551
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Db 2234 ATTTCAATCAGCATCTTGAGAGAGTGAAAGATGATATGATGCAAAAGACCAATTTA 2293
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Qy 772 TyrValAspSerGlyPheProThrArgArgPheProSerLeuArgLysLeuAsnIle 791
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Qy 792 ArgGlnPheGlyAsnLeuLysGlyLeuLeuLysLysGlnGlnGlnGlnGlnGlnGln 811
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RESULT 5

US-10-360-522-48

; Sequence 48, Application US/10360522

; Publication No. US20030221215A1

; GENERAL INFORMATION:

; APPLICANT: Aliefs, Josephus J.H.M.

; APPLICANT: Vossen v.d., Edwin A.G.

TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
 FILE REFERENCE: U 014413-9
 CURRENT APPLICATION NUMBER: US/10/360,522
 PRIOR APPLICATION NUMBER: EP 02075565.8
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: PCT/NL03/00091
 PRIOR FILING DATE: 2003-02-07
 NUMBER OF SEQ ID NOS: 63
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 48
 LENGTH: 2913
 TYPE: DNA
 ORGANISM: Solanum bulbocastanum
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(2913)
 OTHER INFORMATION: /note="Rpi-b1b"
 US-10-360-522-48

Alignment Scores:
 Pred. No.: 0 Length: 2913
 Score: 3766.50 Matches: 753
 Percent Similarity: 83.43% Conservative: 78
 Best Local Similarity: 75.60% Mismatches: 130
 Query Match: 73.46% Indels: 35
 Gaps: 8

US-10-647-268-2 (1-988) x US-10-360-522-48 (1-2913)

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 121 ATTCAAGCCGCTTGAAGATGCTCAGAGAACTCAACACACACCTTACAAAT 180
 61 ThrLeuGlnLeuLeuAsnAlaAlaIleThrGluAlaAspAspIleLeuAspGluCysLeu 80
 181 TGGTTGCAAAATCAATAGCTGCTACATAGAGTCATGACATCTTGATGAAATATA 240
 81 ThrGluAlaProIleArgGlnLeuLeuAsnLeuLeuGlyCysThrPheProAsnValIle 100
 241 ACCAAGGCC---ACAAAGATTCTCCAGTCTGAATATGCGCCTTATCATCAAGTTATC 297
 101 ThrPheArgHISLeuGlyLeuLeuArgMetLeuLeuIleMetGluLeuLeuAspValIle 120
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 121 AlaAlaGluArgGlyIleLeuPheHISLeuAspGluArgThrIleGluArgGluValAlaThr 140
 358 GCTGAGGAAAGAAAGAAATTTTCATTGCAAGAAATAATTGAGAGACAAAGCTTTGA 417
 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValIleGlyArgAspLeuGlyLeuAsp 160
 418 CGGGAACAGAGTTCGTATTACCGAAGCGAGCTTTATGGAAGAGACAAAGAGAAAT 477
 161 GluIleValLeuLeuLeuIleAsnAsnValSerAsnAlaGlnThrLeuProValLeuPro 180
 478 GAGATAGGAAGAAATCTTAATAACATGTAGTATGCCCAACACTTTCAGTCTCCCA 537
 181 IleLeuGlyMetGlyGlyLeuGlyLeuThrThrIleAlaGlnMetValPheAsnAspGln 200
 538 ATACTGGATAGGGGGGATAGGAAAGACGACTCTTGCCCAATGCTTCAATACAG 597
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 RESULT 6
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 ; Sequence 51. Application US/10360522
 ; Publication No. US20030221215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allele, Josephus J.H.M.
 ; APPLICANT: Vossen v.d., Edwin A.G.
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
 ; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
 ; FILE REFERENCE: U 014413-9
 ; CURRENT APPLICATION NUMBER: US/10/360, 522
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: EP 02075565. 8
 ; PRIOR FILING DATE: 2002-02-08
 ; PRIOR APPLICATION NUMBER: PCT/NL03/00091
 ; PRIOR FILING DATE: 2003-02-07
 ; NUMBER OF SEQ ID NOS: 63
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 US-10-360-522-51

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 Best Local Similarity: 68.16% Mismatches: 143
 Query Match: 71.15% Indels: 114
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 QY 21 LeuGlyLeuIleLeuGlyPheLYsAspGluPheGluLYsleuGluSerThrPheThr 40
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 Db 121 ATCCAGACTGTGCTAGAGAGATGCTCAAGAGCACTGAAGTCAAGAGCAATTAAGAAC 180
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 QY 81 ThrGluAlaProIleArgGluLYsAsnLYsTYrGlyCYsTYrHISProAsnValIle 100
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Db 777 ATAAACAATGTTAGTTATCCGAAGAGTCCCAATCTCCCAATCTTGTAAGGGGGA 836
OY 187 LeuGlyserThrThrleuValIleGlymetValPheabaapgluValIleGlnIle 206
Db 837 CTAGAGAAAGACACTAGCCCAATGAGTCTTCAATGATCAAGAAATTAACGATTC 896
OY 207 HisProIyIleTrrpIleCyavaIserGluabPheabngluIyIyArGleuIle 226
Db 897 AATCAAAAGATATGGGTTGTGTCTCAGATGATTTTATGAGAAAGGTTGATTAAGCA 956
OY 227 IleaValIleGluIleGluIySerleuGlyMetAapleuValProleuGluIy 246
Db 957 ATTGAGAAATCTATGAAGAAAGTCACTGGGTGATGATGAGTCCCTCCAGAA 1016
OY 247 LytleuAapleuLeuabngIyIySerIyIleuValleuAapValIlePheab 266
Db 1017 AAGCTTCAGAGTGTGTAATGAAAGAAATGATCTTGTGTTGGATGATGTTGGAAT 1076
OY 267 GluabPgluAapIyTrrpAlalyeIyArGluValIleuIyValIleSerGlyAla 286
Db 1077 GAAATCAAGAAAGTGGATTAATCTTAGACAGATTAAGATTTGAGCTAGTGTCT 1136
OY 287 SerValleuthrThrIyArGleuIyIyValIySerIleMetGlyThrleuGlnPro 306
Db 1137 TCAATTTAATTACTACTGCTCTTGAAGAAATTTGGATCAATTAAGGAATTTGCAACTA 1196
OY 307 TyrGluIleuSerAenIleuSerGlnIyAapCytrpIleuIlePheMetGlnIyAlaPhe 326
Db 1197 TATCAATTAATCAATTTGTCTCAAGAAATTTGTGTGTTGTTCAACCAAGTGCATTT 1256
OY 327 GluIleGlnIyGluIleAenIleuAenIyValIleGlyIyValIleValIyIy 346
Db 1257 TGCACCAACCAAGCAAGTCTTAATCTTAAGAAATCGAAGAGAAATGTGAAGAA 1316
OY 347 CyagIyGlyValIleProleuAlaIalyeThrleuGlyIyIleleuArPheIyArGlu 366
Db 1317 TGTGGGGGTGTGCTCTAGACAGCCAAATCTTGAAGCTTTTACGTTCAAGAGGGA 1376
OY 367 GluIyArGlnThrIyIleValIyArGleuSerGluIleTrrpIyIleuProGlnIyGluIy 386
Db 1377 GAAAGTGAATGGGAACATGTAGAGATGTGATTTGAAATTTTACCTCAAGATGAAAT 1436

OY 387 SerIleuProAlaIeIyArGleuSerIyIyIleuProleuAapleuArGlnIyCy 406
Db 1437 TCTGTTTGCTGCTGAGCTGAGCTGATATCATCTTCCACTGATTTGAGCAAAATGT 1496
OY 407 PheThrIyrcyValIyAlaPheProIyAapThrIyIleuGlyIyGlyIyAenIleuIleSer 426
Db 1497 TTTGATATTTGCGGATTTTCCAAAGGACCAAAATAGAAAGAAATATCTCATGTCT 1556
OY 427 LeuIrrpMetAlaIleGlyPheIleuSerIyGlyAenIleuGluIyAenValIyIy 446
Db 1557 CTCTGATGACACACAGTTTCTTTATCAAAAGAAACATGAGACTGAGAGTGGGC 1616
OY 447 AengluValIyPaengluIleuIyIyIleuArGleuSerPhePheGlnIyIleGluValIySer 466
Db 1617 AATGAAGTATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1676
OY 467 GlyIleThrIyrcyPheIyIleuMetIleAapleuIleIleAapleuAlaIleThrSerIleuPheSer 486
Db 1677 GGTAAACTTATTTCAAGATCATGATCTCATGATGATTTGGCTACATGATGTTTCA 1736
OY 487 AlaSerThrSerSerSerAenIleArGluIle----- 497
Db 1737 GCAGCGCATACAGACAGAAAGTATACCCCAATTAATGTAAGATGAAAGATGATGAT 1796
OY 498 ---IleaValIyAenIyrcIleIleMetIleSerIleGlyPheThrIyValIyIleSer 516
Db 1797 TTCAATTTGAACAATTAATTAAGATATGATGTCATTTGGTTTCTCGAAGTGTGTCTCT 1856
OY 517 TyrSerIleuSerIleIleGluIyPheValSerIleuArGluIleAenIleuSerAapIle 536
Db 1857 TACTCTCTGCTGCTTTAAAGGTTGTCTCGTAAAGGGGCTTAACTGAAGAACTCA 1916
OY 537 LeuIleuIyGlnIleuProSerSerIleGlyAapleuValIleuArGlyIleuAenIleu 556
Db 1917 GAATTTGACAGTATACGCTTCTCGTGAAGATCTAGTACATTTTAAGTACTTGACTTG 1976
OY 557 SerGlyAenThrSerIleArGleuSerIleuProAenIleuCyIyIleuGlnIleuGln 576
Db 1977 TCTGATAT---AAATTTGATGATCTTCCAAAGAGTTGTGCAAGCTTCAAAATCTGCA 2033
OY 577 ThrIleuAapleuIleGlyCyIyIleSerIleuCyIyIleuProIyGluIleThrSerIyIleu 596
Db 2034 ACTCTTATATCAATTAATTTGCACTGACTCTTCTGTTGGCCGAACAAACAAAGTACT 2093
OY 597 GlySerIleuAapleuIleuIleuAapGlyCyIyIyIleuThrCyIyMetProProArG 616
Db 2094 TGTAGTCTCGGAATCTTGATCTTGATCTGT---CCATGACTTCTATGCAACAGCA 2150
OY 617 IleGlySerIleuThrCyIyIleuIyThrIleuSerArGpheValIyGlyIleGlnIyIy 636
Db 2151 ATAGATTTGTTGATGATGCTTAAAGCACTAGCTTAATCTTGTGTTAGGC---GAGAGGAA 2207
OY 637 SerCyGlnIleuGlyIyIleuAapleuAenIleuIyrcIySerIleGluIleThrIle 656
Db 2208 GGTATATCAACTGCTGAACTACGAATTTAACTCCGTGTGCAATTTCAATCAACAT 2267
OY 657 LeuGluIyArGluValIyAaAapMetAapAlalyeGluIleAenIleuSerAlalyeGluIy 676
Db 2268 CTTAGAGAGAGGAAAGATATGAGGCAAAAGCAATTTATCTGCAAAAGCAAT 2327
OY 677 LeuIleSerIleuSerMetIyTrrpAapAapAapIyIyrcIyIleTrrpIyIleTrrpIy 696
Db 2328 CTACACTTTTAAACATGATGAGTGGAT-----AGACCAACAGATATGATCCGAA 2378
OY 697 LyIyValIyGluValIleuGluAlaIleuIyProIleSerAenIleuThrCyIyIleThrIleArG 716
Db 2379 GAAGTTAAAGGCTGTGAAGCCCTCAAAACCATCTCCATCTGAATTTTGAATCATTT 2438
OY 717 GlyPheArGlyIleArGleuProAapIyIleMetAenIleSerValIleuIyAaenValIy 736
Db 2439 GACTTGTGTGATTTCTGTCTCCGACTGATGATATCACTGATTTGAAGAAATGTTGTC 2498
OY 737 SerIleGluIleIleSerCyIyIyAenCySerCyIyIleuProPheGlyIyIleuPro 756

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Db      2499  TCTATTCTAATTAGCGGTTGGAAACGCTGAGCTTACCAACCTTTGGAGAGCTGCT 2558
Oy      757   CysLeuLysSerLeuGluLeuTrpArgGlySerAlaGluValGluTyrVal---AspSer 775
Db      2559  TGTCTGAAAGAGTCTGAGATTACAGAGCGGTCGTGGAGGTGGAGTATGTTGAAGATCTT 2618
Oy      776   GluPheProThrArgArgArgPheProSerLeuAlaGlyLeuAsnIleArgGluPheGly 795
Db      2619  GGATTCTCGACAAAGAAAGAAATTTCCATCCCTGAGAAAACTCATATGAGTGGCTTTGT 2678
Oy      796   AsnLeuLysGlyLeuLeuLysGlyGluGluGluGlnGlyCysProValLeuGluIle 815
Db      2679  AATCTGAAAGAGTCTCAGAGATGAAGAGACGAGCAATTCCTCCCTCTTGAAGAGATG 2738
Oy      816   GluIleLysCysCysProMetPheValIleProThrLeuSerSerValLysLeuVal 835
Db      2739  AAGATTTCGAGATGCGCTTATGTTTCTTTCCGACCTTTCTGTCTCAGAAATTTAGAA 2798
Oy      836   ValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu 855
Db      2799  ATTTGGGGGGAG---GCAAGATGCAAGAGGTTTGACCTCATATCTAATCTCAGACCTTT 2855
Oy      866   ThrSerLeuGlnIleArgTyrAsnLysGluAspAlaSerLeuProGluLysMetPheLys 875
Db      2856  ACATCCCTCAAGATTTTCACTAACACACAGAGACTTCACTCTGGAAGAGATGTTCAA 2915
Oy      876   SerLeuAlaAsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuPro 895
Db      2916  AACCTTGAAGATCTCATATCTAGTGTCTTTCTTGAGAAATCTCAAGAGCTGCT 2975
Oy      896   ThrSerLeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeu 915
Db      2976  ACCACCTCGCTAGTCTCAACAATTTGAAGTCTCGAGATTCGTTATGTTTACCCACTA 3035
Oy      916   GluSerLeuProGluGluValLysGlyLeuIleSerLeuThrGluLeuSerIleThr 935
Db      3036  CAGAGTCTCCCGAGAGAGCGCTGAGAGCTTATATCTCACTCAGAGAGTATTTGTGAA 3095
Oy      936   TyrCysGluMetLeuGlnCysLeuProGluLysGlyLeuGlnHisLeuThrAlaLeuThrAsn 955
Db      3096  CACTGTACATGCTAAATGTTTACCAGAGGATTTGCAGCACTTAACAACCTCTCAGAGT 3155
Oy      956   LeuSerValGluPheCysProThrLeuAlaLysArgCysGluLysGlyIleGlyGluAsp 975
Db      3156  TTAATAAATTCGGGAGATCTCAACAACGATCAAGCGGTGTGAAGAGGAATAGAGAAAGAC 3215
Oy      976   TrpTyrLysIleAlaHisIleProArgValPheIleTyr 988
Db      3216  TGGCACAATAATTCTCACATTCCTTAATGTGAATATATAT 3254

RESULT 7
US-10-360-522-49
; Sequence 49, Application US/10360522
; Publication No. US2003022125A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen V.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 3592
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum

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; FEATURE:
; NAME/KEY: mlec feature
; LOCATION: (1)-(3591)
; OTHER INFORMATION: /note="rpi-blb including intron sequence (position
; OTHER INFORMATION: 428-1106)"
US-10-360-522-49

Alignment Scores:
Pred. No.: 0
Score: 3638.50
Percent Similarity: 68.03%
Best Local Similarity: 61.65%
Query Match: 70.97%
DB: 17
Length: 3592
Matches: 754
Conservative: 78
Mismatch: 129
Indels: 262
Gaps: 9

US-10-647-268-2 (1-988) x US-10-360-522-49 (1-3592)
Oy      1   MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyGlu 20
Db      1   ATGGCTGAGCTTCATTCATCAAGTCTCTGACATCTCACTTCTTCTCAAGGGGAA 60
Oy      21   LeuGlyLeuIleLeuGlyPheLysAspGluPheGluLysLeuGlnSerThrPheThrThr 40
Db      61   CTGTATATGCTTTTCGGTTCACAGATGATCCAAAGGCTTTTCACAGCATTTTCTCA 120
Oy      61   IleGlnAlaValLeuGluAspAlaGlnLysGlnLeuLysAspLysAlaIleGluAsn 60
Db      121  ATTCAAGCGCTCTTGAAGATGCTCAGAGAGCACTCAACAACAGCCCTAGAAAAT 180
Oy      61   TrpLeuGlnLysLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysLys 80
Db      181  TGGTTGCAAAAACCAATGCTGCTACATATGATGATCATGATACATCTTGGAATATATA 240
Oy      81   ThrGluAlaProIleArgGlnLysLeuAsnLysTyrGlyCysTyrHisProAsnValIle 100
Db      241  ACCAAGGCC---ACAAGTTCTCCCACTGCAATATGCGCGTTATCATCCAAAGTTATC 297
Oy      101  ThrPheArgHisLysIleGlyLysArgMetLysLysIleMetGlyLysLeuAspValIle 120
Db      298  CTTTCCGTCACAAAGTCGGGAAAGATGAGCAACAATGATGAAAAAATTAAGGCAATT 357
Oy      121  AlaAlaGluAlaGlyLysPheHisLeuAspGluArgHisIleGluIleValAlaThr 140
Db      358  GCTGAGAAACAGAAATTTTCATTTGCGACGAAAAAATTGTAGAGACAGAGCTTTAGA 417
Oy      141  ArgGlnThrGly----- 144
Db      418  CGGAAACAGAGTCTCATCTTAATTAATAGTATTACACAACAATAAGTTATTAATTTT 477
Oy      144  ----- 144
Db      478  TGGCAATTATCAAAATTCAGAAAAAGGTTAATATATCATCATGCTTATGTAATAGTGA 537
Oy      144  ----- 144
Db      538  TATATACCTCTCGTTGATCTTTCATGTAATATATCTTGAATTCGGCAAGCTCAGAA 597
Oy      144  ----- 144
Db      598  TCAATTTATCAACCCCACTTTTAATATCTGATATCTTTAGAAATCACCCTGTCTAACT 657
Oy      144  ----- 144
Db      658  CATCACTAACCAATTCCTTGTGTAATCTTTCTTTTACCTATTAACCTTGAACACT 717
Oy      144  ----- 144
Db      718  CGATCCGTTTGTCTTTCTTAACAAGAGCTCAGAGAAAAAGAGTTTCTTCTATTCTG 777
Oy      144  ----- 144
Db      778  TTTCTGTGTGTCTGCACTTGGGTCTTAATCCATTAAAAACAGGAGATGTAATCCCA 837

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144 ----- 144
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144 ----- 144
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144 ----- 144
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144 ----- 144
Db TATATTGCGAAAAATATCTTATTTCTGTGTCTCTATAGATTGAATGTAAATA 1077
145 -----Phe-ValLeuAsnGluProGlnValTyrGly 154
Db TATTCTCATGTGACATTGCTTGACACAGTTCTGTATTAACGAAACGCGAGTTATGG 1137
154 YATGAspLysGluLysAspGluIleValLysIleLeuIleAsnAsnValSerAsnAlaGly 174
Db AAGAGACAAAGAAAGAAAGATGAGATGAAATCTTAATAACATGTTAGTACGCCA 1197
174 nThrLeuProValLeuProIleLeuGlyMetGlyLysLeuGlyLysThrThrLeuAlaGly 194
Db ACACCTTTCAGTCCCTCCCAATACCTTGATGGGGGATTAGSAAAAAGACCTTGCCCA 1257
194 nMetValIleAsnAspGlnArgValIleGluIlePheIleAspLysIleTyrIleCysVal 214
Db AATGCTCTTCATGACCGAGAGGTACAGCATTTCCATCCAAATAATGATTTGTGT 1317
214 LSeGluAspPheAsnGluLysArgLeuIleLysGluIleValGluSerIleGluGly 234
Db CTGGAAATTTGTAGAGAGAGGTAAATAAGCAATGTAGAACTATTAGAAAGAG 1377
234 sSer---LeuGlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAs 253
Db GCCACTACTTGGTGAATGAGACTTGGCTCCACTTCAAAAGAAAGCTTCAGAGTTCTGAA 1437
253 nGlyLysLysThrLeuLeuValLeuAspAspValTyrAsnGluAspGlnAspLysTyrAl 273
Db TGGAAAAAGATACCTGCTGTGTCTTAGATGATGTTTGGAAATGAAAGATCAACAGAACTGGGC 1497
273 aLysLeuArgGlnValLeuLysValGlyAlaSerGlyAlaSerValLeuThrThrThrAr 293
Db TAAATTTAAGACAGCTTGAAGGTGAGCAAGTGTCTCTGTCTTAACCACTACTCG 1557
293 GLeuGluLysValGlySerIleMetGlyThrLeuGlnProTyrGlnLeuSerAsnLeuSe 313
Db TCTTGAAAGAGTTGGATCAATTTATGGAAACATTGCAACCATATGAACTGTCAATCTGTC 1617
313 rGlnGluAspCysThrLeuLeuPheMetGlnArgAlaPheGlyIleGlnGluGluIleAs 333
Db TCAAGAAAGATTTGTGTGTGTCTCATGCAACGTCACTTGGACACCAAGAAAGAAATAA 1677
333 nLeuAsnLeuValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAl 353
Db TCCAAACCTTGTGGCAATCGAAGAGATGTGAAAAAAGTGTGTGTGTGCTCTAGC 1737
353 aAlaLysThrLeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnTyrGlnIleVal 373
Db AGCCAAACCTTGTGAGGTATTTTGTCTTCAAGAGAAAGAAAGAAAGCATGGGAACATGT 1797
373 LArgAspSerGluIleTyrLysLeuProGlnGluLysSerIleLeuProAlaLeuArg 393
Db GAGAGACAGCTCGAATTTGGAATTTCTCAAGATGAAGATTCTATTTGCGCGCTGAG 1857
393 GLeuSerTyrThrAsnLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPr 413
Db GCTTAAGTACATCAACTTCACTTGATTTGAAACAAATGCTTGTGTGTGTGTGCGGTGT 1917
413 eProLysAspThrLysMetGluLysGlyAsnLeuIleSerLeuTyrMetAlaIleGlyPr 433

1918 CCCAAAGATGCCAAAAGGAAAAAGAAAGCTAATCTCTCTGAGTGGCGCATGTGTT 1977
433 eIleLeuSerLysGlyAsnLeuGluLeuGluAsnValGlyLysAsnGluValTyrAsnGlyLe 453
1978 TCTTTTATCAAAAGAAAGATGAGAGCTAGAGATGTGGGCGATGAAAGTAAAGAAATT 2037
453 uTyrLeuArgSerPhePheGlnGluIleGluValLysSerGlyGlnThrTyrPheLysMe 473
Db ATACTTGAGTCTTTTTCGAAGAGATTGAAGTTAAAGTGTAAACTTATTTCAGAT 2097
473 hIleAspLeuIleIleAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerAs 493
2098 GCATGATCTCATTCATGATTTGGCAACATCTGTGTTTCACAAACACATCAACAGCAA 2157
493 nIleArgGluIleIleValGluAsnTyrIleIleIleMetSerIleGlyPheThrLysVal 513
Db TATCCGTAAATTAATAAACAAGTTACACATATGATGTCATTTGTTGCGCGAAGT 2217
513 lValSerSerTyrSerLeuSerHisLysGlnLysPheValSerLeuArgValIleAsnLe 533
2218 GGTGTTTTTTTACACTCTTCCCTTGGAAAAAGTTATCTCTTAAGAGTCTTAATCT 2277
533 uSerAspIleLysLysLeuLysGlnLeuProSerSerIleGlyLysLeuValHisLysArgTyr 553
Db AGGTGATTCGACATTAAATTAAGTTACCATCTTCATGAGATCTAGTACATTTAAGATA 2337
553 rLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGlnLeuCysLysLeuGly 573
Db CTTGAACTGTATGGC---AGTGGCATGCGTATGCTTCCAAAGCAGTTATCGCAACTTCA 2394
573 nAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCysCysLeuProLysGlyThr 593
2395 AAATCTGAAACTCTTGATCTCAATATATTGCCAACCAAGCTTTGTGTTGCCAAAAAGAAC 2454
593 rSerLysLeuGlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMe 613
Db AAGTAAACTGTGTAGTCCCAAAATCTTTACTGATGGTGAAGCAGTCACTGATGAT 2514
613 tProProArgIleGlySerLeuThrCysLysLysThrLeuSerArgPheValValGlyIle 633
Db GCCACCAAGATAGATCATTTGACATGCTTAAGCTCTAGCTCAATTTGTGTGGA-- 2572
633 eGlnLysLysSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGly 653
Db -AGGAGAAAGCTTATCACTTGTGAACTAGAACTTAATCTTAATGCTCAATTA 2631
653 uIleThrHisLeuGlnArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAl 673
Db AATCTCGATCTTGAGAGAGTGAAGAAATGATAGAGAACCAAAAGAACCAATTTATCTGC 2691
673 aLysGluAsnLeuHisSerLeuSerMetLysTyrAspAspAspGluArgProArgIleTyr 693
Db AAAAGGAGATCTGATCTTTTAACATCAGATTGG---AATAACTTTGACACCATATATA 2748
693 rGluSerGluLysValGluValLeuGluAlaLeuLysProHisSerLeuLeuThrCysLe 713
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Db TGAATCTGCTGTGTAGAAAGTCTAGAGTTACACTGGGGGCTGCGGAGTGGAGATAGT 2988
773 lAsp-----SerGlyPheProThrArgArgArgPheProSerLe 786

Db 2389 TGAAGAGTGAATTTGATGTTTCATTCGATTCCTCCCAAGAAATAGATTTCATCTT 3048
QY 786 uArGlyLeuAniIleArgIupheGlyAsnLeuIysGlyLeuLeuIysGlyGly 806
Db 3049 GAGGAAATCTATATATGAGACTTTGGTAGTCTGAAAGATTTGCAAAAAGAGAGAGA 3108
QY 806 uGlyGlyCysProValLeuGlyGlyIleGlyIleGlyCysProMetPheValIlePr 826
Db 3109 AGAGCAATTCCTGCTTGAAGATGATATTCACGAGGCTCTTTCTG----- 3160
QY 826 cThIeuserSerValIysIysLeuValIalSerGlyAspIysSerAspAlaIleGlyPh 846
Db 3161 -ACCTTTCT----- 3169
QY 846 eSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlyIleArgIyAsnIysGlyAs 866
Db 3170 -----TCTATCTTAGGGCTCTTACTTCCTCCAGAAATTCCTAATAAAGTAGC 3219
QY 866 pAlaSerLeuProGlyIleuMetPheIysSerLeuIleAsnLeuIysIyrlLeuAniIleSe 886
Db 3220 TACTTCATTCCTCCAGAGAGATGTTCAAAACCTTGCAAAATCTGCAAAATCTGCAATCTC 3279
QY 886 rPheIyrrheaSnLeuIysGlyLeuProThrSerLeuIleSerLeuAniAlaLeuIysHi 906
Db 3280 TCGGTGCAATATATCTCAAGAGCTCTACAGCTTGCTGATGCTGAATGCTTTGAAAAG 3339
QY 906 sLeuGlyIleHisSerCysIyrlAlaLeuGlySerLeuProGlyIleGlyValIysGlyLe 926
Db 3340 TCTAAAATTCATGATGCTGTGCGCACTAGAGAGTCTCCCTGAGAGAGGCTGAGAGGTTT 3399
QY 926 uIleSerLeuThrGlyIleuSerIleThrIyCysGlyIleuLeuGlyCysLeuProGlyIle 946
Db 3400 ATCTTCACCTCAAGAGTTATTTGTAACACTGTAACATGCTAAATGTTTACCGAGAGGG 3459
QY 946 YLeuGlyHisLeuThrAlaLeuThrAsnLeuSerValGlyPheCysProThrLeuAlaIly 966
Db 3460 ATTGAGACCTTAACACCTTCAAGATTTAAATTTGGGAGATTTTCCACAATGATCAA 3519
QY 966 sArgCysGlyIysGlyIleGlyIleAspTrpIyrlIysIleAlaHisIleProArgValPh 986
Db 3520 GGGGTGAGAGAGGAAATGAGAGAGACTGCGACAAATTTCTCATTCCTTAATGTGA 3579
QY 986 eIleIyrr 988
Db 3580 TATATAT 3586

RESULT 8
US-10-360-522-50
Sequence 50, Application US/10360522
Publication No. US20030221215A1
GENERAL INFORMATION:
APPLICANT: Allefs, Josephus J.H.M.
APPLICANT: Vossen v.d., Edwin A.G.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360,522
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02075565.8
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 5191
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence of
OTHER INFORMATION: 5.2 kb Sca I genomic DNA fragment of S.
OTHER INFORMATION: bulbocastanum BAC SPB 4 present in pRG2-b1b
US-10-360-522-50

Alignment Scores:
Pred. No.: 0
Score: 3638.50
Percent Similarity: 68.03%
Best Local Similarity: 61.65%
Query Match: 70.97%
DB: 17
Gaps: 9

US-10-647-268-2 (1-988) x US-10-360-522-50 (1-5191)

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Db 1251 CTGTGATTTGCTTTTGGTTTTCAGATGAGTTCCAAAGGCTTTCAAGCATGTTTCTACA 1310
QY 41 ILeGlyIleValLeuGlyIleAspAlaGlyIleIysGlyIleuIysAspIysAlaIleGlyAsn 60
Db 1311 ATCAAGCCGTCCTTGAAGATGCTCAGAGAGCACTCAACAAAGCCCTGAAAT 1370
QY 61 TrpLeuGlyIysLeuAsnAlaIleAlaIleTyrlAlaIleAspIleLeuAspGlyCysIys 80
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Db 1488 CCTTTCCTCACAAGTCGCGGAAAAGATGAGCAAGATGAAATGAAATGAAAGGCAAT 1547
QY 121 AlaIleArgIleIysPheHisLeuAspGlyIyrlThrIleGlyIleGlyIleValIleThr 140
Db 1548 GCTGAGAAAGAAATTTTTCATTTGACGCAAAAAATTTGAGAGACAAAGCTGTAGA 1607
QY 141 ArgGlyIleIyrl----- 144
Db 1608 CGGAAACAGGACTCATCTTAATTAATTAACAACAATTAATTAATTCATTTT 1667
QY 144 ----- 144
Db 1668 TGGCAATTAATCAATTCAGAAAAGGTTAATATATCATGTCATGTAATATGTGA 1727
QY 144 ----- 144
Db 1728 TATATACCTTCGTGTGATCTTTCGATCGAATATATCTTCAAAATCGGCAAGCTCAGAA 1787
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Db 1788 TCAATTAATCAACCCCACTTTTAATTAATCTGATATCTTTAGAAATCCACCTGTCTACT 1847
QY 144 ----- 144
Db 1848 CATCACTACCAATTCCTTTGTTGAATCTTTCTTACTATAACTTGGAACACT 1907
QY 144 ----- 144
Db 1908 CGATCCGTTTTCCTTTCTTAACAAGAGCTCAGAGAAAGAGTTTCTTATTTCTG 1967
QY 144 ----- 144
Db 1968 TTTCTGTGTGCTGACTTGAGTCTTAATCCATTAATAAAGGAGATGTATATCCA 2027
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Db 2028 ACGAGGATGAGCTTTCGAGAGCTGATGAATTTTGTCTAACAAAGAAAAAAGAGA 2087
QY 144 ----- 144

D 2088 TTAGACATGTTTTCTTTCATGATTAGCGGATTTCTTTCAGAGTGAAACATAGCG 2147
OY 144 ----- 144
D 2148 GATATATTGGACCAAAAGTAGAATGGGTATATATTTAAAGTATTTCTGATGAAACAGAG 2207
OY 144 ----- 144
D 2208 TATATGTGGGAAATAATCTCTATTTTCTGTGTCTCTAATGAGTTGATGAAATATA 2267
OY 145 -----Phe-ValLeuGlnGluProGlnValTyrGlu 154
D 2268 TATTCATGTCGACATTCCTTTCACCAAGGTCTGTATTTAACCGAAGCGGTTTATGG 2327
OY 154 YATGAspArgGluTyrAspArgGluIleValTyrIleLeuIleAsnValIleSerAsnAlaGlu 174
D 2328 AAGAGACAAAGAAAGATGAGATAGTAAATCTTAATTAACAATGTTAGTAGAGCCCA 2387
OY 174 nThrLeuProValIleuProIleLeuGlyMetGlyGlyLeuGlyTyrThrThrLeuAlaGlu 194
D 2388 ACACCTTTCAGTCCCTCCCAATTCCTGTAATGGGGGATTTAGGAAACAGACTCTTGCCCA 2447
OY 194 nMetValPheAsnAspArgIleValIleGluHisPheHisProGlySerIleTyrIleCysVal 214
D 2448 AATGGTCTTCATGACCAAGAGATTACTGACGATTTCCATTCCAAAATATGCAATTTGTGT 2507
OY 214 lSerGluAspPheAsnGluTyrAspArgLeuIleTyrGluIleValGluSerIleGluGluTyr 234
D 2508 CTGCGAAGATTTTATGAGAAAGGTTAATAAGCAATTTGAGATCTTATTTAGGAGAG 2567
OY 234 sSer----LeuGlyGlyMetAspLeuAlaProLeuGlnIleTyrLeuAspLeuLeuAs 253
D 2568 GCCACTACTTGGTGAATGAGATGACTTGCTCCACTCAAAAGAAAGCTTCAGAGAGTCTGAA 2627
OY 253 nGlyTyrLeuTyrLeuLeuValIleuAspAspValIleTyrAsnGluAspArgIleTyrAla 273
D 2628 TGGAAAAAGATATCTGCTGTCTTATGATGATGTTTGGAAATGAAAGATCAACGAAGTGGGC 2687
OY 273 AluLeuAsnArgIleValIleuTyrValIleSerGlyValIleSerValIleuThrThrThrAr 293
D 2688 TAATTTAAGACAGCTTGAAGGTTGAGCAAGTGTCTCTGTCTTCAACACACTACTCG 2747
OY 293 GluGluTyrValGlySerIleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSe 313
D 2748 TCTTGAAGAAAGTTGGATTCATTAATGGAACAATGCAACATATGAACTGTCAAAATCTCTC 2807
OY 313 rGlnGluAspCysTyrPheLeuLeuPheMetGlnArgAlaPheGluTyrHisGlnGluIleAs 333
D 2808 TCAAGAAAGATTGTTGTTGTTGTTTCATGCAACGTGCATTTGGAACCAAGAAATATAA 2867
OY 333 nLeuAsnLeuValAlaIleGlyTyrGluIleValIleTyrAspGlyGlyValProLeuAla 353
D 2868 TCCAAACCTTGTGCAATCGGAAGAGATGTGTGAAAAAAGTGTGTGTGCTCTAGC 2927
OY 353 AlaIleThrThrLeuGlyGlyIleLeuArgPheTyrAspArgGluGluArgGlnTyrPheHisVal 373
D 2928 AGCCAAACCTTGTGAGATATTTGTCTTCAAGAGAAAGAAAGAAAGCAATGGGAACATGT 2987
OY 373 lArgAspSerGluIleTyrPheLeuProGlnGluGluSerSerIleLeuProAlaLeuAr 393
D 2988 GAGAGACAGTCCGATTGGAATTTGCTCAAGATGAAAGTTCTATTTGCGCTGCGCTAG 3047
OY 393 GluSerTyrHisIleLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValAlaPhe 413
D 3048 GCTTATGATCAATCAACTTCATCTGATTTGAAACAAATGCTTTGCGTATTTGCGGTGTT 3107
OY 413 eProGlyAspThrGluMetGluTyrGlyAsnLeuIleSerLeuTyrPheAlaHisGlyPhe 433
D 3108 CCCAAAGATGCGCAAAATGAGAAAAGAAAGTAATCTCTCTCTGAGATGGCGCATGTTT 3167
OY 433 eIleLeuSerTyrGlyAsnLeuGluIleuGluAsnValGluTyrAsnGluValIleTyrAsnGluLe 453
D 3168 TCTTTATCAAAAGGAAACATGAGCTAGAGATGTGGCGCATGTAAAGTATGAAAGAAATTT 3227

OY 453 uTyrLeuArgSerPhePheGlnGluIleGluValTyrSerGlyGlnThrTyrPheTyrMe 473
D 3228 ATACTGAGGCTCTTTTTCAGAGAGATTGAAGCTTAAGATGATAAATCTTATTTCAACAT 3287
OY 473 nHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAlaSerThrSerSerSerAs 493
D 3288 GCATGATCTCATTCATGATTTGGCAACATCTCTGTTTTCACAAACATACAGACAGCA 3347
OY 493 nIleArgGluIleIleValGluAsnTyrIleHisMetMetSerIleGlyPheThrTyrVal 513
D 3348 TATCCGTGAATTAATAATAACACAGTACACACATATGATGTCATTTGTTGCGCGAAGT 3407
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D 3408 GGTGTTTTTTTACACTCTTCCCCCTTGGAATAATTTATCTCGTTAAGAGCTTAACT 3467
OY 533 uSerAspIleLeuLeuGlyGlnLeuProSerSerIleGlyAspLeuValHisLeuArgTyr 553
D 3468 AGTGATTCGACATTTAATAAGTTAACCATCTTTCATTTGAGAGATCATTAAGATA 3527
OY 553 rLeuAsnLeuSerGlyAsnThrHisSerIleArgSerLeuProAsnGlnLeuCysTyrLeuGlu 573
D 3528 CTTGAACCTGTATGAC--AGTGGCATGCGTATGCTTCCAAAGCAATTATGCAAGCTTCA 3584
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OY 613 rProProArgIleGlySerLeuThrCysTyrLeuTyrThrLeuSerArgPheAlaValGlyIle 633
D 3705 GCCACAAAGATAGATCATTTGACATGCTTAAACCTTAGCTCAATTTGTGTTGGA-- 3762
OY 633 eGlnTyrLeuSerCysGlnLeuGlyGluLeuArgAsnLeuAsnLeuTyrGlySerIleGlu 653
D 3763 -AGAAAGAAAGATTATCAACTTGGTGAACCTTAAGAAACCTTAATCTCTATGCTCAATTA 3821
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D 3822 AATCTCGCATCTTGAGAGAGATGAAGATGATTAAGCAAGCAAAAGCAATTTATCTGC 3881
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D 3882 AAAAGGAGATCTGATTTCTTTAAGCATGAGTTGG--AATTAATTTGGAACCAATATA 3938
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OY 753 rGluLeuProCysLeuLeuSerLeuGluLeuTyrArgGlySerAlaGluIleTyrVal 773
D 4119 TGATCTGCTGTGTCTAGAAAGCTTAGAGTACACTGGGGGCTCTGGAGATGTGAGATATGT 4178
OY 773 lAsp-----SerGlyPheProThrArgArgPheProSerLe 786
D 4179 TGAAGAGTGGATATGATGATGTTCAATTCGATTCGCCCAAGAAATTAAGTTTCCATCTT 4238
OY 786 uArgTyrLeuAsnIleArgGluPheGlyAsnLeuTyrGlyLeuLeuTyrGlyGluGly 806
D 4239 GAGGAAACCTTATATACGCACTTGTGTATGCTGAAGAGATTTGCTGAAGAAAGAGAGA 4298

145 ----- 145
Db 1017 TAAACTCAAAATGGAATGAACTTAATATTATGACATATATCATCTTTAATAA 1076
Qy 145 ----- 145
Db 1077 GCTACCAATTTAAATCATGATACAGAGAAACCAAAAAATTAGGGTGAATTATT 1136
Qy 145 ----- 145
Db 1137 GATTCTATGCTTATGACATGCTTCCCATCAACATCAAGAAAAATGTGCCAAAGTAT 1196
Qy 145 ----- 145
Db 1197 AAACGGTCGGTATATTGATTTGAATAAGTAAACAGAGATATACATTGGACTAAAGTA 1256
Qy 145 ----- 145
Db 1257 TAACAATAGTATATTGATCATTTTATGATCAAAATTCATGTGTTTTGGGAGAAAG 1316
Qy 145 ----- 145
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Qy 146 ----- 146
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Db 1497 AAAGAAAAGATGAGATAGTGAATTCCTAATAAACATGTTAGTGGCCCAAAACCTC 1556
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Db 1677 GATTTTGTAGAGAAAGGTGTGTAAGGCAATAGTAAATCTATTTGAAGGGAAGCCCTC 1736
Qy 237 GlyGlyMetAspLeuAlaProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysLys 256
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Qy 337 ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaAlaLysThr 356
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Db 2157 CCGATTTGAAATTTGCTCCAGAGTGAAGTTCTATTTGCTGCTGCTGAGCTTATGAC 2216
Qy 397 HisHisLeuProLeuAspLeuArgGlnCysPheThrYrCysAlaValPheProLysAsp 416
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Db 2637 AACCTAATGATTAATACATCTTCCATGAGATGATGATGATGATGATGATGATGATG 2696
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Db 2757 ACTCTTATCTCAATTAATGAGCTCTCTTCTGTTGCCAAACCAACAAAGTAATTT 2816
Qy 597 GlySerLeuArgAsnLeuLeuLeuAspGlyCysTyrGlyLeuThrCysMetProProArg 616
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Qy 697 LysValGluValLeuGluAlaLeuLysProHisSerLeuLeuThrCysLysThrIleArg 716
Db 3105 -----GAAAGTTCTTGAAGCCCTCAACCAACATCCATCTGAATATTTAGAAATCAAT 3158
Qy 717 GlyPheArgGlyIleArgLeuProAspTTPMetAsnHisSerValLeuLysAsnValVal 736

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Db 3567 ACTTCCTTGACATTAAGCAATTAACCTAGAAAGCTTACTTCCACGAAAGATGTTCAA 3626
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Db 3687 ACCAGCTGGGTAGTCAATGCTAATGCTTTGAAGAGTCTCAATTTGAATTTGTAACCACTA 3746
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Db 3747 GAGAGTCTCCCGAGAGAAAGGGGTGAAGGTTTAACCTTCACTCACAGAGTTGCTGTCAGT 3806
QY TyrCysGluMetleuGlnCysleuProGluGluIleGlnHisleuThrAlaLeuThrAsn 955
Db 3807 AACTGTATGATCTTAATAATGTTTACCGAGGATGTCAGACACTTAACGCTCTCACT 3866
QY leuSerValGluPheCysProThrleuAlaIleArgCysGlyIleGlyGluAsp 975
Db 3867 TTAAACATTAATCAATGTCATATGATTAATTCAGCGGTGAGAGAGAAATAGAGAAAGAC 3926
QY TrpTyrIleGlnIleAlaHisIleProArgValPheIleTyr 988
Db 3927 TGGCACAAAATTCCTCACATTCATATTTGACTCTAATAT 3965

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; LENGTH: 3899
; TYPE: DNA
; ORGANISM: Solanum bulbocastanum
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(3899)
; OTHER INFORMATION: /note="RG4-b1b"
US-10-360-522-53

Alignment Scores:
Pred. No.: 7,236-310 Length: 3899
Score: 3400.00 Matches: 717
Percent Similarity: 62.94% Conservative: 105
Best Local Similarity: 54.90% Mismatches: 159
Query Match: 66.32% Indels: 326
DB: 17 Gaps: 10

US-10-647-268-2 (1-988) x US-10-360-522-53 (1-3899)
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Db 1 ATGGCGAAGCTTTTCTTCAAGTTCTGCTAGAAATCTCACTTCTCATCGAGATAAA 60
QY 21 leuGlyleuIleleuGlyPheIysAspGluPheGluIleuGlnSerThrPheThr 40
Db 61 CTTGATGATTTTCGGTTTCGAAAGAAATGTGAAAGCTGTCGAGTGTGTTTCACA 120
QY 41 IleGlnAlaValleuGluAspAlaIleArglyGlnIleuysAspIleAlaIleGluAsn 60
Db 121 ATTCAAGCTGTCTTCAAGATGCTCAGAGAAAGCAATTTGAAGCAAGCAATTTGAAAT 180
QY 61 TrpLeuGlnIleuysAsnAlaAlaIleArglyGlnIleAspAlaIleleuAspGluCysIys 80
Db 181 TGTTCGCAAGAACCTCAATTCGCTGCTGCTATGAAGTTGATATATGGGGAATGAAA 240
QY 81 ThrGluAlaProIleArgGlnIleAsnlysglyArglyCysTyrHisProAsnValIle 100
Db 241 AATGAGGCA--ATAGATTTGACAGCTTCGATTAAGGTTTATCCACCGGATTAATC 297
QY 101 ThrPheArgHisIleValleuArgMetIleAsnIleMetGluIleuysAspValIle 120
Db 298 AATTTCCGTCACAAATTTGGAGAAAGATGAAAGATATGCGAATCTAGATGCAATA 357
QY 121 AlaAlaGluArgIleIysPheHisleuAspGluArgThrIleGluArgGln----- 137
Db 358 TCTGAGAAAGAGAGAGTTTCATTTCTTGAAAAAATTAACAGAGACAGCTGCGCT 417
QY 137 ----- 137
Db 418 GCTACGCGTGAAGACAGTGTGAGTACTGAGTAATTTAGCTTAATTAATTAATTTGT 477
QY 137 ----- 137
Db 478 TACCAATCATGTTTCAACCGTATCTTACATGAGATGCAATGGGGCTGGCGAGGT 537
QY 137 ----- 137
Db 538 TGAAGTGTGAGGTGTGTGGCGAACCCCAACTTTGAGTCACTAATAGTAGTACTTAA 597
QY 137 ----- 137
Db 598 ATTGTATAGATTGAACAAGTACAAACGCTCTACTTGTGTCTTATGCGATTATG 657
QY 137 ----- 137
Db 658 TCACTTAGATGATGATGTCTAATTGTTCACTTAATATGAGTTAAAGTTCACTGTC 717
QY 137 ----- 137
Db 718 AACCCAAAGTTGAGCGCGTGAATGTCAATTGATACCAAGTTAAAGCATATTTATG 777
QY 137 ----- 137

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Db 778 AATTATGCTTAATATGATTCATTTTGTATGATCTGCCAAAATANGTCTACTG 837
Qy 138 -----ValAlaThrArgGln 142
Db 838 AAAGTTTAACTTAGTGTGATCTGCTATTGAAAGTGAATTTTGTGTGC-ACATAACAA 896
Qy 142 ----- 142
Db 897 TGCATAGGCTCTGATTCATTTTTCATTAACCTTTGTAGACGATTTTCTTATCGAA 956
Qy 142 ----- 142
Db 957 TTTTACTGTATAAATGCAAAAAGCAAAAGAAATTAAGAAATATACAGAGCTGACTTCTTC 1016
Qy 142 ----- 142
Db 1017 ATAGTATCTATCATATATAAAAAACATTGATTAAGATATGAGGCTTTTAATTAAC 1076
Qy 142 ----- 142
Db 1077 AAATTTGTAGTTAAACAGTTCTGTGGAGAGATTAGATACAGTGATATATCTA 1136
Qy 142 ----- 142
Db 1137 GAAGTTTAAATTAATAAATTAGCAAAATATACGGGCTGGGGCGGTTGAAAAACAGCA 1196
Qy 142 ----- 142
Db 1197 ACTTTGCAAGGCTGGCGGGTGCAGAAATCTTTGCAAGTTGTGTGGGTTGCCCTGCACCA 1256
Qy 142 ----- 142
Db 1257 CCCAATCTGCATTCCTGTCTAATATGTTTGTGTATTAATCTGTGACTCATCTT 1316
Qy 143 -----ThrGlyPheValIleu 147
Db 1317 AATGAGCTCAATGTATCAAAATCTTTGTGTCTGCACATTACTTGCAGGTTTGTGTATA 1376
Qy 148 AaenGluProGlnValTyrGlyArgAspIleGluAspGluIleValIleIleuIle 167
Db 1377 ACTGAACCAAAAGTCTACGAAAGGAGCAAAAGAGAGATGATGATTAATAATCTGTATA 1436
Qy 168 AaenValSerAsnIleGlnThrLeuProValIleuProIleLeuGlyMetGlyIleu 187
Db 1437 AACATGTATATGTTGGCGAAGAACTTCAGTCTTCCTATATATGGATGGGGGAGCTA 1496
Qy 188 GlyIleThrThrLeuAlaGlnMetValPheAsnAspGlnArgValIleGlnHisPheHis 207
Db 1497 GGAAGAAGCAGACCTGGCCCAATATGATCTTCAACGATGAGAGATTAACATACTTCAAT 1556
Qy 208 ProIleIleThrIleCysValSerGlnAspPheAsnGluIleValIleGlnIle 227
Db 1557 CCCAAATATGAGGTTGTGTCTCAGATATTTGATGAGAGAGATTATTAACAATTT 1616
Qy 228 ValGlnSerIleGlnGluIleValSerIleuGlyIleMetAspLeuAlaProLeuGlnIle 247
Db 1617 ATAGAAATATGAAAGAGTTCTCCTCATGTGAGAGACTTGGCTTCATTCAAGAAAG 1676
Qy 248 LeuArgAspLeuLeuAsnGlyIleValIleThrLeuValIleAspAspValTrrAsnGlu 267
Db 1677 CTCACAGGATTAATGAAAGCAATACCTGCTTGAAGATGATGATTTGGAATGAT 1726
Qy 268 AspGlnAspIleValIleValLeuArgGlnValIleuValIleValIleValIleSer 287
Db 1737 GATCTAAGAAAGTGGCTTAAGTAAAGCAAGCTTAACTGTGAGCAAGAGGCTTCT 1796
Qy 288 ValIleuThrThrThrArgLeuGluIleValIleSerIleMetGlyThrLeuGlnProIle 307
Db 1797 ATTCTAGCTACTACTCGTCTTGAAGAGTTGATCAATTAAGGAGCTTGCAACCATAT 1856
Qy 308 GluLeuSerAsnLeuSerGlnGluAspCysThrLeuLeuPheMetGlnArgValIleGly 327
Db 1857 CATTTGTCNAATTTGTCTCCACATGATATGTTACTTTTGTATTAGCAACGGCATTTGGG 1916

Qy 328 HisGlnGluIleLeuAsnLeuValAlaIleGlyIleGluIleValIleIleCys 347
Db 1917 CAACAAAAGAGCAAAATCTTAATCTTAGTGGCCATTGGAAAGAGATTTGTGAAGAAATGT 1976
Qy 348 GlyGlyValProLeuAlaAlaIleThrLeuGlyIleLeuArgPheIleArgGluIle 367
Db 1977 GGTGTGTGCTTATGAGAGCCCAAGACTTGTGTGTCTTTTACCTTCAAGAGAGAGAG 2036
Qy 368 ArgGlnTrpGluHisValArgAspSerGluIleTrpIleuProGlnGluIleSer 387
Db 2037 AGTAAATGGGAACATGTGAGAGATTAATGATTTGGAGTGTGCTTCAAGATGAAGATTTCT 2096
Qy 388 IleuProAlaLeuArgLeuSerTyrHisIleuProLeuAspLeuArgGlnCysPhe 407
Db 2097 ATTTGCTGTCTTAAGATGATTAATCACTTCACTTCCACTGATTTGAGCAATGCTTT 2156
Qy 408 ThrTyrCysAlaValPheProIleAspThrGluMetGluIleGlyAsnLeuIleSerIleu 427
Db 2157 GCGTATTTGTCAGATTTCCCAAGAGCACCAAAATGATTAAGAAATTCATTAATCTCTC 2216
Qy 428 TrpMetAlaHisGlyPheIleLeuSerIleGlyAsnLeuGluIleGlnValIleGlyAsn 447
Db 2217 TGGATGGCGCATGGTCTTTTATCAAGGGAAATCTTGAGCTTGAAGATGTGGTAAAT 2276
Qy 448 GluValTrpAsnGluLeuTyrLeuArgSerPheGlnGluIleGlyValIleSerGly 467
Db 2277 GAAGTATGGAATGAATTAATTAATCTTGAAGCTTTCTTCCAAAGAAATGAAGCTTAATCGGCT 2336
Qy 468 GlnThrTyrPheIleMetHisAspLeuIleHisAspLeuAlaThrSerLeuPheSerAla 487
Db 2337 AATCTTATTTCAAGATACATGATCTAATCATGATTTGGCTACATCTGTTTCCGCA 2396
Qy 488 SerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrIleHisMetMetSer 507
Db 2397 AGCGCATCATGCGGCATATCCCGAAATGAATGTCAAATTAATGAATACATACATGCTCC 2456
Qy 508 IleGlyPheThrIleValIleSerSerTyrSerIleuSerHisIleuGlnIlePheValSer 527
Db 2457 ATTGCTTCCGTGACAGTGTGTCTTCTTACTCTTCCCTTCCCTTGAAGAAATTTGTCTCG 2516
Qy 528 LeuArgValLeuAsnLeuSerAspIleIleValIleGlnLeuProSerSerIleGlyAsp 547
Db 2517 TTAAGGCTGCTTAATCAATGAATCTCAAAATCTGAGCAATTAACGCTTCCATTGAGAT 2576
Qy 548 LeuValHisLeuArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsn 567
Db 2577 CTATTACATTTAAGATACCTGAGACTGTCTTGCAT--AACTTCCGTAGCTTCCAGAG 2633
Qy 568 GlnLeuCysIleLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCys 587
Db 2634 AGGTGTGCAAGCTTCAAAATCTTCAGACTTGAAGTACATTAATGTCTACTCACTTAAT 2693
Qy 588 CysLeuProIleGluThrSerIleValIleGlySerIleuArgAsnLeuLeuAspGlyCys 607
Db 2694 TGTGTGCAAAACAACAATTAATTAAGTCTCGAATCTTGTGTGATGCTGT 2753
Qy 608 TyrGlyLeuThrCysMetProProArgIleGlySerLeuThrCysIleuIleThrLeuSer 627
Db 2754 ---CAATGACTTCTACTCCACCAAGATGAGATTGTGACATGACCTTAAGACTTACGT 2810
Qy 628 ArgPheValIleGlyIleGlnIleValSerCysGlnLeuGluIleGluLeuArgAsnLeuAsn 647
Db 2811 TTTCTTATTTGTGGA--AGCAAGAAAGGTTATCACTTGTATACTGAAAAACTTAAT 2867
Qy 648 LeuTyrGlySerIleGluIleThrHisLeuGluArgValIleAsnAspMetCysAlaIle 667
Db 2868 CTCGGGGGCTCAATTTCAATCAACAACCTTGAGAGGTGAAGACATACGATGCA--- 2924
Qy 668 GluAlaAsnLeuSerAlaIleGluAsnLeuHisSerLeuSerMetCysTrpAspAsp 687
Db 2925 GAAGCAATTTATCTCAAAAGCAAAATCTGCAATCTTTAAGCATGAGTTAGATTAACGAT 2984

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Oy 688 GlnarProarglleTyrgInuSerGluuylValGluValleuGlnAlaLeuylsProHis 707
Db 2985 ---GGACCAAAACAGATATGAATCCAAAGAGTTAAAGCTTAAAGCACTCAAAACACAC 3041
Oy 708 SerAnleuThrCysLeuThrIleArgGlyPheArgGlyIleArgLeuProAspTyrMet 727
Db 3042 CCCATCTCGAAATATTATAGATCATCTTCCTCGAGAGATTCCTGTTTCCAGCTGGATA 3101
Oy 728 AsnHisSerValLeuylsAsnValValSerIleGluIleIleSerCysGlyAsnCysSer 747
Db 3102 AATCACTCAGTTTGGAGAGAGTCATCTCTGTAGAAATTAAGTGCAGAAACCTGCTTG 3161
Oy 748 CysLeuProPhePheGluLeuProCysLeuylsSerLeuGluLeuTyrArgGlySer 767
Db 3162 TGCTTACCACTTGGAGAGCTTCTGTCTAGAAATCTAGAGTTCAAAAGGAGTCT 3221
Oy 768 AlaGluValGluTyrValAsp-----SerGlyPheProThrArgArgArg 782
Db 3222 GCGAGGTGGAGTATGTGAAGAGAGTATGTCATCTTAGATTCTCCAGAAAGAGAGC 3281
Oy 783 PheProSerLeuArgGlyLeuAsnIleArgGluPheGlyAsnLeuylsGlyLeuLeuyls 802
Db 3282 TTTCCATCTCCGAAAGAACTTCGTATATGTTTCGAGTTGAAAGGCGTATGATAA 3341
Oy 803 LysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 822
Db 3342 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3401
Oy 823 PheValIleProThrLeuSerSerValIlySylsLeuValValSerGlyAspIlySerAsp 842
Db 3402 TTTGTTTTCACACCTTCTCTCTGTCAGAAATTAAGAGTTCAAGGAGAC--ACAAC 3458
Oy 843 AlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeuThrSerLeuGlnIleArgIyr 862
Db 3459 ACTAGAGTTTGAAGCTCCATATCTATCTTACACTTACTTCTCCCTCGAGCTGTCT 3518
Oy 863 AsnIlySylsAspAlaSerLeuProGluGluMetPheIlySerLeuAlaAsnLeuylsTyr 882
Db 3519 AACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3578
Oy 883 LeuAsnIleSerPheIlyPheAsnLeuylsGluLeuProThrSerLeuAlaSerLeuAsn 902
Db 3579 TTGAGTTTCTTGGACTTCAGAAATCTCAAGATCTGAGCTGACAGCTGCTGCTCAT 3638
Oy 903 AlaLeuylsLeuGluIleIleSerCysTyrAlaLeuGluSerLeuProGluGluGly 922
Db 3639 GCTTTGAAGCGTCTCCAAATTGAAGTTGTGACTGACTGAGAGAGTTCCCTTAACAAG 3698
Oy 923 ValIlySylsLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeuGlnCys 942
Db 3699 CTAGAGAGTTTAATCTTCACTCACTCACTGAGTTGTTTAAATCTGTAAGATGCTAAAG 3758
Oy 943 LeuProGluGlyLeuGlnIleLeuThrAlaLeuThrAsnLeuSerValGluPheCysPro 962
Db 3759 TTACCGAGAGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3818
Oy 963 ThrLeuAlaIlyArgCysGluIlySylsIleGlyIlyAspTyrTyrIleAlaHisIle 982
Db 3819 GAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3878
Oy 983 ProArgValPheIleTyr 988
Db 3879 CCAATCTGATATTTCAT 3896

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; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 60/407,100
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3222
; TYPE: DNA
; ORGANISM: Solanum Bulbocastanum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)..(528)
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (529)..(690)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (691)..(3219)
; US-10-647-268-7

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Alignment Scores:

Pred. No.:	1,66-304	Length:	3222
Score:	3342.00	Matches:	681
Percent Similarity:	74.98%	Conservative:	116
Best Local Similarity:	64.06%	Mismatches:	180
Query Match:	65.18%	Indels:	86
DB:	18	Gaps:	13

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US-10-647-268-2 (1-988) x US-10-647-268-7 (1-3222)
Oy 1 MetAlaGluAlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnIlyGlu 20
Db 58 ATGCTGAGAGCTTTCCTTCAAGTTCTGTCAGCAATATCTCTTTCATCTCAAGGGGAA 117
Oy 21 LeuGlyLeuIleLeuGlyPheIlyAspGluPheGluIlySylsLeuGlnIleSerThrPheThr 40
Db 118 CTTGTATTTGCTTTTGGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 177
Oy 41 IleGlnAlaValLeuGlnAspAlaGlnIlySylsGlnLeuylsAspIlySylsAlaIleGluAsn 60
Db 178 ATCCACTGTGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 237
Oy 61 TyrLeuGlnIlySylsLeuAsnAlaAlaIleTyrGluAlaAspAspIleLeuAspGluCysIys 80
Db 238 TGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
Oy 81 ThrGluAlaProIleArgGlnIlySylsAsnIlySylsTyrGlyCysTyrHisProAsnValIle 100
Db 298 AATGAGGCA--GCAAGATTCATCACTCTTATTAAGGTATATTCATCCAAAGATCATC 354
Oy 101 ThrPheArgHisIlySylsIleGlyIlyArgMetIlySylsIleMetGluIlySylsAspValIle 120
Db 355 ATTTTTCGTTCAAGAGCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
Oy 121 AlaAlaGluArgIleIlyPheHisLeuAspGluArgThrIleGluArgGlnValAlaThr 140
Db 415 GCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
Oy 141 ArgGln----- 142
Db 475 CGTGAACAGGTGCTCATCTTAAACTGTGTTAGCCAGAGTACTTAATAGCTTAGTTT 534
Oy 142 ----- 142
Db 535 TATATTCATCTTTTGTAGTTACAGAGTTCTATACATGTGTTCATGTGAGCCCTTCC 594
Oy 142 ----- 142
Db 595 TTGTGCTTTTGTGTTGCAAAATCTTCTATATTCCTGTGACTCTTTTAGTGAAGT 654
Oy 143 -----ThrglyPheValLeuAsnGluPro 150
Db 655 TGAATTTAATAAATTTGTGTGCTGATGCTTGGAGAGAGGTTTGTGTTAGCAGAGCA 714

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[illegible]

OY	510	PheThrValValIserSerTySerIuseSerHisLeuGlnIleuPheValSerLeuArg	529
Db	1792	TTTGCTGAAGTGGTGCCTTCTTATTCCTCTTAATCTTTAAAGGTTGTCTCGGTAGG	1851
OY	530	ValLeuAsnIuseSerAspIleTyLeuIleuysGlnIleuProSerSerIleGlyAspLeuVal	549
Db	1852	GTTCTGTGATAGAAATTTTCAAGTTGATCAGTTATTCATCTTCCATCGAGATCTATA	1911
OY	550	HisLeuArgTyLeuAsnIleuSerGlyAsnThrSerIleArgSerLeuProAsnGlnIleu	569
Db	1912	CATTAAAGTTGTGAACTTGCGCTGGGC---AGTACGATTCGTACCTTCCAAAGAGTTA	1968
OY	570	CysTyLeuGlnIleAsnLeuGlnThrIleuAspLeuHisIleGlyCysHisSerIleuTyCysLeu	589
Db	1969	TGCAGGCTTCAAAATTCGCAGACACTGTGATATATCATGTTGTTTCTCATCTTTATATT	2028
OY	590	ProIlysgIuThrSerIleTyLeuGlySerIleuArgAsnIleuLeuAspGlyCysTyGly	609
Db	2029	CCAAACCAAAATATTAATTTAGTACGTCTTGAATACTTGCTTCACTGCTGTTGCCA---	2085
OY	610	LeuThrCysMetProProArgIleGlySerIleuThrCysLeuIlysnIleuSerArgPhe	629
Db	2086	ATACTTCTAGTCACACCAAGATAGATCATTTGACATGCTTAGACCTAGATTACTTT	2145
OY	630	ValValGlyIleGlnTyIlySerSerCysGlnIleuGlyIleuAsnIleuAsnIleuTy	649
Db	2146	ATTTTGGGC---GAGAGGAAAGGTTATCATCTTGTTAACTACGGAATCTTAAGCTTCAT	2202
OY	650	GlySerIleGlnIleThrHisIleuGlnArgValIlyAsnAspMetAspAlaTyGlnAla	669
Db	2203	GGTTCACTTTCATCTCATCTTGTAGAGATGAGTAGAGTAAACGATGCCAAAGAAAGCT	2262
OY	670	AsnIleuSerAlaTyGlnAsnIleuHisSerIleuSerMetIlyStrAspAspGluArg	689
Db	2263	AATTATCTACCAAAACAAATTTGTACATATTATGATGATGAGTTGG-----GATTATAGG	2316
OY	690	ProArgIleTyArgIuSerGluTy-----ValGluValLeuGlnAlaLeuIlyPro	706
Db	2317	CCATATGGAATATGATACAGAAACAAATTTGGATGATGAAAGAGCTTGAAAGCCCTCAACA	2376
OY	707	HisSerAsnIleuThrTyIleuThrIleArgGlyPheArgGlyIleArgLeuProAspTrp	726
Db	2377	CACCTCAACTGAAATACATTAAGCTATTTGGCTTCAGAGGTTTTCATTTCCAAATTGG	2436
OY	727	MetAsnHisSerValLeuTyAsnValValSerIleGlnIleIleSerCysIlyAsnCys	746
Db	2437	ATGAGGCTTCGGTTTGAAGAAATGTGTCTCATTTGAA---ATTGAATGGAAGAACTGC	2493
OY	747	SerCysLeuProProPheGlyGlnLeuProCysLeuIysSerLeuGlnIleuTyTrpArgGly	766
Db	2494	TGCGGCTTACACCATTTGGAGAGCTCCTTGCTGAGAAAGTCAAAAGTTATCAACGGA	2553
OY	767	SerIleGlnValGlnTyTrpVal-----AspSerGlyPheProThrArgArgPhePro	784
Db	2554	TCTGCGAGGGGAGATATTTGAAGAGAGATGATGATTCACA---TTAAAGTTCCCA	2610
OY	785	SerIleuArgTyLeuAsnIleArgGluPheGlyAsnIleuTyGlyLeuLeuTyIlyGln	804
Db	2611	TACTTGAAGACACTGCTATTTGAAAGTTTCCAAATCTGAAAGACCTGCTGAGAAAGGAA	2670
OY	805	GlyGlnGlnGlnCysProValIleuGlnGlnIleGlnIleTyCysCysProMetPheVal	824
Db	2671	GGAGAAAGAAATTCCTCATGCTTGAAGAAATGGAAATTTGGCATTCCTCATGTTGTT	2730
OY	825	IleProThrIleuSerSerValTyIlyValLeuValValSerGlyAspTybSerAspAlaIle	844
Db	2731	TTTTCAGCATTTCTTCTGTGCAAGAAATGATGTCTGGGGGGGAA---ATAGATGCAGCA	2787
OY	845	GlyPheSerSerIleSerAsnIleuMetAlaLeuThrSerLeuGlnIleArgTyArgAsnIly	864
Db	2788	AGCTTATAGCTCCATATCTTAAGCTTACACCTTACAGCTCTCTCTATTTGATCATTACTTT	2847
OY	865	GluAspAlaSerLeuProGlnGlnMetPheIlySerIleuAlaAsnIleuTyIlyLeuAsn	884

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Db      2848  GAACCAACACCTCCCAAGAGAGATGTTCAAGCCCTGTAAATCTTGACTCTTACGC 2907
Qy      885  ILeSerPheTyRPhaenLeuLeuGluLeuProThiSerLeuAlaSerLeuAsnAlaLeu 904
Db      2908  ATTATATCTTCAAAAACTCAGAGAGTTGCCAAGAGCCCTGGGTAGCTCAATGCTTTG 2967
Qy      905  LysHisLeuGluIleHisSerCysTyRAlaLeuGluSerLeuProGluGluGlyValLys 924
Db      2968  AAGGTCTAAAAATTCATTATGTGTACCGACTAGAGACTCTCCCGAACAAGGATGGAA 3027
Qy      925  GlyLeuIleSerLeuThiGlnLeuSerIleThiTyRHisGluMetLeuGlnCysLeuPro 944
Db      3028  GGGTTAACTTCACTCAGCACTTATATGTTCAAAACTGTGAGTCTTAAATGTTTACT 3087
Qy      945  GluGlyLeuGlnHisLeuThiAlaLeuThiAsnLeuSerValGluPheCysProThiLeu 964
Db      3088  GAGGATTTGCAGCACTTAAGAGCCCTCACTGTTACAAATTTATGCTGTCCAGCATTTG 3147
Qy      965  AlaTyRArgCysGluLysGlyTyrLeuGluAspTyrTyrLeuIleAlaHisGlyProArg 984
Db      3148  AAAAGCGGTGTGCGAAGGGGATAGAGAGAGTGGCAAAATTTGCTCACAATTCCTAAT 3207
Qy      985  ValPheIle 987
Db      3208  GTAGATATT 3216

RESULT 12
US-10-437-79971
; Sequence 79971, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79971
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1
US-10-437-963-79971

Alignment Scores:
Pred. No.: 3 76e-132 Length: 3333
Score: 1517.00 Matches: 396
Percent Similarity: 51.23% Conservative: 187
Best Local Similarity: 34.80% Mismatches: 345
Query Match: 29.59% Indels: 210
DB: 18 Gaps: 34

US-10-647-268-2 (1-988) x US-10-437-963-79971 (1-3333)
Qy      4  AlaPheLeuGlnValLeuLeuAsnLeuThi-----CysPheIleGln 18
Db      25  GCCTTATGCAAAACCTCTTCAGAAATGTCAAGAGCAACCCCTGATCATTTTCATATCT 84
Qy      19  GlyGluLeuGlyLeuLeuGlyPheLeuAspGluPheGluLeuLeuGlnSerThiPhe 38
Db      85  TGGAGA-----GGCATATCATGTGCATAGAGAGCCCTCTTCCACACCTG 129
Qy      39  ThrThiLeuGlnAlaValLeuGluAspAlaGlnIleLysGlnLeuLysAspLysAlaIle 58

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Db      130  TCTCAGTTACAGGCTTCTCTTGACGACGCTGAGAGAACAGATGTGACATGCAATCTTG 189
Qy      59  GluAsnTrpLeuGlnIleLysLeuAsnAlaAlaIleTyRAlaAspAspIleLeuAspGlu 78
Db      190  AGGGATGGCTTACGAAGCTCAAGATATCGCTATCGACTTATATCTGCTGGACAGC 249
Qy      79  CysLeuThiGluAlaProIleArgGlnLysAsnLysTyRLeuCysTyRHisProAsn 98
Db      250  TATTACGCCAAAGT---ATGGCATGAAGCAGAGCAG-----GTGATATTCCACACA 300
Qy      99  ValIleThiPhe-----ArgHisLysIleGly 107
Db      301  AAGGCAAGTTTCTTTCTTCTCTTCTTCTTGAAGATCTGACAGCAAGCTGATAGCAAG 360
Qy      108  LysArgMetLysLysIleMetGlnLysLeuAspValIleAlaIleArgIleLysPhe 127
Db      361  CATATGATTAACTCATATTGGAGAGATTGATATGATTCGCAABAAGCCGACACAT 420
Qy      128  HisLeuAspGluArgThiIleGluArgGlnValAlaIleThiArg-----GlnThiGly 144
Db      421  GGGCTCCAGATGATATGTGAATGAGCGGTATGATCTCAGAGGCTCCGCAATAGT 480
Qy      145  PheValLeuAsnGluProGlnValTyrGlyArgAspLysGlnLysAspGluIleValLys 164
Db      481  TCTCTTGATATGATTTGGCTGTATTTGTAGAGAGAGGACAGAGAAATGTGAGG 540
Qy      165  ---IleLeuIleAsnValSerAsnAlaGlnThiLeuProValLeuProIleLeuGly 183
Db      541  CTGGTGTCTCTGTATATGACATATATCTCGCAACTATATGTGATTCAGATTGTGGC 600
Qy      184  MetGlyLysLeuGlyLysThiThiLeuAlaGlnMetValPheAsnAspGlnArgValIle 203
Db      601  ATGGGTGGCTGGTGAATAACTCTTATGCTGATGCTGATGATGATGATGATGATGATG 660
Qy      204  GluHisPheHisProLysIleTrpIleCysValSerGlnAspPheAsnGlnLysArgLeu 223
Db      661  GAAACATTTGACTTGAGAGATCTGATCTTATGATCTTAAAGCTTTTGTATGAGAAACCT 720
Qy      224  IleLysGluIleValGlnSerIleGlu---GlnLysSerLeuGlyGlyMetAspLeuAla 242
Db      721  ACACAAAGAACTCTTGAGGCTTGACTGATGACCAATCTGTGCTAGTACTAATCATGAT 780
Qy      243  ProLeuGlnLysLysLeuArgAspLeuLeuAsnGlyLysTyRLeuLeuValLeuAsp 262
Db      781  ATGCTACAGAAACACTCTCCAGAGTATTTGGGGGCAAGAGTACTGCTGTGTGGAT 840
Qy      263  AspValIleTrpAsnGluAspGlnAspLysTrpAlaLysLeuArgGlnValLeuLysValGly 282
Db      841  GATGCTGAAATGAGACCTTGATTAATGGCAGCGCTATAGAGAGCCTTATATTCAAGA 900
Qy      283  AlaSerGlyAlaSerValLeuThiThiArgLeuGlnLysValGlySerIleMetGly 302
Db      901  GGGTTGGAACAGATATAGTGTGATCAATCAGAAATGAGAAATGTGGCAGAAATCATGGGA 960
Qy      303  ThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnGluAspCysTrpLeuLeuPheMet 322
Db      961  GGAATAGAGCCCTTACAGATTACAGAAATCATCAATGATGTGACAGCTGCTGTATTCAG 1020
Qy      323  GlnArgAlaPhe-----GlnHisGlnGlnGlnIleAsnLeuAsnLeu 336
Db      1021  AGCCATGATTTAGGAGATGTGACTGACAGCGCAGATCCGGAG-----TTG 1065
Qy      337  ValAlaIleGlyLysGluIleValLysLysCysGlyGlyValProLeuAlaLysThi 356
Db      1066  GAGGGGATAGGAATGAAATGTGAAAGAGCTGAAGGGATTTGCCCTTGTCAACAAAGCA 1125
Qy      357  LeuGlyGlyIleLeuArgPheLysArgGlnGluArgGlnTrpGlnHisValArgAspSer 376
Db      1126  TTAGGAGAGCTCTCTTTTGGCAAAACAGATGAAGAGGTGAAGAGACATCTCGAAAT 1165
Qy      377  GluIleTrpLysLeuProGlnGlnLysSerIleLeuProAlaLeuArgLeuSerTyr 396

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Db 1186 GACATATGGAGTTACCGGAGATTAAGAAATACATCTGCCAGCCCTCACTTAAGTTAC 1245
OY HisHisLeuProLeuApLeuArgLincysPheThrTyrcysAlaValPheProLysAsp 416
Db 1246 AACCATTTACCAACCATCTTAAGAGATGCTTGGATCTGTCTGTATATCTTAAGAT 1305
OY 417 ThrGluMetGluLysGlyAsnLeuIleSerLeuTPMetAlaHisGlyPheIleLeuSer 436
Db 1306 TATATGTTCAAGAGAGAGAACTGGTTAAGATCTGGCTAGACACTTGGTTTCAGACAG 1365
OY 437 LysGlyAsnLeuGluLeuGluAsnValGlyAsnGluValTPAsnGluLeuTyrlLeuArg 456
Db 1366 TCTAGAAAGAGAGAGATGAAGATCTGAAATGCATCTTAAGATTTTAAGCAGG 1425
OY 457 SerPhePheGluGluIleGluValLysSerGlyInthrTyrcysPheLysMetHisAspLeu 476
Db 1426 TCTTTCTTCAGCCCTATAGAG-----AATACTATGTATGATCATATGCA 1470
OY 477 IleHisAspLeuAlaThrSerLeu----- 484
Db 1471 ATGCACGACCTTGCAAAATCTATCTCCATGGAGAGCTGGACCACTTAAGATTAGGAGA 1530
OY 484 ----- 484
Db 1531 AGACATGACAAATGCCATTAAAGACCCGTCATCTTTCATTCATGACAGAGATGCCAAGTGC 1590
OY 485 -----PheSerAlaSerThrSerSerSerAsnIleArgGluIleIleValGluAsnTyrc 502
Db 1591 ATGCATCTCAATCCATCTGTATGGGTTTAAAGAGAGACCTGACATTA----- 1641
OY 503 IleHisMetMetSerIleGlyPheThrLysValLysSerTyrcysSerLeuSerHisLeu 522
Db 1642 ATCCAT-----GGATACAGATCAAGAGATGCTCAATGCCCTCATGCTATTT 1689
OY 523 GluLysPheValSerLeuArgValLeuAsnLeuSerAspIleLysLeuLysGluLeuPro 542
Db 1690 ATGAAACCTTGATATCTTATAGAGCTGTATATGATGCATGACCAAGGCTTAAAGAGTTACCA 1749
OY 543 SerSerIleGlyAspLeuValHisLeuArgTyrcysLeuAsnLeuSerGlyAsnThrSerIle 562
Db 1750 GAATCTAATAGGAACTTAACCAACTGCGCTTCATGATCTCAGT---AGCCTGAATATC 1806
OY 563 ArgSerLeuProAsnGlnLeuCyrcysLysLeuGluAsnLeuGlnThrLeuAspLeuHisGly 582
Db 1807 GAACATTATCCAGCATCTCTTGTATAGCTCTATATCTTGCAAAATCTAAAGCTGATGAC 1866
OY 583 CysHisSerLeuCyrcysLeuProLysGluInthrSerLysLeuGlySerLeuArgAsnLeu 602
Db 1867 TGCAATTTTCTTAAGGAGATGCCCAAGGACATCACTAGGCTCATTAATCTGGCGCATTTA 1926
OY 603 -----LeuLeuAspGlyCyrcysTyrcysGlyLeuInthrCysMetProProArgIle 617
Db 1927 GAAGCAATACAGACTACTGCTCCAGATACATGAG-----ATT 1965
OY 618 GlySerLeuInthrCysLeuLysThrLeuSerArgPheValIleGlyIleLysLysSer 637
Db 1966 GGAAGTTTGGTATGCTTACAGAACTTAAGAAATTTGTAGTT-----CAGAAAGGCTCA 2019
OY 638 ---CysGluLeuGlyGluLeuArgAsnLeuAsn---LeuTyrcysSerIleGluIleThr 655
Db 2020 GGGCAACAGCTCACAGAACTAAATGAATGATGATGAGCTGCAAGGACCACTTCTATTGCT 2079
OY 656 HisLeuGluArgValLysAsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGlu 675
Db 2080 GGCCCTCAATTAATGATCTTAATGGGCAAGATGCAAGTTTGCAAGTTTGAAGAAAG 2139
OY 676 AsnLeuHisSerLeuSerMetLysTrpAspAspAsp-----GluArgProArgIleTyrc 693
Db 2140 CATCTTGAACCTTACACTTATATGAGATGAGCATGCGTGAAGAACTCT----- 2190
OY 694 GluSerGluLysValGluValLeuGluAlaLeuLysProHisSerAsnLeuInthrCysLeu 713
Db 2191 ---TCAGAGCAGCAGAGATGTTCTTAAGAGTCTTCAACCAATCTCGATCTCAAGAAATTA 2247

OY 714 ThrIleArgGlyPheArgGlyIleArgLeuProAspTrpMetAsnHisSerValLeuLys 733
Db 2248 GTGATTTAAAGGGTCCCGGGGTAGAGTTCCCAAGCTGCGGTGATTTCTTCC 2307
OY 734 AsnValValSerIleGluIleIleSerCyrcysLysAsnCyrcysLeuProProPheGly 753
Db 2308 AAGCTCAAAACCATATCATATATGCAATCTGTAAGC---ACAAGGCTTCCAGCTTTAGC 2364
OY 754 GluLeuProCyrcysLeuLysSerLeuGluLeuInthrTrpArgIleSerAlaGluValGluTyrcVal 773
Db 2365 CAGCTTCCCTTTTAAATATCTTGTCTATA---GCTGAGTAACTGAGGTGACACACTTC 2421
OY 774 AspSer-----GlyPheProThrArgArgPheProSerLeuArgLysLeuAsn 790
Db 2422 AGCAGTGAAGCTTACAGAGATTTGACAAACAAAGGTTTCCAGCTTGAAGATTTCTTA 2481
OY 791 IleArgLysPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGluGluCysPro 810
Db 2482 TTGGAGATATGCAAAATCTGAGCAGAGATTTTGTGATGCTGATCAATGTTTCCA 2541
OY 811 ValLeuGluGluIleGluIleLysCyrcysProMetPhe-----ValIleProThrLeu 828
Db 2542 CAATTAAGTAACTTGTCTCATCAAGTCCACACAGTTGAAGAAAGTTACTCTTAATCCA 2601
OY 829 SerSerValLysLysLeuValSerGlyAspLysSerAspAlaIleGlyPheSerSer 848
Db 2602 TCACACCTTAAGAACACTGTGATTTCTGAATCA-----GGCCTTGAGTCA 2646
OY 849 IleSerAsnLeuMet----- 853
Db 2647 CTTCCAGAGCTTCAGAAATATTTCTGTCCATCTTACCAACATCTCTATACATCAATGAT 2706
OY 854 -----AlaLeuThr 856
Db 2707 TGCCCAATCTAATCTCTAAGTATGTTACTGTGATACAGACCAACAGCTTCAA 2766
OY 857 SerLeuGlnIleArgTyrcysLysGluAspAlaSerLeuProGluGluMetPheLysSer 876
Db 2767 AGCTTAACATATGCCCATGTGGAAGGCTTGTTCACATGCCAGAGAGATGTTCCGTCCA 2826
OY 877 LeuAlaAsnLeuLysTyrcysLeuAsnIle-----Ser 886
Db 2827 TTAATATCATCTCAAGAGCTGACATCTAAGAGTCCCTGTCTGTCCTTGCACACAGA 2886
OY 887 PheTyrcPheAsnLeuLysGluLeuProThrSer----- 897
Db 2887 CTGAGGAGAGGCTTG-----CTTCCCACTTCAATCGAAGATATCCGTAAACTCATGC 2940
OY 898 -----LeuAlaSerLeuAsnAlaLeuLysHisLeu 907
Db 2941 ACTCATTAAGCAAGTGCCTTCTTAATGAGCCTTAAGTACTTCCATCTTAAGCATTTT 3000
OY 908 GluIleHisSerCyrcysTyrcysAlaLeuGluSerLeuProGluGluValLysGlyLeuIle 927
Db 3001 GAAATTGCTGATGTGCTGATATCAATTAATTTCCAGAGAGAGGTTTACTCCAC----- 3054
OY 928 SerLeuInthrGluLeuSerIleThrTyrcysGluMetLeuGlnCysLeuProGluGlyLeu 947
Db 3055 ACACCTCAATTTTGGAGATATCATGCTGATGATCTTCAATGCTTCACTCCGTGCTG 3114
OY 948 GlnHisLeuThrAla----- 952
Db 3115 CACAACATCTCTCACTTGAACACTAGATTAAGTACTGTCGGGGGTTGAAGCTTG 3174
OY 953 -----LeuThrAsnLeuSerValGluPheCysProThrLeu 964
Db 3175 CCAAGAAAGGCTGCGAGATGGGGCTCAACGAGCTTTATCAACAGAGATGTCACAAATTT 3234
OY 965 AlaLysArgCyrcysGlyLysGlyIleGlyGluAspTrpTyrcLysIleAlaHisGly 982
Db 3235 AAGCAACATGCTCAAGAAAGGT---GGGAGATATCATGCAAGAGATATGCTCAATC 3285

RESULT 13

US-10-437-963-51007

Sequence 51007, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Mu, Wei

APPLICANT: Boubharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 51007

LENGTH: 3669

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_53440C.1

US-10-437-963-51007

Alignment Scores:

Pred. No.: 5 44e-132 Length: 3669

Percent Similarity: 48.51% Matches: 408

Best Local Similarity: 32.88% Mismatches: 194

Query Match: 29.57% Indels: 284

Gaps: 35

US-10-647-268-2 (1-988) x US-10-437-963-51007 (1-3669)

QY 1 MetAlaGlu-----AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIle 17

DB 1 ATGGCGGAGTTACTATTCGGCTCTTTGCTGCTCCCTTCAGAGAAAGCAGGTGATCTTC 60

QY 18 GlnGlyLeuLeuGlyLeuLeuLeuGlyPheLeuAspGluPheGluLeuLeuLeuSerThr 37

DB 61 GGCACAGAGTTTATGTTTCAATCGGGGTATTTGAACAGCGCGTTCCGAGCTGATATCCTTG 120

QY 38 PheThrThrIleGlnAlaValLeuGlnAspAlaGlnLeuLeuLeuLeuLeuLeuLeuLeu 57

DB 121 CCGCTTCCGCTCAACAGCATGATCATGATGCCAGGATCAGGATCCAAAGAGCGCTGCT 180

QY 58 IleGluAsnTrpLeuGlnLeuLeuAsnAlaAlaAlaIleThrGluAlaAspAspIleLeuAsp 77

DB 181 GTGAACTCTTGATTCGCAAGCTGAAGCTGCGCTGTGATGCTGATGACCGCTTGAT 240

QY 78 -----GluCysLeuThrGluAlaProIleArgGlnLeuLeuLeuLeuLeuLeuLeuLeu 92

DB 241 GAGCTGCACTACAGAGAGCTCCGCTCGAAGCCCTCCGCTCGGAGCAATAAATCATACT 300

QY 93 Gly-----CysTrpHisProAsnValIleThrPheArgHisIleGly 107

DB 301 GGGGTAAAGGCTTTCTCTCTCTCATTTAATCTTTACTGTTCAAGTATAGGATAGCA 360

QY 108 LysArgMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 127

DB 361 AAGAGACTCCAGAGATAGTCGAGCGGATGATCACTGTTTTCGCAAAATGAATCATTT 420

QY 128 -----HisLeuAspGluArgThrIleGlnArgGlnValAlaThr 140

DB 421 GGGTTCCTTAATTCCTCCATGCCAGTGGATGAGAGG----- 456

QY 141 ArgGlnThrGlyPheValLeuAsnGluProGlnValIleThrGlyArgAspLeuLeuLeuLeuLeu 160

DB 457 ATGCAAACTATTCCTTAAGTCGAGCAGAGCAAGAGTATTTGGAAAGGAGCAAAAGAAAGAT 516

QY 161 GluIleValLysIleLeuIleLeuAsnValSerAsnAlaGlnThrLeuProValLeuPro 180

DB 517 GAAATTTGTCATATGCTTCTTCAACT-----GCCGAGACGAGCAATTTGTAATCTTCTT 570

QY 181 IleLeuGlyMetGlyLeuGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 200

DB 571 ATTGTTGGATAGAGAGCTGGGAAAGACAACTCTTGACACAGCTGCTTCAATGACGTA 630

QY 201 ArgValIleLeuHisPheHisProLysIleTrpIleCysValSerGluAspPheAsnGlu 220

DB 631 AAAGTGAAAGCAATTTTCAAAAGCATATGTGGGTTTGTGTGTGTGTGTGTGTGTGTGTGT 690

QY 221 LysArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 238

DB 691 CCGTTATTTGTCAGAGGATATTTGACACCGCAATTTGGAAATGATTTGTCAGAAATTT 750

QY 239 MetAspLeuAlaProLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 258

DB 751 GATTAACCTCGAATTTGTCACAGCAACGCTTCCGGGAGAACTGGGCGCCAAAGAGGATCTT 810

QY 259 LeuValLeuAspAspValIleTrpAsnGluAspGluAspLeuLeuLeuLeuLeuLeuLeuLeu 278

DB 811 CTGTACTAGATGATGTTTGAATGAAGATTAACAGAAATCGGAGAGCTTTAGAACATTG 870

QY 279 LeuLysValGlyAlaSerGlyAlaSerValLeuThrThrThrArgLeuGlnLysValGly 298

DB 871 CTGCTTCTTGTGGAATGGGAAGTCGGTGGTGTGTGCTACCCGAAACGTGAAGTTGCA 930

QY 299 SerIleMetGlyThrLeuGlnProTyrgluLeuSerAsnLeuSerGlnGluAspCysTrp 318

DB 931 TCATCATGAGAGTCAATTAATGCTCATTTGTGCTGAGAGAACCTTAACCAAGAAATTTCTTGG 990

QY 319 LeuLeuPheMetGlnAspAlaPheGlyHisGlnGluGluLeuLeuLeuLeuLeuValAla 338

DB 991 ATTGTATTCAGCAGAAAGACTTTTGGCAGCAGGTGTGTGAGACTCCAGAGCTGTTGAG 1050

QY 339 IleGlyLysGlnIleValLysLysCysGlyGlyValProLeuAlaAlaLysTrpLeuGly 358

DB 1051 GTTGTAAGAAAGATTTGTTGAGAAATGTTGCGCGGCTCCGTTAGCCATTAAGAGATGAGGA 1110

QY 359 GlyIleLeuAspPheLysArgGlnGluArgGlnTrpGluHisValAspSerGluIle 378

DB 1111 GCGTTGATGAGTCAAAACAGAGACAGCAGAGTGGCTATTCATCTTGAAGAGAACACT 1170

QY 379 TrpLysLeuProGlnGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTrpHisHis 398

DB 1171 TGG-----GATGAAGAAAGCAGATCTGCGAGCGCTGCTTGGGCTACAAAAAT 1221

QY 399 LeuProLeuAspLeuAspArgGlnCysPheThrTyrcysAlaValPheProLysAspThrGlu 418

DB 1222 TTGCTTCTCATATGAAACAAATGTTTGTGCTTGTGCAATATTCGGAAGAGCTTACGAG 1281

QY 419 MetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGly 438

DB 1282 ATGTATTAAGACGATCATATCATCTTTGGGTATCGAATGATTTATTCATCCAAAGAG 1341

QY 439 AsnLeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuTyrlLeuAspSerPhe 458

DB 1342 ATGTCAATATTAAGAAAGAAATGGGAATCATGTTTGGGAGCTGTTGGAGGTCAATTT 1401

QY 459 PheGlnGluIleGluVal-----Lys 465

DB 1402 TTCCAAATGTTAAAGCAATTTGATCAATTTTCCAAAGCTAAAGTACAGGTATGGGCA 1461

QY 466 SerGlyGlnTrpTyrlPheLysMetHisAspLeuIleHisAspLeuAlaThrSerLeuPhe 485

DB 1462 AGTGATGATCACTCAATTAATATCATATCTTATGATGATCTTGACGTTTCATATAGC 1521

QY 486 ---SerAlaSerThrSerSerSerAsnIleArgGluIle-----IleValGluAsnTrp 502

DB 1522 GGTATGATGAGTGTATGCTTGGAAATCTGGCTAAATATTAAGAAATATCCCAAAATATCTC 1581

QY 503 IleHisMet-----MetSerIleGlyPhe-----ThrLysVal 513

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Db 1582 CATCATATGCGCTTTGAGGGTCACAAAGATGGTTCTTGATGACAGCATGTGCGAGTT 1641
Qy ValSerSer---TyrSerLeuSer-----HisLeuGlnIlePheValSer--- 527
Db 1642 ATCCGACATGATATTTGCTTATGATAGATGACATGATATTTGCCAGACATTAATTC 1701
Qy 528 -----LeuArgValIleuValLeuValSerApeIleuValLeuValSerProSer 543
Db 1702 AATGAGTCTCTTGTAGAGTAGTGGCTTCATATTTTCCGACATGAAAATTTCCCTGTT 1761
Qy 544 SerIleGlyApeIleuValHisLeuArgTyrIleuValLeuSerGlyApeThrSerIleArg 563
Db 1762 GAACACGACATTTATGACACATTAAGATATCTTGATTTGCTGGT---AGCTACATTAAT 1818
Qy 564 SerLeuProAenGlnLeuCyValLeuGlnIleAenGlnIleThrLeuApeIleuHisGlyCyVal 583
Db 1819 ACATTAATCTGAAGACAGCTTACGCGACATTAATATTAATTAACAAAGTGTGATCTCAATAGATGC 1878
Qy 584 HisSerLeuCyValLeuProIleuGlnIleSerIleuGlySerIleuArgApeIleu 603
Db 1879 AGGAGCGTGAACCCATCTACAGATGCGATGAATTTATGATTAAGCTTCCGCAATGTGTAC 1938
Qy 604 LeuApeGlyCyValTyrGlyLeuThrCyMetProProApeIleuGlySerLeuThrCyValLeu 623
Db 1939 CTGTATGACTGTGCTGCACTAACAAGCATGCGACGTGCTTACGACATCTCATTAATTTA 1998
Qy 624 LysThrLeuSerApeArgPheValValGlyIleGlnIleValSerCyValLeuGlnIleu 643
Db 1999 CGGACATATGACAAAGTTGCTGACTGCT---AATGAATCTGCGTATAGGATTAACGAATGTG 2055
Qy 644 ArgAenLeuAenLeuTyrGlySerIleGlnIleThrHisLeuGlnIleArgValIleApeApe 663
Db 2056 AATATCACTTAATACTTTGGGGGCAAGCTTCAGATATTTATTTATTTAAGTAACAATATCC 2115
Qy 664 MetApeAlaIleValIleAenLeuSerAlaIleValIleAenLeuHisSerLeuSerMetIle 683
Db 2116 ATAAAGCAAAAGAAAGCAACCTTGAGTGAACAATTTGACAGAGTTGACACTTTGCTGC 2175
Qy 684 ThrApeApeApe-----GluApeProApeIleTyrGlnIleu 696
Db 2176 TGGGGCACATCAAAATCTGCGAGTTACAGACTGAAGATTTGATTAATCTGCATGA 2235
Qy 697 LysValGlnValIleGlnIleAenLeuPheProHisSerAenLeuThrCyValLeuThrIleArg 716
Db 2236 -----GAGATCACTTGAAGCTCTTAAGCTCCCAACGATGACCGTTCTAAAGCTGAG 2289
Qy 717 GlyPheArgGlyIleArgLeuProApeIleThrAenHisSerVal---LeuIleAenVal 735
Db 2290 CAGTATATGGGCACTACGTTCCCATATGATGAAATGGAATGCAATCACTTGCACAACTT 2349
Qy 736 ValSerIleGlnIleIleSerCyValIleAenCySerCyValProProPheGlyGlnIleu 755
Db 2350 GTTAAGCTCAAAAGTACGAGCTCCATTAATTTGTATGAATCTTCATCACTGATGGAAGCTT 2409
Qy 756 ProCyValLeuIleSerLeuGlnIleuThrArgGlySerAlaGlnValIleGlnIleValIleApeSer 775
Db 2410 CCCCTTTCTCAAGGTTCTCCGACTA---AAAGACATGAAGAAGTTGAAATCTTGTGTAAAC 2466
Qy 776 GlyPheProThrArgArgArg-----PheProSerLeuArgIle 788
Db 2467 GGGTTTGTCTGTATTAAGATGATGATCATCAATTAATGAGCATCCCAAAATTAATTAATC 2526
Qy 789 LeuAenIleArgGlnIlePheGlyAenLeuValGlyLeuValGlyIleGlnIleu--- 807
Db 2527 TTGTCACTAGAACATGGAATCTTGTAGAGAACTGCGACAGAAATGATGTTGAAACAGATA 2586
Qy 808 -----GlnCyProValIleGlnIleuGlnIleuValSerCyValPro---MetPhe 823
Db 2587 ACACGGGCTATATTTCCGCTGCTAGATGCAATGAAATCATTAATGTCCAAATTTGACA 2646
Qy 824 ValIleProThrLeuSerSerValIleValLeuValValSerGlyApeIleuSerApeApe 843

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Db 2647 GCTATGCCATAATGCTCCGGTTCTCAAGTCTGTAAGTGTGATAGAAACAAATA---TTG 2703
Qy 844 IleGlyPhe---SerSerIleSerAenLeuMet----- 853
Db 2704 ATTGGCTTATGCTCAAGTGTATGTAATCTGTGATCTATATCTTTGGTGCAGTCAAGG 2763
Qy 853 ----- 853
Db 2764 AGTTTAGAGAGAAAAAACATATATCTATATCAATAAAGAAAACCTGAGAACACACA 2823
Qy 854 ----- 854
Db 2824 GATTCAAAAGATCATGTTTGGCCCATCACTTTTCATCATGAGGGCTCACTCAATAATTA 2883
Qy 859 Gln----- 859
Db 2884 CACCTACAGGATTCAGTGTCTGTAGACACAGAAATATCAAAATATTAAGTGTACAGTGT 2943
Qy 860 -----IleArgTyrAenIleGln 865
Db 2944 ATGTCTGACAGACTTAGATCTAATTTCTGTGACTGCTTCATCAATATGATATACATTTG 3003
Qy 866 ApeAlaSerLeu----- 869
Db 3004 CAGTCACACACTGTGTTCTGAAATCATTTGCGCTGACAGCACTTAACAATGCAATAC 3063
Qy 870 -----ProGlnIleuMetPheIleSerLeuAlaAenLeuIleTyr 882
Db 3064 TGTACACAGCTCACCTTTTGGCCAGGGAGGAGTTCCAAAGCTTGACTTCAATTAACGA 3123
Qy 883 LeuAen----- 884
Db 3124 CTGACATTAAGATATGCAACAACCTTCAACGGGTATGCAACTGCCAAGTCTCAGTGAAG 3183
Qy 885 -----IleSerPheTyrPheAen 890
Db 3184 TCCTTTGAAGATGAGGACATGCAATTAATTTGGACGATAGAAATTCGAATTTGTGCTCAAC 3243
Qy 891 LeuIleGlnIleuProThrSerLeuAlaSerLeuAenIleuValIleuValIleHis 910
Db 3244 TTAGTGGCTTTCCCTTACAGCTTATGC-----TATCTGAGGATATGC 3285
Qy 911 SerCyTyrAlaLeuGlnIleuSerLeuProGln----- 920
Db 3286 AGCTGCAATGATCTTGAAGACTTACCTGAGAGGATGAGGAGTGTGCGGGGCTTAAGAAAGT 3345
Qy 920 ----- 920
Db 3346 CTGTCAATGATTAATTAACCAAGATGGAAGTCCCTGCCACAGATTCACATCTATACA 3405
Qy 921 -----GlnGlyVal 923
Db 3406 AATGTACACAGGCTTACCTGGAACTAATGACAGCTTAACAATTAACCGAAAGGAGTGTG 3465
Qy 924 LysGlyLeuIleSerLeuThrGlnIleuSerIleThrTyrCyValIleuGlnIleu 943
Db 3466 CATTAATGTGACAGCTCTCAATGATCTGTGCTATTTGGAACATGCCCTAATTAAGCTTTA 3525
Qy 944 ProGlnIleu---GlnHisLeuThrAlaLeuThrAenLeuSerValIlePheCyPro 962
Db 3526 CCGGAAAGTCTCCAGCAGAGGCTGACAGCTGGAAAGCTCTTATTAAGACATGAGCCCT 3585
Qy 963 ThrIleuAlaIleArgCyValIleuValGlyIleGlyGlnIleuPheTyrIleuValIleHisIle 982
Db 3586 ACGTGTGTGAGAGATGCAAAACGTGA---GGAAGCTATCTGAGACAAAGTTAAGAGATTT 3642
Qy 983 Pro 983
Db 3643 CCA 3645

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RESULT 14
 US-10-437-963-33659
 / Sequence 33659, Application US/10437963

Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 33659
LENGTH: 3852
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: clone ID: PAT_MKT4530_3774C.1
US-10-437-963-33659

Alignment Scores:
Pred. No.: 2,54e-128 Length: 3852
Score: 1477.50 Matches: 397
Percent Similarity: 50.79% Conservative: 179
Best Local Similarity: 35.01% Mismatches: 348
Query Match: 28.82% Indels: 212
DB: 18 Gaps: 36

US-10-647-268-2 (1-988) x US-10-437-963-33659 (1-3852)
QY 4 AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIleGlnGlyLeuLeuGlyLeu 23
DB GCGTTCATGACGAGCGCTTTTCAGAAAGCGGCGCTGCTTCAGAGCGAGCTGAAATTC 439
QY 24 IleLeuGlyPheLeuAspGlyPheGlyLeuGlnSerThrPheThrThrIleGlnIla 43
DB 440 CCTCAAAACATGAGCTGTGAGAGCTGCAAGATCTATCAGACAGCTGTGCACATTTGCT 499
QY 44 ValLeuGlnAspAlaGlnIleLeuLeuAspAlaIleGlnAsnTrpLeuGln 63
DB 500 CACGTTGAAGATGCAAGAGGAGCGGAGCTGAAAGATCAGCGCGGAGAAAGCTGCTTCC 559
QY 64 LysLeuAsnAlaAlaIleTyrGlnIlaIaAspAspIleLeuAspGlyCysLeuThrGlnIla 83
DB 560 AGCGTGAAGAGCGTGCCTATGATGATGATGATGATGATGATGATGATGATGATGATG 619
QY 84 ProIleAspGlnIleLeuAsnIleTyrGlyCysTyrHisProAsnValIle----- 100
DB 620 ---CTCCGATCCAACTTGCAAGCCCACTCACTCACTCACTCACTCACTCACTCACTGC 676
QY 101 -----ThrPheAsnIleLeuIleGlyLeuAspGlyLeu 111
DB 677 TTCTGCTGATTTGCTGTAATAAGGCTATTTTAAACAGAGATTTTGTAAACAAATATG 736
QY 112 LysIleMetGlnLysLeuAspValIleAlaIleGlnIle-----Ile 125
DB 737 CGGATTAAGAGGAGAGATGAGCTTATTTAAAGACAGATATGTGTCGATCCGATCAG 796
QY 126 LysPheHisLeuAspGlyLeuThrIleGlnIleGlnValAlaIleThrArgGlnIlePhe 145
DB 797 AGGTTTAAACAGGAAAG---ATTAAGAGAGAGCC-----AAGACAGATTCG 841
QY 146 ValLeuAsnGlnProGlnValIleTyrGlyAspAspLysGlnLysAspGlnIleValLysIle 165
DB 842 TTAATTAAGAGATCCGAGCTGTATGCTATGAAGAAGATTAAGAGGTCATTTGAACAATG 901
QY 166 LeuIle---AsnAsnValSerAsnAlaGlnThrLeuProValLeuProIleLeuGlyMet 184
DB 902 TTAAGTACACAGAAATTAATCAAAACCATGTCACCTTTCTATCTCCATAGAGGATAG 961

QY 185 GlyGlyLeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnIleGln 204
DB GAGAGAGTGAAGAGAGCACTTTTAACAGAGCTGTCTACATATGATGAGAGTAAAGAG 1021
QY 205 HisPheHisProLysIleTrpIleCysValSerGlnAspPheAsnGlnLysArgLeuIle 224
DB 1022 CATTTCCAGTTAAGAAATGTGCTGTGTGTCTTGAAGAACTTGTATGAGGCGCAACTACC 1081
QY 225 LysGlnIleValIleGlnSerIleGlu-----GlnLysSerLeuGlyMetAspLeu 241
DB 1082 AAGAAACGATTAAGAAATGATGAGAGCGATTAATCATCCGCCACAAACAACTGAATTC 1141
QY 242 AlaProLeuGlnLysLysLeuAspLeuLeuAsnGlyLysLysTyrIleLeuValLeu 261
DB 1142 -----CTCAAGAGAGCTCTCAACAGCTGAAAGGCAAAAGTTCTTCAATGATTC 1195
QY 262 AspAspValTrpAsnGlnAspGlnAspLysTrpAlaLysLeuArgGlnValIleLysVal 281
DB 1196 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
QY 282 GlyAlaSerGlyLysSerValLeuThrThrThrArgLeuGlnLysValGlySerIleMet 301
DB 1256 GTGCAAAAGAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1315
QY 302 GlyThrLeuGlnProTyrGlnLeuSerAsnLeuSerGlnIleAspCysTrpLeuLeuPhe 321
DB 1316 GCGCGGTGAGCTCTTATCTATCTTAACACATGATCATACATGATGCTGCAATTAATTC 1375
QY 322 MetGlnArgAlaPheGlyHis---GlnGlnGlnIleAsnLeuAsnValAlaIleGly 340
DB 1376 AGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1435
QY 341 LysGlnIleValLysLysCysGlyValProLeuAlaIleLysThrLeuGlyGlyIle 360
DB 1436 AAGAAATTTGCTCAATAGTTGAAGGCTTACACTGATGATGATGATGATGATGATGATG 1495
QY 361 LeuArgPheLysArgGlnIleArgGlnIleTyrGlnIleValArgAspSerGlnIleTrpLys 380
DB 1496 TTAATGCTGAAGAGCAACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1555
QY 381 LeuProGlnGlnGlnSerSerIleLeuProAlaLeuArgLeuSerTyrHisIleLeuPro 400
DB 1556 TTGCATTCAGCAAGAAATTAATATCTTACAGCTGTGAGATGATGATGATGATGATGATG 1615
QY 401 LeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAspTrpGlnMetGln 420
DB 1616 CCCATATTGAAGCATGCTTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1675
QY 421 LysGlnAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerLysGlyAsnLeu 440
DB 1676 AAAGCATATTGTCAGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1735
QY 441 GlnLeuGlnAsnValGlnAsnGlnValTrpAsnGlnLeuTyrLeuArgSerPhePheGln 460
DB 1736 AGGATGAGAGAGATTTGGAATACTATTGTATGATATTAATGACAGACATCTTCTTCCA 1795
QY 461 GlnIleGlnValLysSerGlyGlnThrTyrPheLysMetHisAspLeuIleHisAspLeu 480
DB 1796 -----AAACACAGAGATGGA-----TACGATGATGATGATGATGATGATGATG 1840
QY 481 AlaThrSer-----LeuPheSerAlaSerThr 489
DB 1841 GCGCAGTCTGTCTCCATGAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1900
QY 490 SerSerSerAsnIleArgGlnIleIleVal-----GlnAsnTyrIle 503
DB 1901 ACAGAAAGAAATGCCAGGACCT-ATCATTTCTTTGACAAATAAATGACAAATACATTT 1959
QY 504 HisMetMetSerIleGlyPheThrLysValLysSerTyrSerLeuSerHisLeuGln 523
DB 1960 TGAAGCTTTTGT--GATTTTATATAGACAGAGGCTTTGATGCTGATGATGATGATG 2017

QY 524 Lys-----PheValSerLeuArgValLeuAsnLeuSer 534
 Db 2018 TCAGAGACAGAGCTATCCCGAGTATCGTTCCTCAATTTAAGGTACCTCATCTCCTT 2077
 QY 535 AspIle-----LysLeuLysGluLeuProSerSerIleGlyAspLeuValHisLeu 551
 Db 2078 GATTGGAACCGACAGAAATTAACAGAAATTCGTAAGTCTGTTGGAATTAAGATGCTC 2137
 QY 552 ArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsnGluLeuCysLys 571
 Db 2138 CGATTCCTGAACCTTACAGGC---ACTGTTGTAAGAAAGCTGCTTCAATTCATTTGTTAAG 2194
 QY 572 LeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCys---HisSerLeuCysCysLeuPro 590
 Db 2195 CTCATTGCTTGCAGAACCTTAAGTTAGAAACCTCTGCATTAATCTTGTAAATCTC--- 2251
 QY 591 LysGlnThrSerLysLeuGlySerLeuArgAsnLeuLeuAspGlyCysTyrGlyLeu 610
 Db 2252 -----CTATCCCTCGAAGCAAGAACTGAACCTG 2278
 QY 611 ThrCysMetProProArgIleGlySerLeuThrCysLeuLysThrLeuSerArgPheVal 630
 Db 2279 ATCACTGCGATAGCCAGAAATAGGAAATTAAGTCTGCTTCAAAAGTTGAGAAATTTGTT 2338
 QY 631 ValGlyIleGlnLysSerCysGlnLeuGlyGluLeuArgAsnLeuAsn---LeuTyr 649
 Db 2339 GTTCCT---AAGCAAAAGATACAGAGTTAGTGAATTAAGAAAGCATTAAGATCCGA 2395
 QY 650 GlySerIleGluIleThrHisLeuGlnArgValLysAsnAspMetAspAlaLysGluAla 669
 Db 2396 GGACATATCTGCATTAATAATCTAGAGAGCGTGTAGTGCAGAAAGCAAGATGAACGA 2455
 QY 670 AsnLeuSerAlaLysGluAsnLeuHisSerLeuSerMetLysTrpAspAspArgLys 689
 Db 2456 TTGCTAAGTGAAGAGCAACATCTGACATTCCTAAGCTTAATATGTTTCCAGTAGC----- 2509
 QY 690 ProArgIleTyrGluSerGluLys-----ValGluValLeuGluAlaLeuLys 705
 Db 2510 ---AGGATTTTACTTCAAGAAAGCAACCAAGCAATAGAAACCTCATCCTCTCGAA 2566
 QY 706 ProHisSerAsnLeuThrCysLeuThrIleArgGlyPheArgGlyLysArgLeuProAsp 725
 Db 2567 CCACATGATGAACCTCAAGAGCTGACAGTCAAGCATTTGCAAGATTCATTCACAT 2626
 QY 726 TrpMetAsnHisSerValLeuLysAsnValSerIleGluIleIleSerCysLysAsn 745
 Db 2627 TGG-----ATACTCTCACTTCACTTCAAACTATCTGCTGACGTATCAAT 2674
 QY 746 CysSerCysLeuProProPheGlyLysLeuProCysLeuLysSerLeuGluLeuTrpArg 765
 Db 2675 TGTTCATTTCTGCGACGACTGACAGCTGCTCTACTCAAGGTTATA----- 2722
 QY 766 GlySerAlaGluValGluTyrValAspSerGlyPheProThr----- 779
 Db 2723 -----ATCATTTGGGGGTTTCTTCAACATATTAAATTGAGAT 2761
 QY 780 -----ArgArgArgPheProSerLeuArgLysLeuAsnIleArg 792
 Db 2762 GAGTTTTCAGGTAGTAGTAAGATTAAGGGGTTTCCGTCACTGAAGAAAGATTTGTTGAA 2821
 QY 793 GluPheGlyAsnLeuLysGlyLeuLeuLysGlyGluGluGluGluCysProValLeu 812
 Db 2822 GACACGCTTAATCTGAAAGGTGACCTTCCACACAAAGATGAGTTCCTTCCATTCCTT 2881
 QY 813 GluGluIleGluIleLysCysCysPheMetPheVal---IleProThrLeu---SerSer 830
 Db 2882 AGAGAACTTCAAGTCTGACGTGCTCCAAAGTAACAGATTCCTCTCCCATCAACA 2941
 QY 831 ValLysLysLeuValValSerGlyAspLysSerAspAlaIleGlyPheSerSerIleSer 850
 Db 2942 CTAGTGAACCTGAATAATTTCT-----GAGGCAAGCTTTTCTGTATCTTCT 2986
 QY 851 Asn-----LeuMetAlaLeuThrSerLeuGlnIleArgTyrAsnLys 864

Db 2987 GAAGTCATGCTCCAGATTTCCTACCATCTTGAACAGCTTACAGATTCAACAAATGCCCC 3046
 QY 865 GluAspLysSerLeu----- 869
 Db 3047 AATTCATCTCTTGCAGCAAGAGATTGCTTAGTACAGCAATTAATGACCTCCAGCAACTA 3106
 QY 870 -----ProGluGluMetPheLysSerLeuAla 878
 Db 3107 ACCATCACTAAGTCCAGAACTAATTCACCCCACTGAAGATTAACGAATTTAACT 3166
 QY 879 AsnLeuLysTyrLeuAsnIleSerPheTyrPheAsnLeuLysGluLeuProThrSer--- 897
 Db 3167 GCTCTCAGAGCTTTCACAT---TATGATTGTCCAGAGCTGCGCAACAGAGAA 3217
 QY 897 ----- 897
 Db 3218 CATGTGCTTACTACTCGCATGATTAAGATCTAAGCATCACTCATGCTCCAACTA 3277
 QY 898 -----LeuAlaSerLeuAsnAlaLeuLysHisLeuGluIleHis 910
 Db 3278 ATCAATCCTCTTCTGATGAACCTTAATGAGCTCTTGTCTCAAGATCTTGTCAATCG 3337
 QY 911 SerCysTyrAlaLeuGluSerLeuProGluGlu----- 921
 Db 3338 GATTGCGTTAGCTTAATTAATCTTCCAGAAAGTTACCGGCTACCTCAAAAATTGGAG 3397
 QY 922 -----GlyValLysGlyLeuIleSer-----Leu 929
 Db 3398 ATCTTCATTTGACGATTAATCTGCGCTCTGCTGCTGTTTCAAGAAAGCTCTTGTCTTA 3457
 QY 930 ThrGlnLeuSerIleTyrTyrCysGluMetLeuGlnCysLeuPro---GluGlyLeuGln 948
 Db 3458 AAACTAGATTAATCTTAATTTGTTAGTCAATAAATGCTTCCAGCAATGACTTCCA 3517
 QY 949 HisLeuThrAlaLeuThrAsnLeuSerValGluPheCysProThrLeuAlaLysArgCys 968
 Db 3518 -----CTGCTCTTAAGAAATTAATTAATCAACAAAGAGTCCCATTTCTGCGAGAGGTGT 3571
 QY 969 GluLysGlyIleGlyGluAspTyrTyrLysIleLeuHisIle 982
 Db 3572 CAGAAACAGCTGAGAAAGATTTGCTTAATATCTCATATA 3613

RESULT 15
 US-10-437-963-96697
 ; Sequence 96697, Application US/10437963
 ; Publication No. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ia Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yinhua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ. ID NOS: 204966
 ; SEQ ID NO 96697
 ; LENGTH: 4206
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURES:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9476C.1
 US-10-437-963-96697
 Alignment Scores: 5.89e-125 Length: 4206
 Pred. No.: 1442.50 Matches: 394

Percent Similarity: 46.83% Conservative: 189
 Best Local Similarity: 31.65% Mismatches: 375
 Query Match: 28.14% Indels: 287
 DB: 18 Gaps: 32

US-10-647-268-2 (1-988) x US-10-437-963-96697 (1-4206)

OY 1 MetAlaGlu-----AlaPheLeuGlnValLeuLeuAspAsnLeuThrCysPheIle 17
 DB 1 ATGGCTGAGCTACTCTCAAGCTCTTCTACCTGCGCTTGGAAAGAAAGCTGGGAGCTCTC 60
 OY 18 GlnGluGluLeuGlyLeuIleLeuGlyPheLeuAspGluPheGluGlyLeuGlnSerThr 37
 DB 61 TCCACAGAGCTTGAATTCATTGGGGGATNTGAACACCGGCGCTTGCAGACTGATACCTTG 120
 OY 38 PheThrThrIleGlnAlaValLeuGlnAspAlaGlnIleGlyLeuGlnLeuLeuAspIleVal 57
 DB 121 CTGCTTGGCATCAACCAAGTGAATGATGTCGCCGAGAGAGGCGATCCAAAGAGCTTCT 180
 OY 58 IleGluAsnThrPheGlnIleGlyLeuAsnAlaAlaAlaIleGlyAlaAspAspIleLeuAsp 77
 DB 181 GTGAAGTCTGTGATGACCAAGCTGAAGCTGCTGCTGTGATGCTGATGATGCTTCAT 240
 OY 78 GlnCysIleThrGluAlaProIleArgGlnIleGlyLeuGlySerIleGly----- 93
 DB 241 GAGCTGCACACTGAGGCG---CTTGCAGCGAGGAGCACTCCGTCGGGCGATTAATCAAC 297
 OY 94 -----CysTyrHisProAsnValIleThrPheArgHisIleVal 106
 DB 258 AGTGGCGTAAGGGCTTCTTCTCTCTCTCATTTAAATCCCTTAAGTCAAGATATGAGATA 357
 OY 107 GlnIleAspArgMetLeuIleGlyLeuGlnIleLeuAspValIleAlaAlaGlnArgIleLeu 126
 DB 358 GGAAGAAGAACTCAGACAGATAGTGAACGATTGATCAGCTTGTTCGAAATGAATCAA 417
 OY 127 PheHisLeu-----AspGluArgThrIleGlnArgIleValAla 139
 DB 418 TTGGGGTCTTAATTTGCCCATGCGACAGGATGAGAG----- 456
 OY 140 ThrArgIleThrGlyPheValLeuAsnGluProGlnValIleGlyArgAspArgIleLeu 159
 DB 457 ---ATGCAGACCTATTCTTACGTCGACGAGGAGGATATTGGAAGGCAAAAGAAAGA 513
 OY 160 AspGluIleValIleLeuIleAsnValSerAsnAlaGlnThrLeuProValLeu 179
 DB 514 GATGAATTCACCAATATGCTTCTTAAGT-----GCCAAGCTGACAAATTGTATACTT 567
 OY 180 ProIleLeuGlyMetGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGly 199
 DB 568 CCTATTGTTGGGATAGAGAGATTGGGCAAGACAACTCTGCACAGCTGCTTCAATGAC 627
 OY 200 GlnArgValIleGlnHisPheHisProIleThrIleCysValSerGlnAspPheAsn 219
 DB 628 GTGAAGTGAAGACAACTTTTCMAAAGCATATGTGGTGTGTGTCTCACAAGAACTTCAGT 687
 OY 220 GlnIleArgLeuIleGlyGlnIleValGlnSerIle-----GlnGlnIleSerLeuGly 237
 DB 688 GTTCTCGATATTTGTCAAGGGGATATTTGACACTGCAGCAATTTGGAAATGTTGGACGAG 747
 OY 238 GlnMetAspLeuAlaProLeuGlnIleGlyLeuArgAspLeuLeuAsnGlyIleGlySerIle 257
 DB 748 AGTGATTAAGCTGGAATTGCTACAAACAGCTCTCCGGGAAGAACTGAGCCAAAGAGGTAC 807
 OY 258 LeuLeuValLeuAspAspValIleTrpAsnGlnAspGlnAspIleThrIleValSerLeuArg 277
 DB 808 CTCTCTTGTACTATATATGTTTGGAAATGAAGATGAACAAAATGGGAGGCTCTTAAGACA 867
 OY 278 ValLeuIleValGlyIleSerGlyAlaSerValLeuThrThrArgLeuGlnIleVal 297
 DB 868 TTCTCTTGTCTCTGTAATAAGGAGAGTGGTGTGTGTGCACTACCCGAAATTCGATGTT 927
 OY 298 GlnSerIleMetGlyThrLeuGlnProIleGlnLeuSerAsnLeuSerGlnGlnAspCys 317

DB 928 GCGTCACTCATGGGAGCACTTCTCCATTTGGCTCTAGAACACTTACCAAGAAAGATTCC 987
 OY 318 ThrLeuLeuPheMetGlnArgAlaPheGlnHisGlnGlnIleLeuAsnLeuLeuVal 337
 DB 988 TGGACTTATTTCTGTGAAGAGCGTTCCGTACAGGCGTGGCCAAAGCTTGTGATTTGTC 1047
 OY 338 AlaIleGlyLeuGlnIleValIleGlyLeuGlyLeuGlyLeuGlyLeuGlyLeuGlyLeu 357
 DB 1048 GAGATTGTGCAAAAATTTGTCAAAATATGTTCTGGAGGTCCCATTTAGCAATTAATAGATG 1107
 OY 358 GlnGlyIleLeuArgPheLeuArgGlnGlnArgGlnIleThrGlnHisValArgAspSerGln 377
 DB 1108 GAGGCTGTGTGATGAACAACTAGTGAAGGATTTGGCTGGCGATCTTCAAAACAAT 1167
 OY 378 IleThrIleLeuProGlnGlnIleSerSerIleLeuProAlaLeuArgLeuSerIleHis 397
 DB 1168 ACTTGG-----GAGGAAATTAACATATCTGACAGTCCATATCACTACCTACAA 1215
 OY 398 HisLeuProLeuAspLeuArgIleCysPheThrTyrCysAlaValaPheProIleAspThr 417
 DB 1216 CATCTACCTTCTTTATGAACAGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1275
 OY 418 GlnMetGlnIleGlyLeuLeuIleSerLeuThrMetAlaHisGlyPheIleLeuSerIle 437
 DB 1276 GAGATTATTAAGATGATCTTAATCATCTGTGATATCAATGATTCATTCATCACTAA 1335
 OY 438 GlnIleLeuGlnIleGlnIleValIleGlnIleValIleTrpAsnGlnIleGlyLeuArgSer 457
 DB 1336 GAGACCTCGACATGAAAGAACTGGGACAAAGTCTTGTGAGGCTTGTGGAGATCA 1395
 OY 458 PhePheGlnGlnIleGlnValIleSerGlyLeu----- 468
 DB 1396 TTTTTCMAAATGCGAAACTCGGTCGCGGAGGAGAGATACATATATGGGTACAA 1455
 OY 469 -----ThrTyrPheLeuMetHisAspLeuIleHisAspLeuAlaThrSer----- 483
 DB 1456 GATGTAACATACGAAATATTCATGATCTTATGATGATCTTGCAGTTCTATTAAGCGGG 1515
 OY 484 -----LeuPheSerAlaSerThrSerSerSerAsnIleArg 495
 DB 1516 GATGAGTCTATCTTTCGAAATCTTGTGAAATTAATTAATTAATTAATTAATTAATTAAT 1575
 OY 496 GlnIleIleValIleGlnAsnIleHisMetMetSerIleGlyPheThrIle 512
 DB 1576 CATCTAGTT-----TTCCACATTCACACAAAGTGTGTCGATGACAGCTTGT 1626
 OY 513 -----ValIleSerSerIleSerLeu-----SerHisLeuGlnIleSphaValSerLeu 528
 DB 1627 CCAATTATCCGAAGTCTATTAGTTTACATTAAGAAATCATATGAATTCATGAAGAGAGTCT 1686
 OY 529 -----ArgValIleAsnLeuSerAspIleIleValGlnGlnLeu 541
 DB 1687 AGATTCAATGATGTCCTTGTGAGAGCGCTTGGGCTTCAATCTGTGACAAATGAAGATTTC 1746
 OY 542 ProSerSerIleGlyAspLeuValHisIleuArgTyrLeuAsnLeuSerGlyAsnThrSer 561
 DB 1747 TCAATTGAACACAGATATATGAAGACTTGGGATCTTGAATTATTC---TCTAAGCAC 1803
 OY 562 IleArgSerLeuProAsnGlnLeuCysIleSleuGlnAsnLeuGlnIleThrLeuAspLeuHis 581
 DB 1804 ATAAACACATCCCTGAAGCGGTGACAGTGCATGATTAACAATCTAATGCTCAAT 1863
 OY 582 GlnCysHisSerLeuCysCysLeuProIleGlnIleThrSerIleSleuGlySerLeuArgAsn 601
 DB 1864 AGATGCAAGGCGCTGACCTCACTGCTGACGCGCATGAATTAATTAATCAAGCTTGGCCAT 1923
 OY 602 LeuLeuLeuAspGlyCysTyrGlyIleuThrCysMetProProArgIleGlySerLeuThr 621
 DB 1924 GTGATCTTGAGTGTGTTCTAAGTATCAAAAGATGCCCGCGGTCTAGGCAAGTCAAC 1983
 OY 622 CysLeuIleThrLeuSerArgPheValValGlyIleGlnIleGlySerCysGlnLeuGly 641
 DB 1984 AGTTTACGAACATTCACATGATATATGTTGGC---AATGAATCGATTGATGACTTCAT 2040

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QY 642 GluLeuArgAsnLeuAsnLeuTyrGlySerIleGluIleThrIleLeuGluArgValys 661
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2041 GAACTCAAGCACTTGAACCTTGGGGGCAAGCTCAACAATACATATTTCTGAGGTAACA 2100
QY 662 AsnAspMetAspAlaLysGluAlaAsnLeuSerAlaLysGluAsnLeuHisSerLeuSer 681
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2101 AATCGCTTACAGCAAAAGAGCCAACTTGAGATTAAGAAAAATCTGCAGCACTACACA 2160
QY 682 MetLysTrpAspAsp-----AspGluArgPro 690
DB ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2161 CTTTGTTGGGACTCAGCAAAATTTCACCTGTTCACATTGTCAATTCTGCAGATGAAATTTTG 2220
QY ArgIleTyrGluSerGlyLeuValGluValIleGluAlaLeuLysProHisSerAsnLeu 710
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2221 CAATTATCCGCTCCGAA-----GAACTGCTGAGATGCTCTTAAAGCTCCCAACGATTA 2274
QY 711 ThrCysLeuThrIleArgGlyPheArgGlyIleArgLysProAspTrpMetAsnHisSer 730
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2275 AAAGTTTAAAGCTAAGCAATATATGGGCTCCAACTTCCAAATGTGATGGAAGATGAT 2334
QY 731 Val---LeuLysAsnValSerIleGluIleIleSerCysLysAsnCysSerCysLeu 749
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2335 GTGACACTGCAGAAATATGTTAACTCACTTGAAGAGGCTGTATGTGTCTCAAACTC 2394
QY 750 ProProPheGlyGluLeuProCysLeuLysSerLeuGluLeuTrpArgGlySerAlaGlu 769
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2395 CCACCAAGTGTGGCACTTCCCTTTTGAAGTTCTCCGCTCAACAG---ATGAGAGG 2451
QY 770 ValGluTyrValAspSerGlyPheProThrArgArgArg----- 782
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2452 TTGAATATCTTGTTTACAGGATCAACCCCACTGATGAAGATATGGCAACCAATTAGTGA 2511
QY 783 PheProSerLeuArgLysLeuAsnIleArgGluPheGlyAsnLeuLysGlyLeuLeuLys 802
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2512 TTTCAAAATATTAATTTATGCTACCTAGATGATGATGATGATGATGATGATGATGAT 2571
QY 803 LysGluGlyGluGlu-----GlnCysProValLeuGluGluIleGluLys 818
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2572 TATGACACTCAACAGTACATCACTTCTTTCCAAAGCTGAGAGCCCATGGAATTTATA 2631
QY 819 CysCysPro---MetPheValIleProThrLeuSerSerValLysLeuValValSer 837
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2632 GACGTGCCAAAGCTGACAGCACTGCTTAATGTTCGATTTCTTAAGTTTGACA 2691
QY 838 GlyAspLysSerAspAlaIleGlyPheSerSerIleSerAsnLeuMetAlaLeu----- 855
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2692 GGAACAAAGTACTGCTGGGTTAGTGTACAGTATAGTAACTATCATATCTGTATCTC 2751
QY 856 -----ThrSerLeuGlnIleArg-----TyrAsnLysGlu 865
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2752 GGTGCAAGTCAAGGAGTTCAAGGAGGATGAGACATTAATCTATATATGAGAGA 2811
QY 865 ----- 865
DB 2812 CGTGAAGGAGACATGATACAAAGATGAGCATATTTTCCCGATCACTTGTGTGCATGG 2871
QY 865 ----- 865
DB 2872 GATTCACTCACTAAACTACACTACAGATTCATATACACAGACAGAAAATGTGAAG 2931
QY 866 -----AspAlaSerLeu----- 869
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2932 AGTATAAGTGTGCATATATGTCTGTGCAGACCTTAATGTCTGTCTTGTGTGATGCTTC 2991
QY 869 ----- 869
DB 869 ----- 869
DB 2992 ATCAACAATGAAGATTAACGTACACACTATGTCTGTGATATCATTTGAGATGCTACAA 3051
QY 870 -----ProGluGluMetPheLysSer 876
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3052 CAATTGAAGAAATCTGGTACTGTATGATGCTCACTTTTGGCCAGAGAGAGTTCCGAAGC 3111

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QY 877 Leu----- 877
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DB 3112 TTGACTTCTTGAAGAAAACCTTCATGTTGATGATGCAAAAACCTTCACGGGTGACCACT 3171
QY 878 -----AlaAsnLeuLysTyrLeuAsn 884
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3172 GACCGACTGTGAGAGCCCTTACAGATGAGAGCCCATGTATTAATTGGAATTACTTACAG 3231
QY 885 IleSerPheTyrPheAsnLeu----- 891
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3232 ATGATGCTGCTCCCACTTAATGTGATTCCTTACAAACTTCATCTGCTACGATCCTT 3291
QY 891 ----- 891
DB 3292 GTGATTAACAGATTAATGTAATTGAGGGCTGCTGAGGATTTGTTGCCAGGGCACT 3351
QY 892 -----LysGluLeuProThrSerLeuAla 899
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3352 CTAAACACTCTGTAAATTTTGGGTGGCCAAAGTTTAACTCCCTGCTGCCAGCATTTGG 3411
QY 900 SerLeuAsnAlaLeuLysHisLeuGluIleHisSerCysTyrAlaLeuGluSerLeuPro 919
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3412 TGTCTTCAAAATCTGAAGAGCTTGAAGCTGACAGATTAATACAGCTTAACCTTGTGCT 3471
QY 920 GluGluGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCysGluMet 939
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3472 ---GAGGGATGCAAGATCTAAAGCTGTCAAAACACTACATTTATTAATGTCTGCT 3528
QY 940 LeuGlnCysLeuProGluGlyLeu---GlnHisLeuThrAlaLeuThrAsnLeuSerVal 958
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3529 ATAAACCGCTTTACAGAGAGTCTCCAGCAAGAGCTGCATGCTCCAAACGTTCAACGTT 3588
QY 959 GluPheCysProThrLeuAlaLysArgCysGluLysArgGlyIleGlyLysAspTrpTyrLys 978
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3589 GAAGATGCTCCCTGCTGTGGCGAGAGATGACAGCTGG---GAGATTAATTTGGAGAAA 3645
QY 979 IleAlaHisIlePro 983
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3646 GTCAGAGCAATTCTCT 3660

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Search completed: April 17, 2005, 07:25:47
Job time : 1329 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 16, 2005, 23:27:47 ; Search time 6346 Seconds
(without alignments)
5926.174 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFLOVLNLTCTFIOGE.....EKIGEDWYKIAHPRVFTY 988

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 segs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgn2_1/USPFO_spool_p/US10647268/runat_15042005_154720_26496/app_query.fasta_1.1159
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10647268 @CGN 1.1 5180 @runat_15042005_154720_26496 -NCPU=6 -ICPU=3
-NO WMAP -LARGSEQQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_estc1: *
2: gb_estc2: *
3: gb_hc: *
4: gb_estc3: *
5: gb_estc4: *
6: gb_estc5: *
7: gb_estc6: *
8: gb_gss81: *
9: gb_gss82: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	1401	27.3	3408	9	CL976585 OsIFRC029
3	1335.5	26.0	3795	9	CL958853 OsIFRC036
4	1307.5	25.5	3319	9	CL975408 OsIFRC027
5	1293	25.2	3708	9	CL958564 OsIFRC001
6	1252	24.4	3354	9	CL975407 OsIFRC027
7	1241.5	24.2	3975	9	CL958562 OsIFRC001
8	1233.5	24.0	3003	9	CL966185 OsIFRC013
9	1212	23.6	3222	9	CL961820 OsIFRC037

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11	1145.5	22.3	3546	9	CL945091 OsIFRB001
12	1102.5	21.5	3273	9	CL962672 OsIFRC038
13	1101.5	21.5	3576	9	CL978496 OsIFRC031
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16	1061.5	20.7	4557	9	CL975789 OsIFRC028
17	1061	20.7	2409	9	CL979800 OsIFRC044
18	1058.5	20.6	4050	9	CL980521 OsIFRC034
19	1054.5	20.6	3264	9	CL964592 OsIFRC038
20	1052	20.5	2499	9	CL944015 OsIFRB001
21	1052	20.5	2499	9	CL965216 OsIFRC011
22	1051.5	20.5	3480	9	CL966533 OsIFRC039
23	1035	20.2	3459	9	CL947688 OsIFRB000
24	1025.5	20.0	1714	9	CL955053 OsIFRC029
25	1021	19.9	2628	9	CL976586 OsIFRC032
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ALIGNMENTS

RESULT 1
LOCUS CL960744 3333 bp DNA linear GSS 21-SEP-2004
DEFINITION OsIFRC037153 Oryza sativa Expressed library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

ACCESSION CL960744
VERSION CL960744.1 GI:52376202

KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 3333)

REFERENCE Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Wang, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen

TITLE JOURNAL COMMENT
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.

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Location/Qualifiers
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ORIGIN

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US-10-647-268-2 (1-988) x CL960744 (1-3333)

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 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL976585
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 Euphorbiaceae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 3408)
 AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Zhao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.
 TITLE An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
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Db      1666 TTATTCGAAGACACTCTCTACGAGCACTGAGCCTCATCAA---TCGATTAATTAATTA 1722
Oy      542 ProSerSerIleGlyAspLeuValHisLeuArgTyrglyLeuAsnLeuSerGlyAsnThrSer 561
Db      1723 CCAATTCAGGGCAAGGTACCTTCACACCTTAAGATATCTTGTATATCTCAAAAACGATTTGT 1782
Oy      562 IleArgSerLeuProAsnGlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHis 581
Db      1783 ATGAAAGAACTCTCGAAGATATATGCAATTTGTATGACATCTGCGAGCTTGAACCTTTCT 1842
Oy      582 GlyCysHisSerLeuCysCysLeuProLysGlnThrSerLysLeuGlySerLeuArgAsn 601
Db      1843 AATTGCCATTTTCTTGTACACTACCAAGAGATGAAATATATGACACAGCTTACGTACAC 1902
Oy      602 LeuLeuLeuAspGlyCysTyrglyLeuThrCysMetProProArgIleGlySerLeuThr 621
Db      1903 CTTATACAAATGATGTCTTAATTTTGAAGTCAAGCTTCCAGAGCTTGGCAAAATTAATCT 1962
Oy      622 CysLeuLysThrLeuSerArgPheValGlyIleGlnLysLysSerCysGlnLeuGly 641
Db      1963 TCTCTCCGCAATGACAGATTTTGTAGTGTGTATAGCTCTGTGTGAGTACCTTGA 2022
Oy      642 GlnLeuArgAsnLeuAsnLeuTyrglySerIleGlnIleThrHisLysGlnArgValLys 661
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Oy      662 AsnAspMetAspAlaLysGlnAlaAsnLeuSerLysGlnLysGlnLeuHisSerLeuSer 681
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Qy 758 LeuLysSerLeuGluLeuTrpArg----- 765
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Qy 766 -----GlySerAlaGluVal----- 770
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Qy 771 -----GluTrpValAspSerGlyPheProThrArgArgArg--- 782
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Db 2668 TATGAAATGGCTTCCACAGCATTTCCATCATTTAAAGAAATCAGTTATGATTAGG 2727
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Qy 901 ---LeuAsnAlaLeuLysHisLileuGluLileHisSerCysTrpAlaLeuGluSerLeuPro 919
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CJ958853
LOCUS
DEFINITION
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ACCESSION
CJ958853
VERSION
CJ958853.1 GI:52372461
KEYWORDS
GSS.
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 3795)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomic
Chinese Academy of Sciences, Beijing 10300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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/note="Oryza sativa exon trapped genomic sequences "
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Query Match: 26.05% Indels: 355
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Qy 52 GlnLeuLysAspLysAlaLileGluAsnTrpLeuGlnLysLeuAsnAlaLalaTrpGlu 71
Db 61 GCCGCGCGGACGCGCGCGCTGCGGAGCTGCGGAGCTCAGGAGCGTGGCCACGAC 120
Qy 72 AlaAspAspLileuAspGluCysLysThrGluAlaProLileArgGlnLysLysAsnLys 91

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121 ATCGACGAGCTTCTCGACCGCTCGCACCGAC-----CTCCCGCGCGGCGAGCGCGG 174
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Db 175 GCGCAGCTGCTCGGTGTGGCGGCGGCTCTACGCGCGCTGCTCGCATGGCCACAGCGCTG 234
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Oy 111 LysIlyIleMetGluIlyLeuAspValIleAlaIleGluArgIleIlyPheHisIleu--- 129
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Oy 130 ---AspIlyArg---ThrIleGluArgIleValIleAlaThr-----ArgGlnThr 143
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Oy 164 LysIleIleuIleAsnAsnValSerAsnAlaGlnThr-----LeuProVal 178
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Db 655 TCGGACCTCGCGCACCAACCAACCACTGAGGCGCATGCGCGCTTCTTCTTCATG 714
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Oy 488 -----SerThrSerSerAsnIle 494
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RESULT 4

LOCUS CL975408 3318 bp DNA linear GSS 21-SEP-2004
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 cultivar-group) genomic, genomic survey sequence.

ACCESSION CL975408
 VERSION CL975408.1 GI:52405341

KEYWORDS

Oryza sativa (indica cultivar-group)
 Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE

1 (bases 1 to 3318)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G. K. S., Deng, X. W. and Wang, J.

TITLE

An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis

JOURNAL

Unpublished (2004)
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 Chinese Academy of Sciences, Beijing 101300, China
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 Email: chenchen@genomics.org.cn

FEATURES

Class: exon-trapped.
 Rice genomic sequence.

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Location/Qualifiers
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 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G. K. S., Deng, X. M. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 Unpublished (2004)
 JOURNAL CONTACT: Chen Chen
 COMMENT Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80486766
 Email: chenchen@genomics.org.cn
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VERSION CL975407.1 GI:52405339
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Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS 1 (bases 1 to 3354)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
COMMENT
Contact: Chen Chen
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Percent Similarity: 45.37% Conservative: 192
Best Local Similarity: 29.21% Mismatches: 361
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Oy 511 ThrLysValIleSerSerTyrgSerLeuSerHisIleuGlnLysPheValSerLeuArgVal 530
Db 1606 -----CTTCACAGACAGATGCATCTGTGCAGAAATGTCCGTACAC 1641
Oy 531 LeuAsnLeuSerAsp-----IleLysLeuLysGlnLeuProSerSerIleGlyAsp 547
Db 1642 ATGAATATATCTGACACTTTGTATCTTTCTAATAATATTTACCGGAAAGATAGGGA--- 1698
Oy 548 LeuValHisIleuArgTyrlleuAsnLeuSerGlyAsnThrSerIleArgSerLeuProAsn 567
Db 1698 ----- 1698
Oy 568 GlnLeuCysLysLeuGlnAsnLeuGlnThrLeuAspLeuHisGlyCysHisSerLeuCys 587
Db 1698 ----- 1698
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Oy 687 AspGlnArgProArgIleTyrgLysSerGlu-----LysValGlnValIleu 701
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QY 845 Gly-----PheSerSerIleSerAsnLeuMetAlaLeu----- 855
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RESULT 7
LOCUS CL958562 3975 bp DNA linear GSS 21-SEP-2004
DEFINITION OaIFCC001685 Oryza sativa Express Library Oryza sativa (indica

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ACCESSION CL958562
VERSION CL958562.1 GI:52371872
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE 1 (bases 1 to 3975)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Wang, Y., Sun, N., Zhang, X., Bao, D., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
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Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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location/Qualifiers
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/clone_lib="Oryza sativa Express Library"
/notes="Oryza sativa exon trapped genomic sequences"
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Score: 1241.50 Matches: 335
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Best Local Similarity: 31.02% Mismatches: 364
Query Match: 24.21% Indels: 185
DB: Gaps: 29
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QY 46 GluAspAlaGlnLysLysGlnLeuLysAspLysAlaIleGluAsnTrpLeuGlnLysLeu 65
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QY 66 AsnAlaAlaIleTyrGlnAlaAspAspIleLeuAspGluCysLysThrGlnAlaProIle 85
Db 211 AAGGCTGTGCTTCAAAAGCTAATGACATATTGATGATGATCAAGTAAAGCCCTTCGT 270
QY 86 ArgGlnLysLysAsnLysTyrGlyCysTyrHisProAsnValIleThr----- 101
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QY 116 LysLeuAspValIleAlaIleAlaGluArgIleLysPheHisLeuAspGluArgThrIleGlu 135
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QY 136 ArgGlnValAlaThr-----ArgGlnThr---GlyPheValIleAsnGluPro 150
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OY 191 Thrleumlaglnmevalpheasnarpblnargvalilleuglnhsphehisprolystle 210
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Db 820 -----ATTATG 825
OY 291 ThrItrargleuglnulysvalgllyserillemetglythrleuglnprotyrleugluser 310
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OY 311 AsnleuserglnulysaspCysItrleuileuphemetglnargalpheglnhlsnglnlu 330
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Db 1420 GTTCTGTATTGAAAGAAATGTTTACTATAGCTGAGGGTCACAAATTACATTGAGTTT 1479
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Db 1480 TTGCCAATACTGTTCTGCATTTGTTGTTGCTGTGATCGTCCAGAAACCTCTCAGAT 1539
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Db 1540 GTTTCACATAAGCAGAGATGTCAAGTATGCAAAACATTTTGTGCATTTATGAAATACAGC 1599
OY 516 SerIySerIeuserSerhIaleuglnIysPhevalaserleuargvalleuasnleuserasp 535
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Qy      789 uAsnIleArgGluPheGlyAsnLeuIlybGlyLeuLeuIlybGlyGluGlnGlnCys 809
Db      2403 CCAATTACATGATTTAAGAGAGCTTCGAGAGCTGGGTGGCAACACAGAAAGAAAGAGCT 2462
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Db      2805 CGTAGATATGCGGAGCTGCAATTAAGTTGACATCG---CTGATTTGGGGG-----AACT 2855
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 DEFINITION OsJFCC037780 Oryza sativa Express Library Oryza sativa (indica
 cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL961820
 VERSION CL961820.1 GI:52378383
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 3222)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G. K. S., Deng, X. W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
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 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
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 QY 67 AlAlaAlaTyrGluAlaAspAspIleLeuAspGluCysLysThr----- 81
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QY 98 AsnValIleThrPheArgHisLysIleGlyLysArgMetLys----- 111
 Db 331 -----CTCAATTTTCAGCTCGTCCCGGAGCGGTGGCGCTGACGCGAAG 378
 QY 112 -----LysIleMetGluYlyLeuAspValIleAlaAlaGluArgIleLysPheHisLeu 129
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Oy      643 LeuArgAsnLeuAsnLeuTyRLeuGlySerIleGlnIleThrHisLeuGlnLysValLysAsn 662
Db      2092 TTGAAGGACATCAATATACGTGTGAACTTGGCTGCTGAAATTGGAATCTGCCACCAT 2151
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Oy      683 LysThrAspAspArgGlnArgProArgIleTyRGlusSerGlyLysValGlnValLeuGln 702
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DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL962156
VERSION 1
KEYWORDS GSS.
ORGANISM Oryza sativa (indica cultivar-group)
SOURCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enharoidae; Oryzae; Oryza.
1 (bases 1 to 4236)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis

```

JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
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Oy 150 ProGlnValTyrgLysArgAspLysGlnLysAspGluIleValLysIleLeuIleAsn-- 168
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Db 2638 ATTAACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2697
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Db 3502 -----GAGTTTGAAGAACATGCCAAATGGGAGTGAGTCACTGGAGTTTTCATGCTGAC 3555
Oy 809 CysProvalleuGlnleuGlnleuLyS---CysCySProMetPheValIlePro--- 826
Db 3556 TTCCTTCACTTCGAGAGCTGAATAATCAAGACAGCGGATGATGAGAACTTCACAT 3615
Oy 827 ---ThrlleuSerleuVallySylleuVallySylSerleuAspAspAlaIle--- 844
Db 3616 CAATTATCATCTCTTTGAAAAAATTTGGTCATCAAG-----AAATGTGAAAAAGCTGCA 3669
Oy 845 GlyPheSerleuSerAsnleuMetAlaLeuThrsleuGlnIleArgTyAsnLyS 864
Db 3670 AGACTGCCAACATATTCACCACTTAACATCTTATTTGATG----- 3711
Oy 865 GlnAspAlaSerleuProGlnleuMetPheLySserleu-----AlaAsnleuLyS 882

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Db 3712 -----GGCAATCTTTAGCGAAGAAATACAAATATGCTGTGANTTTCCATGCTCCAAATA 3765
Oy 883 LeuAsnIleSerPheTyTrPheAsnleuLySgluLeuProThrsleuAlaSerleuAsn 902
Db 3766 TTAAGAGTGTTTACAGCAAAACCTTGTGCTTGAATTTGACATATAGAACCTTACCA 3825
Oy 903 AlaLeuLySleuGlnleuIleHsSerCySyleuAlaLeuGlnleuProGlnleuGly 922
Db 3826 ATCTGGAGGCACTTAGCTATTAAGTATGATGCCGGGGCTATTTCTGTG-----GTAGCA 3879
Oy 923 VallySylleuIleSerleuThrcysleuSerleuThrcysGlyMetleuGlnCys 942
Db 3880 TTGTTAGCTTTGAATCTTCAAGCTTCTTAAATAAAGATTTGCCAACTGCACTGC 3939
Oy 943 LeuProGlnleuGlnleuIleThrsleuThrsleuSerValGluPheCysPro 962
Db 3940 CTTTACACCACTTCAACAG-----CACTTCAGCAATGATTTATACAGAACTGTCTCT 3993
Oy 963 ThrlleuAlaLySArgCysGln 969
Db 3994 CAATTACAGGAATGATTTGAG 4014

RESULT 11
CL945091 3546 bp DNA linear GSS 21-SEP-2004
LOCUS
DEFINITION
OaIFSB001967 Oryza sativa Expressed library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION
CL945091.1 GI:52357100
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretoidae; Oryzaceae; Oryza.
1 (bases 1 to 3546)
AUTHORS
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
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Location/Qualifiers
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Best Local Similarity: 30.84% Mismatches: 398
Query Match: 22.34% Indels: 161
DB: 9 Gaps: 34

US-10-647-268-2 (1-988) x CL945091 (1-3546)
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Db 22 GCTTTTTCGAAAGTCTTTTTCAGAAATCCATGAGCTGTGAAAGAAAGAACTGAGTTT 81

```


24 IleuGlyPheLeuAspGluPheGluYleuGlnSerThrPheThrThrIleGlnAla 43
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 44 ValLeuGluAspAlaGlnIleYleuYleuYleuYleuYleuYleuYleuYleu 63
 DB GTTCTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 198
 64 YleuLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 83
 DB GATCTGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258
 84 -----ProIleArgGlnYleuAsnYleuYleuYleuYleuYleuYleuYleu 95
 DB CAGGACAGTAAGTATCATCTTCCCACTCGGTAACCAATTAAGTCTGCTTTG 318
 96 HisProAsnValIleThrPheArgHisYleuYleuYleuYleuYleuYleuYleu 115
 DB AATCTTCACTGCTTAAATTTATGATATATGAAAGGAGGAGGAGGAGGAGGAGG 378
 116 YleuLeuAspValIleAlaAlaGluArgIleYleuYleuYleuYleuYleuYleu 135
 DB AAAATTTGATGATTTGAAAAATTAAGCGCTTAACCTTCAAGTAGAG-----GTCCAT 429
 136 ArgGlnValAlaThrArgGlnThrArgIlePheValLeuAsnGlu-----ProGln 151
 DB GATCAAAAGATCAACAACATGAAGAGTATGTGTAACGAGAGTACCTCTCTCTCA 489
 152 Val-----TyrGlyArgAspYleuYleuYleuYleuYleuYleuYleuYleu 169
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 DB ATATGGGCTCATGATCACTGATTTCAATATTAAGAGATATGATGATCTATCTTAC 726
 230 SerIleGluGluYleuSerLeuGlyMetAspLeuAlaProLeuGlnYleuYleuYleu 249
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 250 AspLeuLeuAsnGlyYleuYleuYleuYleuYleuYleuYleuYleuYleuYleu 269
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 290 ThrThrThrArgLeuGluYleuYleuYleuYleuYleuYleuYleuYleuYleu 309
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 310 SerAsnLeuSerGlnIleAspCysThrPheLeuPheMetGlnArgAlaPheGlyHisGln 329
 DB AAACCTCATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023
 330 ---GluGluIleAsnLeuAsn-----LeuValAlaIleGlyYleuGluIleValYleu 346
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 347 CysGlyGlyValProLeuAlaAlaYleuYleuYleuYleuYleuYleuYleuYleu 366
 DB TGTAAAGGATGCTTCTTCAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1128

367 GluArgGlnThrGlnHisValArgAspSerGluIleTrp---YleuProGlnGluGln 385
 DB -----CACCAAGAGATAAAGTACGTGGGTGCTATTTCTGCAAGAGGA 1173
 386 -----SerSerIleLeuProAlaLeuArgLeuSerTyrHisIleu 399
 DB ATTGCGATGCCATCCCAATTTATTTCTGGGCGCTGCACTGAGCTATGACAGTTA 1233
 400 ProLeuAspLeuAspGlnCysPheThrTyrCysValAlaPheProYleuAspThrGluMet 419
 DB CACTCCCATCTCAAGCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1293
 420 GluYleuGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSerYleuYleu 439
 DB GAGAGAGAGTGGCTTATCAAGCATTTGATGGCTCATGGTTTCATTCAGTCTCAGCTGGC 1353
 440 LeuGluLeuGluAsnValGlyAsnGluValTrpAsnGluLeuYleuYleuYleuYleu 459
 DB GATGTAGCCAGAGCCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1413
 460 Gln---GluIleGluValYleuSerGlyGlnThrTyr---PheYleuMetHisAspLeuIle 477
 DB CAGAGAGACTGGTTCACCATGCTGGGAGAGACACCGTTATAGCATGTCGGAATGATG 1473
 478 HisAspLeuAlaThrSerLeuPheSerIleSerThrSerSer----- 491
 DB CATAGAGTCTGGT-----TTGACGCTCACTGATGATGATGATGATGATGATGATG 1524
 492 -----SerAsnIleArgGluIleVal----- 499
 DB CCTGCAAAAGTTCCAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1584
 500 -----GlyPheThrYleuValValSerSerYleuSerIleSerHisIleGluYleuPheVal 526
 DB TTGCGGACCCAAACATTTGAGACAAATTTCCCAATTAAGCATTTATCACTCTTA 1644
 509 -----GlyPheThrYleuValValSerSerYleuSerIleSerHisIleGluYleuPheVal 526
 DB GTCACTGGTGGCACAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1704
 527 ---SerLeuArgValLeuAsnLeuSerAspIleYleuYleuYleuYleuYleuYleu 545
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 546 GlyAspLeuValHisIleuArgTyrLeuAsnLeuSerGlyAsnThrSerIleArgSerIle 565
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 586 LeuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleu 604
 DB CTTGAGAAAGTTGCCACGAGAGATAAAGTCTTGGCAAGCTTAAGGATATGATGATG 1941
 605 -----AspGlyCysTyrGlyLeuThrCysMetProProArgIleGlySer 619
 DB CTGATGATCTTCCCTCGATATATCATGATTTGAAGATATGATGATGATGATGATG 2001
 620 LeuThrCysLeuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleu 636
 DB TTGACTATCTTCAAGACCTTCAAGGTTTCTCAAGCAAGCAAGCAAGCAAGCAAGCA 2061
 637 SerCysGlnLeuGlyGluYleuYleuYleuYleuYleuYleuYleuYleuYleuYleu 655
 DB CACAGCAGTATTAAGAGCTAGATTAATTTGACATATATCGGGGAACTACTCATTTCA 2121
 2062 CACAGCAGTATTAAGAGCTAGATTAATTTGACATATATCGGGGAACTACTCATTTCA 2121
 656 HisIleuGluArgValYleuYleuYleuYleuYleuYleuYleuYleuYleuYleuYleu 675
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QY 128 HisLeuArgGluArgThrIleGluArgIleValAlaThrArgGlnThrGlyPheValIleu 147
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 QY 148 AengIuProGlnValTyrGlyArgAspIlySerGluIleValIlePheIleu 167
 DB 535 ---CATGGGGAATCTTCGGGCGAAGATCAGAAATCCAAAGTTGGTAAGTACTCTTTA 591
 QY 168 Aasn---ValSerAsnIleGlnThrLeuProValIleuProIleLeuGlyMetGlyIle 186
 DB 592 AGCTTCAGGTGATGATGATTAATCCAGTCTCGGTGCTCCATGTTGGAGTGGTGC 651
 QY 187 LeuGlyIleThrThrLeuAlaGlnMetCysIlePheAsnArgGlnArgValIleGlnIlePhe 206
 DB 652 GTGGCAAGATCTGCTTCAGCAGCATGTGTACAAACACACTAGGTAGCAGACACTTT 711
 QY 207 HisProIlyIleTyrIleCysValSerGluAspPheAsnGluIleValIleGlu 226
 DB 712 GACATGAAATGTGTGATCTGTGTACTGATGCTTGTATGATCCAGATCCAGAGAG 771
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 DB 772 ATGCTAGAGTCAATTTCCAGACATGCTGATTTAGGCATGACAGCATTAACAAG 831
 QY 244 LeuGlnIlyIleLeuArgAspLeuIleuAsnGlyIleIlyIleValIleuAsp 263
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 QY 264 ValIleProGlnIleAspGln-----AspIlyIleValIleValIle 276
 DB 892 GTCTGAGACATGACAAAGATACCTGCGCATAGACAGCAAGAACTGGCAGAGCTTCT 951
 QY 277 GlnValIleuIleValIleAlaSerGlyIleValIleThrThrArgLeuIle 296
 DB 952 TCTCCCTCAAGGCTGACAGCAATGAGCAAGAACTTGTGACCAACCGGATCCAGTATG 1011
 QY 297 ValIleSerIleMetGlyThrLeuGlnProTyrGluLeuSerAsnLeuSerGlnIle 316
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 QY 317 CysIleLeuLeuPheMetGlnArgAlaPheGlyIleGlnIleGlu---IleAsnLeuAsn 335
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 QY 336 LeuValAlaIleGlyIleValIleValIleValIleValIleValIleValIle 355
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 QY 356 ThrLeuGlyIleIleLeuArgPheIleValArgIleGlnIleProGlnIleVal---Arg 374
 DB 1192 GTGGTCTGTAACAGCTGAATGTAACACACACAGATGAGTGAACAAAGTCTTAAG 1251
 QY 375 AspSerGluIleTyrIleLeuProGlnIleGlnIleSerIleLeuProAlaLeuArgIle 394
 DB 1252 AGAATATGAGATG-----GATGAATCAAGCCCAATTTTACAGAT 1293
 QY 395 SerTyrIleIleLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPhePro 414
 DB 1294 AGCATATGAAATCTCCAGTCCACCTTCACAAATGCTTGCATATGAGATCTTCCC 1353
 QY 415 LysAspThrArgIleMetGlnIleValIleAsnIleSerLeuIleMetAlaIleGlyPheIle 434
 DB 1354 AAGGATCGGGAATTTGAAGCTGAGAGATTAATCTCATGTGAGTGAAGCAAGTATGTA 1413
 QY 435 LeuSerIlyGlyAsnIleLeuGluIleValIleValIleValIleValIleValIle 454
 DB 1414 TACCAGATGTTGAGGAGAGATGAGAACTGGGAGCAATATGTTGATGAGATTAAGT 1473
 QY 455 LeuArgSerPheIleGlnIleIleGluValIleSerGlyIleThrTyrPheIleMetHis 474
 DB 1474 AGTGGTCAATTTT---GCCATTCAGAAAGAAACAAATTTGTACGATTAATGATGCT 1530

QY 475 AspLeuIleIleAspLeuAlaThrSerLeuPheSerAlaSer----- 488
 DB 1531 CCCGTATTCACAACTTGGCCAAATCAGTTTCAGCCGAAGATGTTCCGAATAGAGGT 1590
 QY 489 -----ThrSerSerAsnIleArgGluIleIleValGlu----- 500
 DB 1591 GATGAACAGAGAGAGATCCCATCTCTGTAGCCATCTATCAATCCATAGATAGCCTT 1650
 QY 501 -----AsnTyrIleIleMetSerIleGlyPhe-----Thr 511
 DB 1651 TCAATGCTTACGACAGACATATCCATACATGAACTCGGCATCTTCATTTCTTTACGAGC 1710
 QY 512 LysValIleSerSerTyrSerLeuSer-----HisLeuGlnIlyPheValSer 527
 DB 1711 AAGATGGGTGCTCAATTCACATTTCCATCCACAGAGATGTTGATTAACCTTCAAGC 1770
 QY 528 LeuArgValIleLeuAsnLeuSerAspIleIleValIleGluIleProSerSerIleGlyAsp 547
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 QY 726 TrpMetAsnIleSerValIleuIlyAsnValIleSerIleGluIleIleSerCysIlyAsn 745
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 QY 786 LeuArgIlyLeuAsnIleArgGluPheGlyAsnLeuIlyGlyLeuIlyIlyGly 805
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Db      2539 TTACGAGAGATGTTCTTACATGACATGACAGAACTAAATGATGTCATGACAGCGCCAG 2558
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Qy      812 -----LeuGluGlu11Glu11Leu11CysCys----- 820
      |||:::
      |||:::
Db      2599 GAAATGATGAATCTCCGCAATATGTGATTAAGACATCCAAAAGCTCAAGAGCTGCTT 2658
      |||:::
      |||:::
Qy      821 Promet-----PheVal11LeuPro-- 826
      |||:::
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Db      2659 CCACCTACTCCAAAGCTTACAGAGCTGACAAATGCAAAAAAGGGTCTCGGGTTCATAC 2718
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Qy      827 -----ThrLeuSerSerVal11LeuVal11 836
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Db      2779 TTCAATGCCCCCAAGCTACTTCCGAGATTTCTCTGCGCAAGTGAACCAATGAGTTGAGAA 2838
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Db      2839 AGCTTTCAGTACCTTAGAAGCTTATCGTTGATCATATGAGAAATCTCACATGCCCCCTTT 2898
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      |||:::
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Db      2959 ACCTTCATCGACAGACATGAGAGATGTTCTTCAATCTTAAGATCTACCTCAAAAGCTCTGC 3018
      |||:::
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Qy      885 11LeuSerPheTyrPheAsnLeuLysGluLeuProThrSerLeu11SerLeuAsnAlaLeu 904
      |||:::
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Db      3019 ATAAATGGCTGCAACATCTCAATCGCTGCTTCCATATGTCAGAGCTGAGTCCCTG 3078
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Qy      905 LysHisLeuGlu11HisSerCysTyrAlaLeuGluSerLeuProGluGlu11Val11Lys 924
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      |||:::
Qy      925 GlyLeu11SerLeuThrGlnLeuSer11LeuTyrTyrCysGluMetLeuGlnCysLeuPro 944
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Qy      945 GluGlyLeuGlnHisLeuThrAlaLeuThrAsnLeuSerValGluPheCysAspProThrLeu 964
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RESULT 13
CL978496 3576 bp DNA linear GSS 21-SEP-2004
LOCUS OsIFCC031988 Oryza sativa Expressed Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL978496
VERSION CL978496.1 GI:52411494
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Bukayocia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Oryzaceae; Oryza.
1 (bases 1 to 3576)
Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and

```

```

JOURNAL
COMMENT
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
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/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
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Alignment Scores:
Pred. No.: 3.57e-108 length: 3576
Score: 1101.50 Matches: 332
Percent Similarity: 45.57% Conservative: 203
Best Local Similarity: 28.28% Mismatches: 380
Query Match: 21.48% Indels: 259
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US-10-647-268-2 (1-988) x CL978496 (1-3576)
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      |||:::
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      |||:::
      |||:::
Qy      58 11LeuGluAsnThrLeuGlu11LysLeuAsnAla11AlaTyrGlu11AspAsp11LeuAsp 77
      |||:::
      |||:::
Db      211 ATCAAAAGCGGGCTACAG-----TCTGAGAAACATACACACAGTATATGATCGGAC 261
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Qy      78 GluCysLysThrGluAlaPro11LeuArgGlnLysLysAsnLysTyrGlyCysTyrHisPro 97
      |||:::
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Db      262 AAGTATGCTGTCCTCAATACATTCGCGCAAAA-----CCA 297
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      |||:::
Qy      98 AsnVal11LeuThrPheArgHisLys11LeuLysArgMetLysLys11MetGluLysLeu 117
      |||:::
      |||:::
Db      298 AAACTAGCAGATGTTCAACATCAAAATGCGCAACAGATTAAGACAAATCAAAACAGATT 357
      |||:::
      |||:::
Qy      118 AspVal11LeuAlaGluArg-----11LeuSerHisLeuAspGluArgThr11Leu 135
      |||:::
      |||:::
Db      358 GCTGCAATTTGCGAGCAAAAGGCGGATGTCATATATTGATTCATATCCAAATCGAT 417
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      |||:::
Qy      136 ArgGlnVal11AlaThrArgGlnThrGlyPheVal11LeuAsnGluProGlnVal11TyrGly--- 154
      |||:::
      |||:::
Db      418 CATATGTTTCAATAAAACAAG-----ATTATCAGTAGGCAATCTTATTTGGGCAT 468
      |||:::
      |||:::
Qy      155 -----ArgAspLysGluLysAspGlu11Val11Leu 166
      |||:::
      |||:::
Db      469 GTTGATGACTCAAAATATCATGTGAGAGATGAGAGCAACAGATCATACGTAACTTA 528
      |||:::
      |||:::
Qy      167 11LeuAsnVal11SerAsnAlaGlnThrLeuProVal11LeuPro11LeuGlyMetGlyGly 186
      |||:::
      |||:::
Db      529 ATAGAT-----GACCAACAGAAATTCATATGTTCAATTTGTTGAGCTTGCGAGA 579
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      |||:::
Qy      187 LeuGlyLysThrThrLeuAlaGlnMetValPheAsnAspGlnArgVal11LeuHisPhe 206
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Db      580 ACCGTTAAATCTATCATGCGCACACATCTGTATGCAACAAATTAAGAGCAATTTT 639
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      |||:::
Qy      207 HisProLys11Leu---Trr11CysValSerGluAspPheAsnGluLysArgLeu11Lys 225
      |||:::
      |||:::
Db      640 GAAGGCTCAATATTTTGGGTTCAAGTTCACAGAAATTTGATTAACAAACTGCTGCGC 699
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Qy      226 Glu11Val11GluSer11GluGluLysSerLeuGlyMetAspLeuAla11ProLeuGln 245
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Db      700 AAGCTGTATGAAGCAATTTTAAAGAAACATCATATCTTCGACGCAACACAGATGTT 759
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Db      2866 ATCATCGGAGACCTCACCCTCCAGATCTTTGATCTCGGGTGGCCAGTTCTTGGC 2925
Oy      844 Tle-----GlyPheSerSerIleSerAnleu----- 852
Db      2926 ATGCTGCAGAGTGCGCTGGGGGATTCGCGCTCTCGCAACCTGATTTCTGAAAGAAATC 2985
Oy      853 -----MetAlaLeuThrSerLeuGlnIleArgTyr 862
Db      2986 CCACTATTGCTAGCCTCCCAAGTCGATCATGCTCTTACATCCCTGAGAGAGTTGGCT 3045
Oy      863 AsnLysGluAepAlaSerLeuProGlu-----GluMetPheLysSerLeuAlaAnleu 880
Db      3046 ATTGTGTGAATGCAACATCTAAAGAGTTGCTGTGAGGTGAATCATCTACCTCCCTC 3105
Oy      881 LysTyrLeuAnlIleSerPheTyrPheAnleuLysGluLeuProThrSerLeuAlaSer 900
Db      3106 AAGGAATTGATATTCTAGTTGCAGAAATCTGAGCCAGTTGCCCTGAGGGAATTCAGCAT 3165
Oy      901 LeuAnlAlaLeuLysHisLeuGlnIleHisSerCysTyrAlaLeuGluSerLeuProGlu 920
Db      3166 CTTCACCAACTTGAAGACCTTAAGTATACAGACATGTCTTGGCTCCACAGCTGCCAGAA 3225
Oy      920 ----- 920
Db      3226 GAGCTGGGGATGTTAGTCTCTAGAGACCTTATGATCAATATCTTGCTGCTCTTACG 3285
Oy      921 -----GluGlyValLysGlyLeuIleSerLeuThrGlnLeuSerIleThrTyrCys 937
Db      3286 ACCCTTCTGAGAGTCCATGACGGGGCTCACTCATCCCGACATCATCACTTATGAGCTGC 3345
Oy      938 GluMetLeuGlnCysLeuProGluGlyLeu----- 947
Db      3346 CCTATGCTCACCGCTGCTGCAGAGTCATCTCAGACAACTCTCGCGCTCCAGTCTTAT 3405
Oy      948 ----- 948
Db      3406 ATGCAAGCTGCATCGGCTTGATCTTGCCAGCTCCATCATACACCTTACTCTCTT 3465
Oy      954 ThrAsnLeuSerValGlnPheCysProThrLeuAlaLysArgCysGlnLysGlyIleGly 973
Db      3466 CAGCATTTGGTGATTAAGTTACCAACCTTACCTTGAAGGCAATTACAAATAATGAGGTGCG 3525
Oy      974 GluAspTyrPyrLysIleAlaHisIleProArgValPheIle 987
Db      3526 AAGGACTGGACATCATCTCCATATTCTGTTGTGGAGATA 3567

RESULT 14
CL957401 3996 bp DNA linear GSS 21-SEP-2004
LOCUS OsIRFCC000538 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
CL957401
ACCESSION CL957401.1 GI:52369776
VERSION GSS.
KEYWORDS Oryza sativa (indica cultivar-group)
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 3996)
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676

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FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1,51e-106 Length: 3996
Score: 1087.50 Matches: 355
Percent Similarity: 41.60% Conservative: 187
Best Local Similarity: 27.24% Mismatches: 370
Query Match: 21.21% Indels: 391
DB: Gaps: 44

US-10-647-268-2 (1-988) x CL957401 (1-3996)
Oy      5 PheLeuGlnValLeuAepAsnLeuThrCysPheIleGlnGlyLeu----- 21
Db      37 TTCATGCAAGTAATCTTCGACCAAG-----TACCTAAGCTCCAGATTAGAGCACTGG 87
Oy      22 -----GlyLeuIleLeuGlyPheLysAspGluPheGlnLysLeuGlnSerThrPheThr 39
Db      88 GCAATGCTGCAACTTACGA-----GTTGAATTTCAAAACCTGTGCGACCTGAT 141
Oy      40 ThrIleGlnAlaValLeuGluAepAlaGlnLysLysGlnLeuLysAspIleAlaIleGlu 59
Db      142 ATGCTAAGGCAATATCTTATGACCCCTGAAGGCACTGCTGTGATGAGGAGGCGATCTGG 201
Oy      60 AsnTyrLeuGlnLysLeuAnlAlaIleTyrGlnLysAspIleLeuAspGlyCys 79
Db      202 CAACTATTGGAGTTTGAAGCTTTCAGCTTATGATGACAGAGATGCTTGATGATGATTA 261
Oy      80 Lys-----ThrGlnAlaProIleArgGlnLysAsnLys----- 91
Db      262 GACTACATTGCGCTTATGAGAAATAGTGGAACAAGAGCGAAACAGACTGTGCTAGC 321
Oy      92 TyrGlyCysTyrHisProAsnValIle----- 100
Db      322 ATTGGATTATCAATCTTAAAGCTTTCGGAACCTTTGACAGCAGGTTCTCCTT 381
Oy      101 -----ThrPheArgHis-----Lys 105
Db      382 TTCCTCCATTCAAAAACCGACCAACCTTTGATTATGTGTCATGTCGAGCTGGATTCA 441
Oy      106 IleGlyLysArgMetLysLysIleMetGlnLysLeuAspValIleAlaIle-----Glu 123
Db      442 GTCTCTTGCAAGATGAATTCATTTCCGATGCTTCAAAAGAGCTACCGCCCATATTGAG 501
Oy      124 ArgIle-----LysPheHisLeuAspGluArgThrIleGluArgGlnValAla 139
Db      502 CGTGTGTGCTCAGTTCAAGAGTTGTGTAGCTGATATATGACGAAACCAAAATTTCCAAAC 561
Oy      140 ThrArgGlnThrGlyPheValLeuAnlGluProGlnValTyrGlyLysAspLysGlyLys 159
Db      562 TCAAGACCAACACAGCTCATCTTTACGAAACAGAGGTGTACCGGACAGATGAGAGAGAG 621
Oy      160 AspGlnIleValLysIleLeuIle-----AsnAsnValSerAsnAlaIle-----Gln 174
Db      622 AACACCAATTTGAAGATATCTCTGGAACAAAGTTTCAATATATCAAAATAGGTACAAAG 681
Oy      175 ThrLeuProValLeuProIleLeuGlyMetGlyLysGlyLeuGlyLysThrThrLeuAlaGln 194
Db      682 AGCTTCTGTGCTCCCGCATGTGTAGGCAATGTGTGTGGAGAAAGACAACTTGTGTGAG 741
Oy      195 MetValPheAnlAspGlnArgValIleGluHisPheHisProLysIleTyrIleCysVal 214
Db      742 TATGTATATATGATCTAGTCAACATCACTTGTTTTGAAGTAAAGGCAATGGCATGTGTG 801

```

Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.


```

Db      |||      :|||      |||      :|||
2890 CCTAGCCTGATCAATTCCTCCACTTCACATTTCTTCAAGCTTCAAGGATAGTTTG 2949
Qy      832      -----LysylserineValylserine 838
Db      2950 AAAAAATCAGAGGATATCTCTCTCATGAGTTGAAATGATGAAGATTTGATTTCTGGC 3009
Qy      839      Asp----- 839
Db      3010 ATATCTGATTTGTCGTGAAAACATATTTCTGCATTTCAATTACTTGAGAGCCTTC 3069
Qy      840      LysSerAspAlaile----- 844
Db      3070 AAGAGTTTCAGCATACCAAGTTTGATTAATTTCACTGACTACCACTGAAAGCCAGGGA 3129
Qy      845      -----GlyPheSerSerIleSerSer 851
Db      3130 AAGCATGATTTTCTGAGTATCCAGCATATGATGATGATTCGATCTCCTCACTGCTAAC 3189
Qy      852      LeuMetAlaLeu----- 855
Db      3190 ATCAGTGAACCTCAAGATATGCGGTTCTGGATATCTGAGATGTAATCAATGAAATTTTA 3249
Qy      856      -----ThrsSerLeu 858
Db      3250 TCMAATGTTGGATCTTCTGACTGTTGTCATAAAGACGCCCCAGGTTACTTCCCTT 3309
Qy      859      Gluile----- 860
Db      3310 GAGCTGAACCCAAATGTAAGATGATTAACGATTAATGAAGATTTGCTAGAGCTCAG 3369
Qy      860      ----- 860
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Qy      860      ----- 860
Db      3430 AAGTTGATGAGAGGATGCAAAAAATCTGCTGTAAGGAGGATCACAATCTCAGAAAT 3489
Qy      861      -----ArgTyrAsnLysGluAspAlaSerLeu----- 869
Db      3490 ACTGCCTCATGAAAAGATGATGATTAATGATTAATCTTCAACATGCCAATTTGT 3549
Qy      869      ----- 869
Db      3550 AGAACACTTGGTATCTCAATATTTGATGATGACAGGATCAGCAACATATGCTTA 3609
Qy      870      -----ProGluLysSerLeuAlaAsnLeuLysTyrLeuAsnIleSer 886
Db      3610 ACTCCAGACGACGAGACAGATTTGTTACACTGACTTCAATGAAAACACTCGTTCACT 3669
Qy      887      PheTyrPheAsnLeuLysGluLeuProThrSerLeuAlaSerLeuAsnAlaLeuLysHis 906
Db      3670 GAATGCTCATATCTCGCTCATCTGCAACGCTGCAACCAAGATTTCTCCCTGGAAGAC 3729
Qy      907      LeuGluLysHisSerCysTyrAlaLeuGluSerLeuProGluGluGlyValLysGlyLeu 926
Db      3730 CTGCATTTATCATCGGTAGAGCATGACCTCCATCCACACACTGGAGTTGCCAGAGA--- 3786
Qy      927      IleSerLeuThrGlnLeuSerIleThrTyrCysGluMetLeu-----GlnCysLeuPro 944
Db      3787 ---TCACTGAAAAGTTGTTCACTTGTCTGATGTGACCTGTGAGACAGCAAGTCCGTAGAA 3843
Qy      945      GluGlyLeu 947
Db      3844 GAAAGAGTA 3852

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RESULT 15
LOCUS      CK861977      670 bp      mRNA      linear      EST 09-MAR-2004
DEFINITION 33106 In vitro Root Solanum tuberosum cDNA, mRNA sequence.
ACCESSION  CK861977
VERSION     CK861977.1 GI:45291634

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KEYWORDS      EST.
SOURCE      Solanum tuberosum (potato)
ORGANISM      Solanum tuberosum
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                asterids; Lamiales; Solanales; Solanaceae; Solanum.
AUTHORS      1 (bases 1 to 670)
                Film, B., Rothwell, C., Sardana, R., Griffiths, R., Laque, M., De
                Keyser, D., Andy, P., Goyer, C., Li, X.-O., Wang-Pruski, G. and Regan, S.
                Generation of ESTs from in vitro root tissues of potato
                Unpublished (2004)
TITLE      The Canadian Potato Genome Project - BioAtlantech
JOURNAL      Contact: Barry Film
COMMENT      921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA
                Email: bfilm@bioatlantech.nb.ca
                Seq primer: T3.
FEATURES
    source
        1..670
            Location/Qualifiers
                /organism="Solanum tuberosum"
                /mol_type="mRNA"
                /culivar="Shepody"
                /db_xref="taxon:4113"
                /tissue_type="Root"
                /lab_host="XLI0-Gold"
                /clone_id="In vitro Root"
                /notes="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
                Site 2: XhoI; supplier: Developmental series. Sterile stem
                sections from pathogen-free Solanum tuberosum var.
                Shepody, clone 1756; nuclear stock were cultured in
                Magenta boxes containing 1/10 strength MS medium,
                solidified with 0.8% (w/v) Phytagar. Roots of all sizes,
                originating from the stem bottoms were collected from
                these cultures, washed to remove residual Phytagar, and
                used in RNA isolations and library construction."

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ORIGIN
Alignment Scores:
Pred. No.:      3,43e-105      Length:      670
Score:          1062.00      Matches:      203
Percent Similarity: 95.50%      Conservative: 9
Best Local Similarity: 91.44%      Mismatches: 10
Query Match:      20.71%      Indels:      0
DB:              7      Gaps:      0

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US-10-647-268-2 (1-988) x CK861977 (1-670)
Qy      297      ValGlySerIleMetGlyThrLeuGlnProThrGluLeuSerAsnLeuSerGlnLys 316
Db      1      GTTGATCAATATATGGAACCTTGCAACCATATGATTTGTTCAATTTGTTCTCAAGAGAT 60
Qy      317      CysTrpLeuLeuPheMetGlnArgAlaPheGlyHisGlnGluGluLysLeuAsnLeu 336
Db      61      TGTTCGTTGTTGTTTCATTCACAGCGCATTTGGGACCAAGAAATTAATCATTAATCTT 120
Qy      337      ValAlaIleGlyLeuGluIleValLysLysCysGlyGlyValLProLeuAlaIleThr 356
Db      121      ATGGCTATCGAAGAGAGATTTGTAAGAAATGTGTGTGTGCTTCAAGCCTTAATCT 180
Qy      357      LeuGlyGlyIleLeuArgPheLysArgGluGluArgGlnTPGluHisValArgAspSer 376
Db      181      CTGGAAGGATATTTGCGCTTCAAGAGAGAAAGACAGTGGAGACATGTGAGATAGT 240
Qy      377      GluIleTPlysLeuProGlnGluLysSerIleLeuProAlaLeuArgLeuSerTyr 396
Db      241      GAGATTGGAAGTTACCTCAAGAGAAAGTTCTATCTGCTTGCCCTGAGACTTAGTTAC 300
Qy      397      HisHisLeuProLeuAspLeuArgGlnCysPheThrTyrCysAlaValPheProLysAsp 416
Db      301      CATCATCTTCCACTTGATTTGACAAATGCTTGCAATTTTGACAGTATTTCCAAAGAT 360
Qy      417      ThrGluMetGluLysGlyAsnLeuIleSerLeuTrpMetAlaHisGlyPheIleLeuSer 436
Db      361      ACCGAAATGAAAGAAATTAATCTCTCTCTGATGACACAGGTTTCTTTTATCG 420

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - protein search, using sw model

Run on: April 16, 2005, 01:05:58 ; Search time 178 Seconds
(without alignments)
2146.737 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFQLVLDNLTCFIGE.....EKIGEDMYKIAHPRVFIY 988

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5127	100.0	988	ADK98517	ADK98517 S Bulboca
2	5120	99.9	988	ADK98519	ADK98519 S Bulboca
3	5120	99.9	988	ADK98525	ADK98525 S Bulboca
4	4521.5	88.2	1003	ADK98521	ADK98521 S Bulboca
5	3798	74.1	979	ADK98521	ADK98521 S Bulboca
6	3798	74.1	979	ADK98521	ADK98521 S Bulboca
7	3787	73.9	979	ADK98521	ADK98521 S Bulboca
8	3766.5	73.5	970	ADK98521	ADK98521 S Bulboca
9	3766.5	73.5	970	ADK98521	ADK98521 S Bulboca
10	3752.5	72.9	945	ADK98521	ADK98521 S Bulboca
11	3736.5	72.8	992	ADK98521	ADK98521 S Bulboca
12	3730.5	72.8	992	ADK98521	ADK98521 S Bulboca
13	3730.5	72.8	992	ADK98521	ADK98521 S Bulboca
14	3708.5	72.3	945	ADK98521	ADK98521 S Bulboca
15	3654.5	71.3	945	ADK98521	ADK98521 S Bulboca
16	3625	70.7	972	ADK98521	ADK98521 S Bulboca
17	3542	69.1	1040	ADK98521	ADK98521 S Bulboca
18	3542	69.1	1040	ADK98521	ADK98521 S Bulboca
19	3369	65.7	1000	ADK98521	ADK98521 S Bulboca
20	1244	24.3	1266	AAW25157	AAW25157 Tomato im
21	1244	24.3	1266	AAW25157	AAW25157 Tomato im
22	1235	24.1	1240	AAW03665	AAW03665 I2C-2 pro
23	1176	20.3	1402	AAW03664	AAW03664 I2C-1 pro
24	1041.5	20.3	1402	AAW64150	AAW64150 Lettuce r
25	1041	20.3	1402	AAU95463	AAU95463 Lettuce p

26	969.5	18.9	784	2	AAW64151	AAW64151 Lettuce r
27	969.5	18.9	784	5	AAU95464	AAU95464 Lettuce p
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34	736.5	14.4	979	8	ADL57168	ADL57168 Oryza mlt
35	735.5	14.3	993	8	ADM72239	ADM72239 O. minuta
36	729.5	14.2	552	2	AAW64155	AAW64155 Lettuce r
37	729.5	14.2	553	5	AAU95468	AAU95468 Lettuce p
38	700.5	13.7	993	8	ADL57170	ADL57170 Oryza mlt
39	685.5	13.4	342	3	AAW09957	AAW09957 Rice lisp
40	685	13.4	1032	8	ADM72241	ADM72241 O. minuta
41	683	13.3	1031	8	ADL57172	ADL57172 Oryza mlt
42	671	13.1	1032	8	ADM72245	ADM72245 O. minuta
43	665.5	13.0	1091	8	ADL57176	ADL57176 Oryza mlt
44	657	12.8	901	2	AAW80251	AAW80251 An antidi
45	657	12.8	901	2	AAV01965	AAV01965 A protein

ALIGNMENTS

RESULT 1	ADK98517	ADK98517 standard; protein, 988 AA.
ID	ADK98517	
AC	ADK98517	
DT	03-JUN-2004	(first entry)
DE	S Bulbocastanum Shu11 protein sequence SegID2.	
XX	plant disease resistance polypeptide; solanaceous plant; potato;	
KW	late blight disease; fungus; Phytophthora infestans;	
KW	conferring pathogen resistance; Shu11.	
XX		
OS	Solanum bulbocastanum.	
XX		
PN	MO2004020594-A2.	
PD	11-MAR-2004.	
XX		
PF	28-AUG-2003; 2003WO-US027045.	
XX		
PR	29-AUG-2002; 2002US-0407100P.	
PR	20-AUG-2003; 2003US-00647268.	
XX		
PA	(USDA) US SRC OF AGRIC.	
EA	(DRYC-) DRY CREEK LAB.	
PI	Osumi T, Belknap WR, Rockhold DR, Maccree MW;	
XX		
DR	WPI; 2004-239179/22.	
XX	N-PSDB; ADK98516.	
PT	New isolated Solanum bulbocastanum late blight resistance nucleic acid	
PT	molecule encoding a plant disease resistance polypeptide, useful for	
PT	conferring pathogen resistance to Phytophthora infestans in plants.	
XX		
PS	Claim 10; SEQ ID NO 2; 103bp; English.	
XX		
CC	This invention relates to a novel isolated nucleic acid molecule encoding	
CC	a plant disease resistance polypeptide. The preferred plant is a	
CC	solanaceous plant that is potato. The resistance is to late blight	
CC	disease, caused by the fungus Phytophthora infestans. The invention is	
CC	useful for conferring pathogen resistance in plants using a Solanum	
CC	bulbocastanum late blight resistance gene. The present sequence is the	
CC	protein encoded by the S bulbocastanum cDNA sequence of the invention.	
XX		
XX	Sequence 988 AA:	

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Query Match      100.0%; Score 5127; DB 8; Length 988;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEAFLOVLDMNLTCFIOGELILGFDEBEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
DB 1 MAEAFLOVLDMNLTCFIOGELILGFDEBEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
QY 61 WLQKLNAAAYEADDIIDBECKTEAPIRQKNKYGCHYHNVITFRHKIGRMKKIMEKLDVI 120
DB 61 WLQKLNAAAYEADDIIDBECKTEAPIRQKNKYGCHYHNVITFRHKIGRMKKIMEKLDVI 120
QY 121 AAEIKFHLDBERTTEROVATROTFVLANEPQVYGRDKKDEIVKLLINNSNAQTLPLVP 180
DB 121 AAEIKFHLDBERTTEROVATROTFVLANEPQVYGRDKKDEIVKLLINNSNAQTLPLVP 180
QY 181 ILGNGGIGKTTLAQVFNVDQVIEHFHPKIWICVSEDFNEKRLLIKEIVESIEEKSIGMD 240
DB 181 ILGNGGIGKTTLAQVFNVDQVIEHFHPKIWICVSEDFNEKRLLIKEIVESIEEKSIGMD 240
QY 241 LAPLOKRLDLNKGKYLVLVDVWNEODQKAKLRQVLKYGASGASVLTTRLEKVGSI 300
DB 241 LAPLOKRLDLNKGKYLVLVDVWNEODQKAKLRQVLKYGASGASVLTTRLEKVGSI 300
QY 301 MGLTQPYELSNLSQEDCWLTFMORAFGHOEINLNLVAGKEIYKKGCGVPLAAKTLGGI 360
DB 301 MGLTQPYELSNLSQEDCWLTFMORAFGHOEINLNLVAGKEIYKKGCGVPLAAKTLGGI 360
QY 361 LRFKREERQWHEHVRDSEIMKLPQEBSSILPALRLSYHHLPLDLROCFYCAVFPDTEME 420
DB 361 LRFKREERQWHEHVRDSEIMKLPQEBSSILPALRLSYHHLPLDLROCFYCAVFPDTEME 420
QY 421 KGNLISLMAAGFIISKGNLELVNGVGNVWELIYRSFOEIEVKSQGTFRMDLHDL 480
DB 421 KGNLISLMAAGFIISKGNLELVNGVGNVWELIYRSFOEIEVKSQGTFRMDLHDL 480
QY 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVVSSYSLSHQKRVSLRNLNLSIKLQ 540
DB 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVVSSYSLSHQKRVSLRNLNLSIKLQ 540
QY 541 LPSSIGDLVHLRYNLISGNTSIRSLPNQLCKLQNLQTLIDHGCHSLCCLPKETSKLGSIR 600
DB 541 LPSSIGDLVHLRYNLISGNTSIRSLPNQLCKLQNLQTLIDHGCHSLCCLPKETSKLGSIR 600
QY 601 NLILDGCGTLCMPPRISLTCTKLSRFVVGIOKKSQGLGELRLNLYGSIETHTHERV 660
DB 601 NLILDGCGTLCMPPRISLTCTKLSRFVVGIOKKSQGLGELRLNLYGSIETHTHERV 660
QY 661 KNDMDAKEANTSAKENLHSLSMKMDDDERPRIYSEKVEVLEALKPHSNLTCLATIRGFRG 720
DB 661 KNDMDAKEANTSAKENLHSLSMKMDDDERPRIYSEKVEVLEALKPHSNLTCLATIRGFRG 720
QY 721 IRLPDMWNSVYKUNVSIIEIISCKNCSCLPPGELPCLKSLHLMWGSAAVEVDSGFPTR 780
DB 721 IRLPDMWNSVYKUNVSIIEIISCKNCSCLPPGELPCLKSLHLMWGSAAVEVDSGFPTR 780
QY 781 RRFPSIRKLTANIREGNLKGILKKGEEQCPVLEIEIKCCMPFVITPLSSVKKLIVSGDK 840
DB 781 RRFPSIRKLTANIREGNLKGILKKGEEQCPVLEIEIKCCMPFVITPLSSVKKLIVSGDK 840
QY 841 SDALGSSISNMLALTSQIRRNKEDALPEEMFSLANLKYLNLSFNFKELEPTSLAS 900
DB 841 SDALGSSISNMLALTSQIRRNKEDALPEEMFSLANLKYLNLSFNFKELEPTSLAS 900
QY 901 LNALKHLIEHSYALLESIPBEGVKGLISLTQLSITYCEMLQCLPBGLOHLTALNLSVEF 960
DB 901 LNALKHLIEHSYALLESIPBEGVKGLISLTQLSITYCEMLQCLPBGLOHLTALNLSVEF 960
QY 961 CPTLAKCEKIGEDWYKIAHPRVFY 988
DB 961 CPTLAKCEKIGEDWYKIAHPRVFY 988

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RESULT 2
ADK98519
ID ADK98519 standard; protein; 988 AA.
XX
XX AC ADK98519;
XX
XX DT 03-JUN-2004 (first entry)
XX
DE S Bulbocastanum Shu11 protein sequence SegID4.
XX
XX plant disease resistance polypeptide; solanaceous plant; potato;
XX late blight disease; fungus; Phytophthora infestans;
XX conferring pathogen resistance; Shu11.
XX
XX Solanum bulbocastanum.
XX
XX WO2004020594-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US027045.
XX
XX 29-AUG-2002; 2002US-0407100P.
XX
XX 20-AUG-2003; 2003US-00647268.
XX
XX (USDA ) US SEC OF AGRIC.
XX (DXYC-) DRY CREEK LAB.
XX
XX Osumi T, Belknap WR, Rockhold DR, Maccree MM;
XX WPI; 2004-239179/22.
XX
XX N-PSDB; ADK98518.
XX
XX New isolated Solanum bulbocastanum late blight resistance nucleic acid
XX molecule encoding a plant disease resistance polypeptide, useful for
XX conferring pathogen resistance to Phytophthora infestans in plants.
XX
XX Claim 10; SEQ ID NO 4; 103bp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX a plant disease resistance polypeptide. The preferred plant is a
XX solanaceous plant that is potato. The resistance is to late blight
XX disease, caused by the fungus Phytophthora infestans. The invention is
XX useful for conferring pathogen resistance in plants using a Solanum
XX bulbocastanum late blight resistance gene. The present sequence is the
XX protein encoded by the S bulbocastanum cDNA sequence of the invention.
XX
XX Sequence 988 AA;
XX
Query Match      99.9%; Score 5120; DB 8; Length 988;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEAFLOVLDMNLTCFIOGELILGFDEBEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
DB 1 MAEAFLOVLDMNLTCFIOGELILGFDEBEKLOSTFTTIOAVLEDAOKKQKLDKAIEN 60
QY 61 WLQKLNAAAYEADDIIDBECKTEAPIRQKNKYGCHYHNVITFRHKIGRMKKIMEKLDVI 120
DB 61 WLQKLNAAAYEADDIIDBECKTEAPIRQKNKYGCHYHNVITFRHKIGRMKKIMEKLDVI 120
QY 121 AAEIKFHLDBERTTEROVATROTFVLANEPQVYGRDKKDEIVKLLINNSNAQTLPLVP 180
DB 121 AAEIKFHLDBERTTEROVATROTFVLANEPQVYGRDKKDEIVKLLINNSNAQTLPLVP 180
QY 181 ILGNGGIGKTTLAQVFNVDQVIEHFHPKIWICVSEDFNEKRLLIKEIVESIEEKSIGMD 240
DB 181 ILGNGGIGKTTLAQVFNVDQVIEHFHPKIWICVSEDFNEKRLLIKEIVESIEEKSIGMD 240
QY 241 LAPLOKRLDLNKGKYLVLVDVWNEODQKAKLRQVLKYGASGASVLTTRLEKVGSI 300
DB 241 LAPLOKRLDLNKGKYLVLVDVWNEODQKAKLRQVLKYGASGASVLTTRLEKVGSI 300

```


QY 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGSVPLAAKTLGSI 360
DB 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGSVPLAAKTLGSI 360
QY 361 LRFKREBQMEHVDSIEWKLPQEESSILPALRSYHHLPLDLROCFYCAVFPDTEME 420
DB 361 LRFKREBQMEHVDSIEWKLPQEESSILPALRSYHHLPLDLROCFYCAVFPDTEME 420
QY 421 KGNLISLMMAHGFIILSKGNLELVNENGVNENELVLRSPFOEIEVKSQGYTFPMHDLJHD 480
DB 421 KGNLISLMMAHGFIILSKGNLELVNENGVNENELVLRSPFOEIEVKSQGYTFPMHDLJHD 480
QY 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKQVSRVNLSDIKKQ 540
DB 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKQVSRVNLSDIKKQ 540
QY 541 LPSSTIGDLVHLRYNLNGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGLR 600
DB 541 LPSSTIGDLVHLRYNLNGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGLR 600
QY 601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQGLGELRNLYSGSIEITHLERY 660
DB 601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQGLGELRNLYSGSIEITHLERY 660
QY 661 KNDMDAKKANLSAKENLSLSMKWDDBRPRIYSEKVEVLEALKPHSNLTCITIRGFRG 720
DB 661 KNDMDAKKANLSAKENLSLSMKWDDBRPRIYSEKVEVLEALKPHSNLTCITIRGFRG 720
QY 721 IRLPDMNHSVYLKNVYSIEIISCKNCSCLPPGELPCLKSLJELMWSAEVEYVDSGFPTR 780
DB 721 IRLPDMNHSVYLKNVYSIEIISCKNCSCLPPGELPCLKSLJELMWSAEVEYVDSGFPTR 780
QY 781 RRPFLRLKLNIREPNLKGILKKEBEOCPVLEIEICCPFPVPTLSSYKLVSGDK 840
DB 781 RRPFLRLKLNIREPNLKGILKKEBEOCPVLEIEICCPFPVPTLSSYKLVSGDK 840
QY 841 SDATGSSISNLMALTSLOIRYNKEDASLPEEMFKSLNLKYNISFYENKELPTSLAS 900
DB 841 SDATGSSISNLMALTSLOIRYNKEDASLPEEMFKSLNLKYNISFYENKELPTSLAS 900
QY 901 LNALKHLIEHSCYALLESPEBGKGLISLTQISITYCEMLQCLPBGLOHLYALNLSYEF 960
DB 901 LNALKHLIEHSCYALLESPEBGKGLISLTQISITYCEMLQCLPBGLOHLYALNLSYEF 960
QY 961 CPTLAKRCEKGIGBEWYKIAHPRFIY 988
DB 961 CPTLAKRCEKGIGBEWYKIAHPRFIY 988

RESULT 3

ADK98525 ID ADK98525 standard; protein; 988 AA.

AC ADK98525;

DT 03-JUN-2004 (first entry)

DE S Bulbocactanum Shu1 protein-related chimeric transgene protein Segid10.

KW plant disease resistance polypeptide; solanaceous plant; potato;
KW late blight disease; fungus; Phytophthora infestans;
KW conferring pathogen resistance; transgenic.

OS Solanum bulbocactanum.

OS Chimeric.

PN MO2004020594-A2.

PD 11-MAR-2004.

PF 28-AUG-2003; 2003WO-US027045.

PR 29-AUG-2002; 2002US-0407100P.
PR 20-AUG-2003; 2003US-00647268.
XX (USDA) US SEC OF AGRIC.
PA (DRIC-) DRY CREEK LAB.
XX Osuni T, Belknap WR, Rockhold DR, Maccree NM;
XX WPI; 2004-239179/22.
DR N-PSDB; ADK98524.
XX New isolated Solanum bulbocactanum late blight resistance nucleic acid
PT molecule encoding a plant disease resistance polypeptide, useful for
PT conferring pathogen resistance to Phytophthora infestans in plants.
XX Claim 10; SEQ ID NO 10; 103pp; English.
XX This invention relates to a novel isolated nucleic acid molecule encoding
CC a plant disease resistance polypeptide. The preferred plant is a
CC solanaceous plant that is potato. The resistance is to late blight
CC disease, caused by the fungus Phytophthora infestans. The invention is
CC useful for conferring pathogen resistance in plants using a Solanum
CC bulbocactanum late blight resistance gene. The present sequence is that
CC of a protein encoded by a chimeric transgene of the invention.
XX
SQ Sequence 988 AA;
Query Match 99.9%; Score 5120; DB 8; Length 988;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 987; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAEAFLOVLNLCFCFIGSELGLILGFDEFEKLOSTFTTIOAVLEDAQKKQKDAIEN 60
DB 1 MAEAFLOVLNLCFCFIGSELGLILGFDEFEKLOSTFTTIOAVLEDAQKKQKDAIEN 60
QY 61 WLQKLNAAVYADLDLDECKTEAPRIQKKNYGCYHNVITFRHKIGRMKKINEKLDVI 120
DB 61 WLQKLNAAVYADLDLDECKTEAPRIQKKNYGCYHNVITFRHKIGRMKKINEKLDVI 120
QY 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDKEDIVKLLINNVNAQTLPLVP 180
DB 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDKEDIVKLLINNVNAQTLPLVP 180
QY 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDKEDIVKLLINNVNAQTLPLVP 180
DB 121 AAEIKPHLDERTIERQVATQGTGVNLNEPOVYGRDKEDIVKLLINNVNAQTLPLVP 180
QY 181 ILGNGGLAKTTLAQMVFNDQVIEHFPKIKWICVSEDFNEKRLIKEIYESIEEKSIGMD 240
DB 181 ILGNGGLAKTTLAQMVFNDQVIEHFPKIKWICVSEDFNEKRLIKEIYESIEEKSIGMD 240
QY 181 ILGNGGLAKTTLAQMVFNDQVIEHFPKIKWICVSEDFNEKRLIKEIYESIEEKSIGMD 240
DB 181 ILGNGGLAKTTLAQMVFNDQVIEHFPKIKWICVSEDFNEKRLIKEIYESIEEKSIGMD 240
QY 241 LAPLOKRLDLLNGKTYLLVLDVWNEBQDMAXLRQYLKVGASGASVLTTRLEKVGSI 300
DB 241 LAPLOKRLDLLNGKTYLLVLDVWNEBQDMAXLRQYLKVGASGASVLTTRLEKVGSI 300
QY 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGSVPLAAKTLGSI 360
DB 301 MGLTQPYELSNLSQEDCMLFMQRAFGHQBIEINLVAIGKEIVKCGSVPLAAKTLGSI 360
QY 361 LRFKREBQMEHVDSIEWKLPQEESSILPALRSYHHLPLDLROCFYCAVFPDTEME 420
DB 361 LRFKREBQMEHVDSIEWKLPQEESSILPALRSYHHLPLDLROCFYCAVFPDTEME 420
QY 421 KGNLISLMMAHGFIILSKGNLELVNENGVNENELVLRSPFOEIEVKSQGYTFPMHDLJHD 480
DB 421 KGNLISLMMAHGFIILSKGNLELVNENGVNENELVLRSPFOEIEVKSQGYTFPMHDLJHD 480
QY 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKQVSRVNLSDIKKQ 540
DB 481 ATSLFSASTSSNIREIIVENYIHMMSIGFTKVSSYSLSHLQKQVSRVNLSDIKKQ 540
QY 541 LPSSTIGDLVHLRYNLNGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGLR 600
DB 541 LPSSTIGDLVHLRYNLNGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLGLR 600
QY 601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQGLGELRNLYSGSIEITHLERY 660
DB 601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKKSQGLGELRNLYSGSIEITHLERY 660

Db 601 NLLIDGCTGTCMPPRIGSLTCLKTLRSFVVGIOKKSQGLBELNLANVGSIEITHLERY 660
 QY 661 KNDMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPAKPHSNLTCLTITRGRG 720
 Db 661 KNDMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPAKPHSNLTCLTITRGRG 720
 QY 721 IRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLKSLIEMWGSALVEVYDSGFPTR 780
 Db 721 IRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLKSLIEMWGSALVEVYDSGFPTR 780
 QY 781 RRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFVITLSSVKKLVSGDK 840
 Db 781 RRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFVITLSSVKKLVSGDK 840
 QY 841 SDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLINSFYFNKLPTSLAS 900
 Db 841 SDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLINSFYFNKLPTSLAS 900
 QY 901 LNALKHLHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLPBGLOHLTALTVLSVEF 960
 Db 901 LNALKHLHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLPBGLOHLTALTVLSVEF 960
 QY 961 CPTLAKRCEKIGEDMYKLAHLPVFIY 988
 Db 961 CPTLAKRCEKIGEDMYKLAHLPVFIY 988

RESULT 4
 ADK98521
 ID ADK98521 standard; protein; 1003 AA.

ADK98521;

03-JUN-2004 (first entry)

S Bulbocastanum Shu12 protein sequence SeqID6.

plant disease resistance polypeptide; solanaceous plant; potato;
 late blight disease; fungus; Phytophthora infestans;
 conferring pathogen resistance; Shu12.

Solanum bulbocastanum.

MO2004020594-A2.

11-MAR-2004.

28-AUG-2003; 2003WO-US027045.

29-AUG-2002; 2002US-0407100P.

20-AUG-2003; 2003US-00647268.

(USDA) US SEC OF AGRIC.

(DRYC-) DRY CREEK LAB.

Oseunt T., Belknap WR, Rockhold DR, Maccree MM;

WPI, 2004-239179/22.

N-PSDB; ADK98520.

New isolated Solanum bulbocastanum late blight resistance nucleic acid molecule encoding a plant disease resistance polypeptide, useful for conferring pathogen resistance to Phytophthora infestans in plants.

Example; SEQ ID NO 6; 103bp; English.

This invention relates to a novel isolated nucleic acid molecule encoding a plant disease resistance polypeptide. The preferred plant is a solanaceous plant that is potato. The resistance is to late blight disease, caused by the fungus Phytophthora infestans. The invention is useful for conferring pathogen resistance in plants using a solanum bulbocastanum late blight resistance gene. The present sequence is the protein encoded by the S bulbocastanum Shu12 gene sequence which was used

CC in the exemplification of the invention.

XX Sequence 1003 AA;

Query Match 88.2%; Score 4521.5; DB 8; Length 1003;
 Best Local Similarity 88.0%; Pred. No. 0;
 Matches 883; Conservative 37; Mismatches 66; Indels 17; Gaps 2;

QY 1 MAEAFLOVLDNITCFIOGELILGFDEFEKLOSTFTTQAVLEDAQKQKDAIEN 60
 Db 1 MAEAFLOVLDNITCFIOGELILGFDEFEKLOSTFTTQAVLEDAQKQKDAIEN 60
 QY 61 WLQKLNAAVEADDIIDECKTEAPIROKNNKGYCHPNVITPFRKIKRKKIMKLDVI 120
 Db 61 WLQKLNAAVEADDIIDECKTEAPIROKNNKGYCHPNVITPFRKIKRKKIMKLDVI 120
 QY 121 AAEIKFHLDERTIERQVATROT-----GFVINEPOVGRDKEKDIYK 164
 Db 121 AAEIKFHLDERTIERQVATROT-----GFVINEPOVGRDKEKDIYK 164
 QY 165 ILINNVNAOTLPVLPILMGGLGKTTLAQVFNDOQVIEHFHFKIWCVSEDFNEKRLI 224
 Db 165 ILINNVNAOTLPVLPILMGGLGKTTLAQVFNDOQVIEHFHFKIWCVSEDFNEKRLI 224
 QY 181 ILINIVDAOTLSVLPILMGGLGKTTLAQVFNDOQVIEHFHFKIWCVSEDFNEKRLI 240
 Db 181 ILINIVDAOTLSVLPILMGGLGKTTLAQVFNDOQVIEHFHFKIWCVSEDFNEKRLI 240
 QY 225 KEIVESIIEKSLGSGMDLAPLOKRLDLNKKTLIVDDVWNBODKRAKLRQVLKYGAS 284
 Db 225 KEIVESIIEKSLGSGMDLAPLOKRLDLNKKTLIVDDVWNBODKRAKLRQVLKYGAS 284
 QY 241 KEIVESIIEKSLGSGMDLAPLOKRLDLNKKTLIVDDVWNBODKRAKLRQVLKYGAS 300
 Db 241 KEIVESIIEKSLGSGMDLAPLOKRLDLNKKTLIVDDVWNBODKRAKLRQVLKYGAS 300
 QY 285 GASVLTTRLEKYSINGTLQPYELSNLSQEDCMLFMORAFGHOEININLVAGKEIV 344
 Db 285 GASVLTTRLEKYSINGTLQPYELSNLSQEDCMLFMORAFGHOEININLVAGKEIV 344
 QY 301 GASVLTTRLEKYSINGTLQPYELSNLSQEDCMLFMORAFGHOEININLVAGKEIV 360
 Db 301 GASVLTTRLEKYSINGTLQPYELSNLSQEDCMLFMORAFGHOEININLVAGKEIV 360
 QY 345 KKGCGVPLAAKTGGILRFKREERQWEHVDSIWKLPQESSILPALRLSYHHLPLDLR 404
 Db 345 KKGCGVPLAAKTGGILRFKREERQWEHVDSIWKLPQESSILPALRLSYHHLPLDLR 404
 QY 361 KKGCGVPLAAKTGGILRFKREERQWEHVDSIWKLPQESSILPALRLSYHHLPLDLR 420
 Db 361 KKGCGVPLAAKTGGILRFKREERQWEHVDSIWKLPQESSILPALRLSYHHLPLDLR 420
 QY 405 QCFYTCVAVFPKOTMEKGNLSLMMAGFLISKNTLELVNGVNMELVRSFQETEV 464
 Db 405 QCFYTCVAVFPKOTMEKGNLSLMMAGFLISKNTLELVNGVNMELVRSFQETEV 464
 QY 421 QCFYTCVAVFPKOTMEKGNLSLMMAGFLISKNTLELVNGVNMELVRSFQETEV 480
 Db 421 QCFYTCVAVFPKOTMEKGNLSLMMAGFLISKNTLELVNGVNMELVRSFQETEV 480
 QY 465 KSGOTYFPMHDLHDLTSLFSASTSSNIREIIVENVIHMSIGFTKVVSSYSLHLOK 524
 Db 465 KSGOTYFPMHDLHDLTSLFSASTSSNIREIIVENVIHMSIGFTKVVSSYSLHLOK 524
 QY 481 TYGKTYFPMHDLHDLTSLFSASTSSNIREIIVENVIHMSIGFTKVVSSYSLHLOK 540
 Db 481 TYGKTYFPMHDLHDLTSLFSASTSSNIREIIVENVIHMSIGFTKVVSSYSLHLOK 540
 QY 525 FVSLRVNLSDIKLKQLEPSIGDLVHLRYNLGNTSIRSLPNOLCTIQNTQTDLHGCH 584
 Db 525 FVSLRVNLSDIKLKQLEPSIGDLVHLRYNLGNTSIRSLPNOLCTIQNTQTDLHGCH 584
 QY 541 FVSLRVNLSDIKLKQLEPSIGDLVHLRYNLGNTSIRSLPNOLCTIQNTQTDLHGCH 600
 Db 541 FVSLRVNLSDIKLKQLEPSIGDLVHLRYNLGNTSIRSLPNOLCTIQNTQTDLHGCH 600
 QY 585 SLCCLPKETSGLGSLRNLLDGCYGLTCMPPRIGSLTCLKTLRSFVVGIOKKSQGLER 644
 Db 585 SLCCLPKETSGLGSLRNLLDGCYGLTCMPPRIGSLTCLKTLRSFVVGIOKKSQGLER 644
 QY 601 RLSCLPKETSGLGSLRNLLDGCYGLTCMPPRIGSLTCLKTLRSFVVGIOKKSQGLER 659
 Db 601 RLSCLPKETSGLGSLRNLLDGCYGLTCMPPRIGSLTCLKTLRSFVVGIOKKSQGLER 659
 QY 645 NLNLYGSIETHLBRVKNMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPA 704
 Db 645 NLNLYGSIETHLBRVKNMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPA 704
 QY 660 NLNLYGSIETHLBRVKNMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPA 719
 Db 660 NLNLYGSIETHLBRVKNMDAKKANLSAKENHLSLSMKMDDERPRIYSEKVEVTLPA 719
 QY 705 KPHSNLTCLTITRGRGIRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLNSIQLW 764
 Db 705 KPHSNLTCLTITRGRGIRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLNSIQLW 764
 QY 720 KPHSNLTCLTITRGRGIRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLNSIQLW 779
 Db 720 KPHSNLTCLTITRGRGIRLPDMNHSVLYKNNVSIIEISCKNCSCLPPGGLPCLNSIQLW 779
 QY 765 RGSAAVEVYVDSGFPTRRRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFV 824
 Db 765 RGSAAVEVYVDSGFPTRRRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFV 824
 QY 780 SGSAAVEVYVDSGFPTRRRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFV 839
 Db 780 SGSAAVEVYVDSGFPTRRRPFSRLKNTREFNGLKGLKKEGEEOCPVLEIEIKCCPMFV 839
 QY 825 IPTLSSVKKLVVSGDKSDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLIN 884
 Db 825 IPTLSSVKKLVVSGDKSDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLIN 884
 QY 840 IPTLSSVKKLVVSGDKSDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLIN 899
 Db 840 IPTLSSVKKLVVSGDKSDAIGFSSISNIMALTSLQIRYNKEDASLPBEMFSLANLKLIN 899
 QY 885 ISFYFNKLPTSLASLANLHLETHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLP 944
 Db 885 ISFYFNKLPTSLASLANLHLETHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLP 944
 QY 900 IYFFNLKELPPLNLAALNKLHLETHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLP 959
 Db 900 IYFFNLKELPPLNLAALNKLHLETHSCYALLESIPBEGVKGLISLTOLSTIYCEMLQCLP 959
 QY 945 EBLQHLTALTNLSVFCPTLAKRCEKIGEDMYKLAHLPVFI 987

[illegible][illegible]

KM Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
 XX Solanum bulbocastanum.
 OS US2003221215-A1.
 XX 27-NOV-2003.
 PD 07-FEB-2003; 2003US-00360522.
 XX 07-FEB-2003; 2003US-00360522.
 XX 07-FEB-2003; 2003US-00360522.
 XX (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
 PA Allefs JHM, Van Der Vossen EAG;
 PI WPI, 2004-010903/01.
 DR New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.
 XX Example 7; SEQ ID NO 55; 98bp; English.
 XX This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of a protein which
 CC was used for homology purposes in the exemplification of the invention.
 XX Sequence 979 AA;
 SO
 Query Match 74.1%; Score 3798; DB 8; Length 979;
 Best Local Similarity 77.1%; Pred. No. 1,9e-304;
 Matches 763; Conservative 75; Mismatches 139; Indels 12; Gaps 8;
 QY 1 MAEAFQVLLNLTGFIQEGELIIGFDEFEKLOSTFTTQAVLEDAQKQKXDAIEN 60
 DB 1 MAEAFQVLLNLTGFIQEGELIIGFDEFEKLOSTFTTQAVLEDAQKQKXDAIEN 60
 QY 61 WLQKLNAAAYEADDLDECKTEAPRQKKNKGYCYHPNVTFRHKTGKMKIMEKLDVI 120
 DB 61 WLQKLNAAAYEADDLDECKTEAPRQKKNKGYCYHPNVTFRHKTGKMKIMEKLDVI 120
 QY 121 AERIKFHLDEKTERQVATROTGFVLAINEPQVYGDGKDEIVKLLINNVSAQQLPVL 180
 DB 121 AERIKFHLDEKTERQVATROTGFVLAINEPQVYGDGKDEIVKLLINNVSAQQLPVL 180
 QY 120 AERIKFHLDEKTERQVATROTGFVLAINEPQVYGDGKDEIVKLLINNVSAQQLPVL 179
 DB 120 AERIKFHLDEKTERQVATROTGFVLAINEPQVYGDGKDEIVKLLINNVSAQQLPVL 179
 QY 181 ILGWGSLGKTTAAQVNFQVRIEHPHPIKIVCSDENEFKRLIKEYISTEKSIGGMD 240
 DB 181 ILGWGSLGKTTAAQVNFQVRIEHPHPIKIVCSDENEFKRLIKEYISTEKSIGGMD 240
 QY 180 ILGWGSLGKTTAAQVNFQVRIEHPHPIKIVCSDENEFKRLIKEYISTEKSIGGMD 239
 DB 180 ILGWGSLGKTTAAQVNFQVRIEHPHPIKIVCSDENEFKRLIKEYISTEKSIGGMD 239
 QY 241 LAPLOKRLDLNGLGKYLVLVDVNNEDQDKMAKLRQVLKVGASGASVLTTRLEKVGSI 300
 DB 241 LAPLOKRLDLNGLGKYLVLVDVNNEDQDKMAKLRQVLKVGASGASVLTTRLEKVGSI 300
 QY 240 LAPLOKRLDLNGLGKYLVLVDVNNEDQDKMAKLRQVLKVGASGASVLTTRLEKVGSI 299
 DB 240 LAPLOKRLDLNGLGKYLVLVDVNNEDQDKMAKLRQVLKVGASGASVLTTRLEKVGSI 299
 QY 301 MGTLOPYELISNLSQEDCWLLEWQARAGHOEINLVAIGKIVKKGCVPLAATLGGI 360
 DB 301 MGTLOPYELISNLSQEDCWLLEWQARAGHOEINLVAIGKIVKKGCVPLAATLGGI 360
 QY 361 LRFKEERQWHEVRSEIWKLPQESSILPRLSTVHNLPLDROCFYCAVFPKOTEME 420
 DB 361 LRFKEERQWHEVRSEIWKLPQESSILPRLSTVHNLPLDROCFYCAVFPKOTEME 420
 QY 360 LRFKEERQWHEVRSEIWKLPQESSILPRLSTVHNLPLDROCFYCAVFPKOTEMA 419
 DB 360 LRFKEERQWHEVRSEIWKLPQESSILPRLSTVHNLPLDROCFYCAVFPKOTEMA 419
 QY 421 KGNLISLWMAHGFIISKNLLELVNENVEWNLVYLSFPOEIVKSGQTYFRQDHLIHD 480
 DB 421 KGNLISLWMAHGFIISKNLLELVNENVEWNLVYLSFPOEIVKSGQTYFRQDHLIHD 480

DB 420 KENLIAFWMAHGFIISKNLLELVNENVEWNLVYLSFPOEIVKSGQTYFRQDHLIHD 479
 QY 481 ATSLFASSTSSNNREIIVENYIMMSIGFTKVVSYSLSHLOKFSRLVNLSDIKKO 540
 DB 480 ATSLFASSTSSNNREIIVENYIMMSIGFTKVVSYSLSHLOKFSRLVNLSDIKKO 539
 QY 541 LPSSIGDLVHLRYNLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLSLR 600
 DB 540 LPSSIGDLVHLRYNLNLSGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSKLSLR 599
 QY 601 NLIDGCGYLTCPMPRIIGSLTCLKLSRFVYVGIQKSCQGLPRLNLYGSIETHLERY 660
 DB 600 NLIDGCGYLTCPMPRIIGSLTCLKLSRFVYVGIQKSCQGLPRLNLYGSIETHLERY 657
 QY 661 KNDMDAKEANLSAKENHSLSMKWDDDRPRIYSEKVEVLEALKPNSNTLCLTIRGFRG 720
 DB 658 KNDMDAKEANLSAKENHSLSMKWDDDRPRIYSEKVEVLEALKPNSNTLCLTIRGFRG 713
 QY 721 IRLPDMNNSVLRKXVNSIIEIISCKNCSCLPPFGLPCLKLSIELWRSABEVRY-DSGFP 779
 DB 714 IRLPDMNNSVLRKXVNSIIEIISCKNCSCLPPFGLPCLKLSIELWRSABEVRY-DSGFP 772
 QY 780 RRRPPLKLNIRFNGUKGLKKEGBOCPVLEIEIKCPMFVPIPLSSVKTLVSGD 839
 DB 773 -GRPPSLRKLVITWDPNSLKGILKKEGBOCPVLEIEIKCPMFVPIPLSSVKTLVSGD 830
 QY 840 KSDAIGFSSISNLMALTSLOIRYKEDASLPPEMFKSLANLYNISFYFNKELPTSLA 899
 DB 831 -TDLTVLRSLISNLMALTSLOIRYKEDASLPPEMFKSLANLYNISFYFNKELPTSLA 889
 QY 900 SLNLKLEHLSHCYALBSLPBEGVGLISLTQLSITYCEMLQCLPEGLQHLTALNLSVE 959
 DB 890 SLNLKLEHLSHCYALBSLPBEGVGLISLTQLSITYCEMLQCLPEGLQHLTALNLSVE 949
 QY 960 FCPLTARCEGEGEDWYKTAHIRVRIY 988
 DB 950 QCPVIFKRCERGIGEDWYKTAHIRVRIY 978
 RESULT 7
 ADH51541
 ID ADH51541 standard; protein, 979 AA.
 XX
 AC ADH51541;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Plant infection-related protein sequence Segid58.
 XX
 KW plant disease; oomycete infection; Phytophthora infestans; fungicide;
 KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
 XX
 OS Solanum bulbocastanum.
 XX
 PN US2003221215-A1.
 XX
 PD 27-NOV-2003.
 XX
 PD 07-FEB-2003; 2003US-00360522.
 PF 07-FEB-2003; 2003US-00360522.
 XX
 PR 07-FEB-2003; 2003US-00360522.
 XX
 PA (KMEB-) KMEB EN RESEARCHBEDRIJF AGRICO BV.
 XX
 PI Allefs JHM, Van Der Vossen EAG;
 XX
 DR WPI, 2004-010903/01.
 XX
 PT New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.
 XX Example 7; SEQ ID NO 58; 98bp; English.
 PS

XX This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of a protein which
 CC was used for homology purposes in the exemplification of the invention.

XX Sequence 979 AA;

Query Match 73.9%; Score 3787; DB 8; Length 979;
 Best Local Similarity 76.9%; Pred. No. 1.5e-303;
 Matches 761; Conservative 76; Mismatches 140; Indels 12; Gaps 8;

1 MAAFAIQLVLDNLTCFIOGELILGFQDEPEKLOSTFTTIOAVLEDAQKKLQKDAIEN 60
 1 MAEAFIOVLDNLTSFLKGLVLFQDEPQRLSSMSTIOAVLEDAQKKLQKDAIEN 60
 61 WLQKLNAAAYEADILDECKTEAPLRQKKNKYCYHPNVITFRHKGKMKIMEKLDVI 120
 61 WLQKLNAAAYEADILDECKTEAPLRQKKNKYCYHPNVITFRHKGKMKIMEKLDVI 120
 61 WLQKLNAAAYEADILDECKTEAPLRQKKNKYCYHPNVITFRHKGKMKIMEKLDVI 120
 61 WLQKLNAAAYEADILDECKTEAPLRQKKNKYCYHPNVITFRHKGKMKIMEKLDVI 120
 121 AAEIRIKHLDERTERQVATQGTGVLNEPOVYGGDKDEIVKLLINNSNAQTLPLPLP 180
 120 AAEIRIKHLDERTERQVATQGTGVLNEPOVYGGDKDEIVKLLINNSNAQTLPLPLP 179
 181 ILGWGSGKTLTAQVNFQDVIEHFKIWIQVSEBDENERKLEIYEISEEKSLGMD 240
 180 ILGWGSGKTLTAQVNFQDVIEHFKIWIQVSEBDENERKLEIYEISEEKSLGMD 239
 241 LAPLOKRLDLNKGKYLVLVDVWNEQDQKMAKLRQVLKYGASGASVLTTRLEKXGSI 300
 240 LAPLOKRLDLNKGKYLVLVDVWNEQDQKMAKLRQVLKYGASGASVLTTRLEKXGSI 299
 301 MGTLOPYELNLSQEDCWLLFMQRAFGHQBIEINLVAIGEIYKCCGVPLAAKTLGGI 360
 300 MGTLOPYELNLSQEDCWLLFMQRAFGHQBIEINLVAIGEIYKCCGVPLAAKTLGGI 359
 361 LRFKREEROMEHVDESEIWKLPQESSITLPLRLSYHNLPLDLQCCFYCAVFPDQTEME 420
 360 LRFKREEROMEHVDESEIWKLPQESSITLPLRLSYHNLPLDLQCCFYCAVFPDQTEME 419
 421 KGNLISLMAHGFILSKNLELENGVNEVMNELYLRSFQIEVKSQTYFKMDLIHDL 480
 420 KGNLISLMAHGFILSKNLELENGVNEVMNELYLRSFQIEVKSQTYFKMDLIHDL 479
 481 ATSLFSASTSSSNIREIIVENYIHMSIGFTKVVSSYSLSHLQKRFVSRVNLSDIKLQ 540
 480 ATSLFSASTSSSNIREIIVENYIHMSIGFTKVVSSYSLSHLQKRFVSRVNLSDIKLQ 539
 541 LPSISGLVHRYNLNGNTSIRSLPNOLCLQNLQTLDLHGCSICCLPETSGLSLR 600
 540 LPSISGLVHRYNLNGNTSIRSLPNOLCLQNLQTLDLHGCSICCLPETSGLSLR 599
 601 NLLDGCGTLCMPPRISLTCLKTLRSFVVGIOKKSQGLGELNMLNYSIEITHLERY 660
 600 NLLDGCGTLCMPPRISLTCLKTLRSFVVGIOKKSQGLGELNMLNYSIEITHLERY 657
 661 KNDMDAKENLISAKENLISLMSKMDDDRPRITYSEKAVLLEALKPHSNLTLCTIRGRG 720
 658 KNDMDAKENLISAKENLISLMSKMDDDRPRITYSEKAVLLEALKPHSNLTLCTIRGRG 713
 721 IRLPDMMHSTLVKXNVVSIIEISCKNCSGLPPRGELPCKSLIEWRGSAEVEYV-DSGPT 779
 714 IRLPDMMHSTLVKXNVVSIIEISCKNCSGLPPRGELPCKSLIEWRGSAEVEYV-DSGPT 772
 780 RRRPFSJLKNIRFENGLKGLKKEGEGCVLEIEIETKCCPMFVIFPLSSVKKLVSGD 839

DB 773 -GRPPSLAKVIMWPFNSMLKGLKKEGEGCVLEIEIETKCCPMFVIFPLSSVKKLVSGD 830
 QY 840 KSDAIGFSSISNMLATSLQIRYNKEDASLPEEMFKSLANIKYINISFYMLKEPLTSLA 899
 DB 831 -TDAITVARSINMLALSLSDISNNVEATSLPDEEFKSLANIKYINISFYMLKEPLTSLA 889
 QY 900 SLNMLKLEIHSYALBSLPBEGVKGSLISLTQSLITYCEMLQCLPEGIQHLTALTNLISVE 959
 DB 890 SLNMLKLEIHSYALBSLPBEGVKGSLISLTQSLITYCEMLQCLPEGIQHLTALTNLISVE 949
 QY 960 FCPILARCEKGEIDPWYKIAHIRVFLY 988
 DB 950 QCPVFRKRCERIGEDWIKIAHIRVFLY 978

RESULT 8

ADFI7765
 ID ADFI7765 standard; protein; 970 AA.

AC ADFI7765;

DT 12-FEB-2004 (first entry)

DE Solanum bulbocastanum Rpi-b1b protein sequence.

KW Rpi-b1b; Rpi-b1b gene cluster; growth regulant; oomycete infection;
 introgression breeding; plant; late blight.

OS Solanum bulbocastanum.

FN Key Location/Qualifiers

FT Misc-difference 143 /note= "Encoded by Gn"

EP1334979-A1.

PD 13-AUG-2003.

PE 08-FEB-2002; 2002EP-00075565.

PR 08-FEB-2002; 2002EP-00075565.

PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

PI Van Der Vossen EAG, Allefs JHM;

DR WPI; 2003-714439/68.

DR N-PSDB; ADFI7759, ADFI7760.

PT New resistance gene conferring resistance against an oomycete pathogen,
 useful for producing plants, especially potatoes and tomatoes, resistant
 PT against oomycete pathogens such as Phytophthora infestans.

PS Example 5; SEQ ID NO 41; 86pp; English.

XX This invention relates to novel isolated polynucleotides that confer
 CC resistance against late blight caused by the oomycete pathogen
 CC Phytophthora infestans, which threatens both tomato and potato crops.
 CC Specifically, it refers to a gene cluster (namely Rpi-b1b) that encodes
 CC leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
 CC and which cause disease resistance to bacteria, fungi, nematodes etc.
 CC These R genes, namely Rpi-b1b, RGC1-b1b, RGC3-b1b and RGC4-b1b, can be
 CC described as plant growth regulators. They are useful in providing
 CC resistance to Phytophthora infestans, especially in Solanum tuberosum
 CC (potato) plants to protect against oomycete infection or to demonstrate
 CC disease susceptibility. Resistance can be conferred by transformation of
 CC existing potato and tomato cultivars with the gene, a procedure that is
 CC more straightforward and faster than conventional introgression breeding.
 CC This polynucleotide sequence is the Solanum bulbocastanum Rpi-b1b protein
 CC of the invention.

XX Sequence 970 AA;

Query Match 73.5%; Score 3766.5; DB 7; Length 970;
 Best Local Similarity 75.6%; Pred. No. 7.5e-302;
 Matches 753; Conservative 78; Mismatches 130; Indels 35; Gaps 8;

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QY 1 MAEAFIQVLDNLTCFIOGELILGFDEFEKLGSTFTTIOAVLEDAQKQKQKAIEN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEAFIQVLDNLTCFIOGELILGFDEFEKLGSTFTTIOAVLEDAQKQKQKAIEN 60
QY 61 WLQKLNAAAYEADIDLECKTEAPRQKKNKYGCHPNVITFRHKGKMKIMEKLDVI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 WLQKLNAAAYEADIDLECKTEAPRQKKNKYGCHPNVITFRHKGKMKIMEKLDVI 120
QY 121 AAEKIKFHLDRTERQVATQGTQFVLNEPQVYGDKEKDEIVKLLINNSNAQTLPTLP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 AAEKKNFHLHKKIYERQAVRRETSVLTPEQVYGDKEKDEIVKLLINNSDAQHLSTLP 179
QY 181 ILGNGGLGKTTLAQWVFNDOQVIEHFPKMIWCVSEDFNEKRLIKEIVESIEEKS-LOGM 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 180 ILGNGGLGKTTLAQWVFNDOQVTEHFFHSKIMICVSEDFNEKRLIKEIVESIEGRPLLGEM 239
QY 240 DLAPLQKKDLNLNGKTYLLVLDVYMNEDQDKMAKLROYLKVGSAGSVLTTRLEKVG 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 240 DLAPLQKKDLNLNGKTYLLVLDVYMNEDQDKMANLRAVLKVGSAGSVLTTRLEKVG 299
QY 300 IMGTLOPVELNLSGEDCMLFMORAFGHOEINLVAIGKEIVKCGGYPLAKTIGG 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 300 IMGTLOPVELNLSGEDCMLFMORAFGHOEINLVAIGKEIVKCGGYPLAKTIGG 359
QY 360 ILRFREERQWEHVDSEIMKLPBESSILPALRLSYHMLPLDLRQCTTYCAVPRKOTEM 419
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 360 ILCFRERARAEHVDSDIPWMLPQDESSILPALRLSYHMLPLDLRQCPAYCAVPRKADAM 419
QY 420 EKGNLISLWMAHGFLLSKGNLELVNGEVMWMLYLRFPQEIYKSGQTYFKMDLHD 479
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 420 EKEKILISLWMAHGFLLSKGNMELVDGVMKEILYLRFPQEIYKSGQTYFKMDLHD 479
QY 480 LATSLFSASTSSNIREITIVENYIMMSIGFTKVVSYSLSHLQKFSVLRYLNLSDIMLK 539
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 480 LATSLFSANTSSNIREINKSHSYTMMSIGRAEVFFTLTLPLEKFIILRYLNLSDISFEN 539
QY 540 QLPSSIGDLVHLRYLNLSGNTSIRSLEPNQCTQNLQTLDLHGHSICCLPETSIGLSL 599
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 540 KLPSSIGDLVHLRYLNLGV-SGMRSLEPKQLCTQLQTLDLQYCTKLCCLPETSIGLSL 598
QY 600 RNLLIDGCGYGLTCMPPRIGSLTCLKTLRSFVYVGIQKSCQGLRNLMYGSIRTHIER 659
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 599 RNLLIDGQSGLTCMPPRIGSLTCLTLDQFVVG-RKKGYQLGELGNLMYGSIKISHLER 657
QY 660 VKNDMDAKEANLSAKENLSHSMKWDDBRPRIYSEKVEVLEALKPHSNITCLTIRGFR 719
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 658 VKNDMDAKEANLSAKGNLSHLSMSH-NNFGPHIYSEEVKULEALKPHSNITSLKIYGR 716
QY 720 GIRLPDMWNSHVLKNVSIIEIISCKNCSCLPEFGELPCLKSLLEWRGSAEVEYVD----- 774
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 717 GIHLPEMNWNSHVLKNVSIILSNFRNCSCLPEFGDLPCLESLELWGSADVEYVEYVDID 776
QY 775 --SGPPTRRRPPSLKNIIRERGNLKGILKKGEGQCYLEIEIKCCPMFVIPTLSSVK 832
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 777 VHSQGPTRIRPPSLRKLDIMWFGSLKGLKKGEGBQFVLEBEMIHEBCPL---TLS--- 830
QY 833 KLIVVSGDSDAIGPSSINIMALTSLQIRYNKEDASLEPEMFKSLANKYINISFYFNK 892
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 831 -----SNLRALTSIRLCYNKVNATSPBEPMFKLANLIKLTISCNLIK 873
QY 893 ELPTSLASINLKHLEIHSYVALBSLPEBGVGLISLTQSLITYCEMLQCLPEGLQHLTA 952
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 874 ELPTSLASINLKLKSLQCLCALBSLPEBGLEGLSLNELFVEHCNMLKCLPEBGLQHLTT 933
QY 953 LTNLSVERCPTLAKGCEKIGEDWYKIAHPRVFYI 988
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 934 LTLKIRGCPOLIRKCEKIGEDWYKISHIPVNIYI 969
  
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RESULT 9
 ADH51537
 ID ADH51537 standard; protein; 970 AA.
 AC ADH51537;
 DT 25-MAR-2004 (first entry)
 DE S bulbocastanum Rpi-b1b protein SegID54.
 XX plant disease; oomycete infection; Phrytophthora infestans; fungicide;
 KW Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.
 XX Solanum bulbocastanum.
 XX US2003221215-A1.
 EN 27-NOV-2003.
 PD 07-FEB-2003; 2003US-00360522.
 XX 07-FEB-2003; 2003US-00360522.
 PE 07-FEB-2003; 2003US-00360522.
 PR (KWE-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
 PA Allefs JHM, Van Der Vossen EAG;
 PI WPI, 2004-010903/01.
 XX N-PSDB; ADH51531.
 DR New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
 PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
 PT with resistance against oomycete infection.
 XX Claim 2; SEQ ID NO 54; 98pp; English.
 XX This invention relates to a novel DNA sequence in the field of plant
 CC disease, in particular oomycete infections. The DNA sequence encodes a
 CC protein which may provide a plant or its progeny with at least partial
 CC resistance against an oomycete infection caused by Phytophthora
 CC infestans. The invention may be useful for the development of compounds
 CC with a fungicide activity. The DNA sequence of the invention encodes an
 CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
 CC cell, protein or binding molecule is useful for providing a plant or its
 CC progeny with resistance against an oomycete infection such as late blight
 CC (a disease of major importance to production of Solanaceae such as potato
 CC and tomato cultivars). The present sequence is that of the S
 CC bulbocastanum Rpi-b1b protein of the invention.
 CC
 SQ Sequence 970 AA;

Query Match 73.5%; Score 3766.5; DB 8; Length 970;
 Best Local Similarity 75.6%; Pred. No. 7.5e-302;
 Matches 753; Conservative 78; Mismatches 130; Indels 35; Gaps 8;

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QY 1 MAEAFIQVLDNLTCFIOGELILGFDEFEKLGSTFTTIOAVLEDAQKQKQKAIEN 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MAEAFIQVLDNLTCFIOGELILGFDEFEKLGSTFTTIOAVLEDAQKQKQKAIEN 60
QY 61 WLQKLNAAAYEADIDLECKTEAPRQKKNKYGCHPNVITFRHKGKMKIMEKLDVI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 WLQKLNAAAYEADIDLECKTEAPRQKKNKYGCHPNVITFRHKGKMKIMEKLDVI 120
QY 121 AAEKIKFHLDRTERQVATQGTQFVLNEPQVYGDKEKDEIVKLLINNSNAQTLPTLP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 AAEKKNFHLHKKIYERQAVRRETSVLTPEQVYGDKEKDEIVKLLINNSDAQHLSTLP 179
QY 181 ILGNGGLGKTTLAQWVFNDOQVIEHFPKMIWCVSEDFNEKRLIKEIVESIEEKS-LOGM 239
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 180 ILGNGGLGKTTLAQWVFNDOQVTEHFFHSKIMICVSEDFNEKRLIKEIVESIEGRPLLGEM 239
QY 240 DLAPLQKKDLNLNGKTYLLVLDVYMNEDQDKMAKLROYLKVGSAGSVLTTRLEKVG 299
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 240 DLAPLQKKDLNLNGKTYLLVLDVYMNEDQDKMANLRAVLKVGSAGSVLTTRLEKVG 299
  
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Dh 240 DLAPLQKQDLGELNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTLTKYKGS 299
Qy 300 IMGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 359
Dh 300 IMGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 359
Qy 360 LRFKREEROMEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 419
Dh 360 ILCKFERBARAEVHRDSPITWMLPODESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 419
Qy 420 EKGMLISLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 479
Dh 420 EKEKXLSLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 479
Qy 480 LATSLSFASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 539
Dh 480 LATSLSFASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 539
Qy 540 QLPSSIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 599
Dh 540 KLPSSIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 599
Qy 600 RNLIDGCGYGLTCCPPIRGSLTCLKTLSRPVVGIOKKSQGLGELRNMLYGSIEITHLER 659
Dh 600 RNLIDGCGYGLTCCPPIRGSLTCLKTLSRPVVGIOKKSQGLGELRNMLYGSIEITHLER 659
Qy 660 VKNDMDAKEALSAKENHSHSMKDDDERPRIYESERVEYELALKPHSNLTCLTINGFR 719
Dh 660 VKNDMDAKEALSAKENHSHSMKDDDERPRIYESERVEYELALKPHSNLTCLTINGFR 719
Qy 720 GIRLPDMNHSVLRKNVSIETISCKNSCCLPPFGELPCLKSLMLRGSAAVEYVD---- 774
Dh 720 GIRLPDMNHSVLRKNVSIETISCKNSCCLPPFGELPCLKSLMLRGSAAVEYVD---- 774
Qy 775 --SGPPTRRRPPSLRKLNIREFGNLSKGLLKKEGEBOCVLEIEIKCCPMFVPIPLSSVK 832
Dh 775 --SGPPTRRRPPSLRKLNIREFGNLSKGLLKKEGEBOCVLEIEIKCCPMFVPIPLSSVK 832
Qy 777 VHSQFPTRIRPPSLRKLDIMDFGSLKGLLKKEGEBOCVLEIEIKCCPMFVPIPLSSVK 830
Dh 777 VHSQFPTRIRPPSLRKLDIMDFGSLKGLLKKEGEBOCVLEIEIKCCPMFVPIPLSSVK 830
Qy 833 KLVVSGKSDAIGSSISNLMALTSLOIRYAKEDASLPBEMFKSLANIKYINISFYPLK 892
Dh 833 KLVVSGKSDAIGSSISNLMALTSLOIRYAKEDASLPBEMFKSLANIKYINISFYPLK 892
Qy 831 -----SNLRALTSRLRCYNKVAITSPBEMFKSLANIKYINISFYPLK 873
Dh 831 -----SNLRALTSRLRCYNKVAITSPBEMFKSLANIKYINISFYPLK 873
Qy 893 ELPTSLASLNLKHEIHSYALSLPEEGVKGILSLTQLSITYCEMLQCLPEGLQHLTA 952
Dh 893 ELPTSLASLNLKHEIHSYALSLPEEGVKGILSLTQLSITYCEMLQCLPEGLQHLTA 952
Qy 874 ELPTSLASLNLKHEIHSYALSLPEEGVKGILSLTQLSITYCEMLQCLPEGLQHLTA 933
Dh 874 ELPTSLASLNLKHEIHSYALSLPEEGVKGILSLTQLSITYCEMLQCLPEGLQHLTA 933
Qy 953 LTNLSEFCPTLAKRCEKIGEDWYKLAHIDPVPIY 988
Dh 953 LTNLSEFCPTLAKRCEKIGEDWYKLAHIDPVPIY 988
Qy 934 LLSLKGCGPOLIRKCEKIGEDWYKLAHIDPVPIY 969
Dh 934 LLSLKGCGPOLIRKCEKIGEDWYKLAHIDPVPIY 969

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PR 07-FEB-2003; 2003US-00360522.
PA (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX Allele JHM, Van Der Vossen EAG;
XX WPI; 2004-010903/01.
XX New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
PT for providing members of the Solanaceae family e.g. Solanaceae tuberosum
PT with resistance against oomycete infection.
XX Example 7; SEQ ID NO 63; 98pp; English.
PS This invention relates to a novel DNA sequence in the field of plant
CC disease, in particular oomycete infections. The DNA sequence encodes a
CC protein which may provide a plant or its progeny with at least partial
CC resistance against an oomycete infection caused by Phytophthora
CC infestans. The invention may be useful for the development of compounds
CC with a fungicide activity. The DNA sequence of the invention encodes an
CC Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
CC cell, protein or binding molecule is useful for providing a plant or its
CC progeny with resistance against an oomycete infection such as late blight
CC (a disease of major importance to production of Solanaceae such as potato
CC and tomato cultivars). The present sequence is that of a protein which
CC was used for homology purposes in the exemplification of the invention.
SQ Sequence 945 AA:
Query Match 73.2%; Score 3752.5; DB 8; Length 945;
Best local Similarity 76.6%; Pred. No. 1e-300;
Matches 745; Conservative 82; Mismatches 113; Indels 33; Gaps 7;
Qy 1 MAEAFQVLVDNLTCTFQGLGILGFKDERKQSNFTTQAVLEDAOKKOLKDAIEN 60
Dh 1 MAEAFQVLVDNLTCTFQGLGILGFKDERKQSNFTTQAVLEDAOKKOLKDAIEN 60
Qy 61 WLOQLNAAAYEADDIIDECKTEAPIROKKNKYGCVHNVTFRHRIKRMKIMKIDVI 120
Dh 61 WLOQLNAAAYEADDIIDECKTEAPIROKKNKYGCVHNVTFRHRIKRMKIMKIDVI 120
Qy 61 WLOQLNAAAYEADDIIDECKTEAPIROKKNKYGCVHNVTFRHRIKRMKIMKIDVI 117
Dh 61 WLOQLNAAAYEADDIIDECKTEAPIROKKNKYGCVHNVTFRHRIKRMKIMKIDVI 117
Qy 121 AAEIKFHLDERTIERQVARTQGTGVINEPQVGRDKDEIKYLINNVSNAOTLPVLP 180
Dh 121 AAEIKFHLDERTIERQVARTQGTGVINEPQVGRDKDEIKYLINNVSNAOTLPVLP 180
Qy 118 AKERTDHLHEKTIERQVAPETGPVLTPEQVGRDKDEIKYLINNVSNAOTLPVLP 177
Dh 118 AKERTDHLHEKTIERQVAPETGPVLTPEQVGRDKDEIKYLINNVSNAOTLPVLP 177
Qy 181 ILGWSGIGKTTLAQVNVNDQVIRHFRPKIYICSEDPNEKRLIKEIYESIEESIGMD 240
Dh 181 ILGWSGIGKTTLAQVNVNDQVIRHFRPKIYICSEDPNEKRLIKEIYESIEESIGMD 240
Qy 178 ILGWSGIGKTTLAQVNVNDQVIRHFRPKIYICSEDPNEKRLIKEIYESIEESIGMD 237
Dh 178 ILGWSGIGKTTLAQVNVNDQVIRHFRPKIYICSEDPNEKRLIKEIYESIEESIGMD 237
Qy 241 LAPLQKQDLGELNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTLTKYKGS 300
Dh 241 LAPLQKQDLGELNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTLTKYKGS 300
Qy 238 LASFOKQDLGELNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTLTKYKGS 297
Dh 238 LASFOKQDLGELNGKRYLLVLDVWMDQOKMANLRAVLVVGASGASVLTTLTKYKGS 297
Qy 301 MGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 360
Dh 301 MGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 360
Qy 298 MGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 357
Dh 298 MGTLPYELSNLSOEDCMLFMORAFGHOEINLVAIGKEIYKKGVPYLAKTIG 357
Qy 361 LRFKREEROMEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 420
Dh 361 LRFKREEROMEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 420
Qy 358 LRFKREEROMEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 417
Dh 358 LRFKREEROMEHVADSEIWKLPQESSILPALRLSYHMLPLDLROCTTYCAVPEKOTEM 417
Qy 421 KGNLISLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 480
Dh 421 KGNLISLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 480
Qy 418 KGNLISLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 477
Dh 418 KGNLISLMAHAGFLSKGNLELVNGEVMNELYLSFFOEIYKSGQTYFKMDLTHD 477
Qy 481 ATSLFSASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 540
Dh 481 ATSLFSASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 540
Qy 478 ATSLFSASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 537
Dh 478 ATSLFSASNTSSNIREIIVENYIMMSIGFTKVSSYSLSHLOKVSILRYLNSDLTK 537
Qy 541 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 600
Dh 541 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 600
Qy 538 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 597
Dh 538 LPSISIGDLVHLRYLNSGNTSIRSLPNQLCKLQNLQTLDHGCHSLCCLPKETSKLSL 597

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QY NLILDGCVGLTCTMPRIISLTCTLSRFVVGIOKKSQCOLGELNINLYGSIIRITHLERV 660
DB 598 NLLHGHCHRLTRTPRIGSLTCTLTGQFVVG-RKKGQOLGELNINLYGSIIRITHLERV 656
QY 661 KNDMDAKEANISAKENIHSLSMKWDDDERPRIYSEKYEVLKALKPHSNLTCTLTIGFRG 720
DB 657 KNDXAKEANISAKENIHSLSMKWDDDE-PRHYSEBEVEVLKALKPHSNLTCTLTIGFRG 715
QY 721 IRLDPMMNHSVLKNNVSIIEISCKNCSGLPPRGELPCIKSLIEMRGSAE-VEX-----VDS 775
DB 716 IRLDPMMNHSVLKNNVSIIEISCKNCSGLPPRGELPCIKSLIEMRGSAEVEVDIVDS 775
QY 776 GPTRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLSSVKLV 835
DB 776 GPTRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLSSVKLV 826
QY 836 VSGDKDAIGFSSISNIMALTSLQIRYNKEDASLPEEMFKSIANKIYNISFYENKELP 895
DB 827 -----SNLKALTSINISDNKEATSPPEEMFKSIANKIYNISFYENKELP 872
QY 896 TSLASINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQHTLTALTN 955
DB 873 TSLASINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQHTLTALTN 932
QY 956 LSVFCPTLAKRC 968
DB 933 VKINGCPOLIKRC 945

RESULT 11

ADHS1543
ADHS1543 standard; protein; 992 AA.

ADHS1543;
25-MAR-2004 (first entry)

Plant infection-related protein sequence SeqId60.

plant disease; oomycete infection; Phytophthora infestans; fungicide;
Rpi-b1b protein; plant; late blight; Solanaceae; potato; tomato.

Solanum bulbocastanum.

US2003221215-A1.

27-NOV-2003.

07-FEB-2003; 2003US-00360522.

07-FEB-2003; 2003US-00360522.

(KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.

Allefs JHM, Van Der Vossen EAG;

WPI; 2004-010903/01.

New isolated or recombinant Rpi-b1b nucleic acids and proteins, useful
for providing members of the Solanaceae family e.g. Solanaceae tuberosum
with resistance against oomycete infection.

Example 7; SEQ ID NO 60; 989p; English.

This invention relates to a novel DNA sequence in the field of plant
diseases, in particular oomycete infections. The DNA sequence encodes a
protein which may provide a plant or its progeny with at least partial
resistance against an oomycete infection caused by Phytophthora
infestans. The invention may be useful for the development of compounds
with a fungicide activity. The DNA sequence of the invention encodes an
Rpi-b1b protein comprising 970 amino acids. The nucleic acid, vector,
cell, protein or binding molecule is useful for providing a plant or its
progeny with resistance against an oomycete infection such as late blight

CC (a disease of major importance to production of Solanaceae such as potato
and tomato cultivars). The present sequence is that of a protein which
was used for homology purposes in the exemplification of the invention.

XX Sequence 992 AA;

Query Match 72.9%; Score 3736.5; DB 8; Length 992;

Best Local Similarity 74.8%; Pred. No. 2,4e-299;

Matches 747; Conservative 92; Mismatches 141; Indels 19; Gaps 8;

QY 1 MAEFLOVLDNLTCFIOGELGLGKDFEKLQSFITTIQAVLEDAOKKOLDKAIEN 60
DB 1 MAEFLOVLDNLTCFIOGELGLGKDFEKLQSFITTIQAVLEDAOKKOLDKAIEN 60
QY 61 WLOKLNAAVEADDIIDCKTEAPIRQKNKYGCYHNVTFRKIKGRMKIKMDLVI 120
DB 61 WLOKLNAAVEADDIIDCKTEAPIRQKNKYGCYHNVTFRKIKGRMKIKMDLVI 119
QY 61 WLOKLNAAVEADDIIDCKTEAPIRQKNKYGCYHNVTFRKIKGRMKIKMDLVI 120
DB 61 WLOKLNAAVEADDIIDCKTEAPIRQKNKYGCYHNVTFRKIKGRMKIKMDLVI 119
QY 121 AAEIRKHELDERTTERQVARTQGFVINEPQVYGRDYEKDEIVKILINNSNAQTLEVL 180
DB 120 AAEIRKHELDERTTERQVARTQGFVINEPQVYGRDYEKDEIVKILINNSNAQTLEVL 179
QY 120 AAEIRKHELDERTTERQVARTQGFVINEPQVYGRDYEKDEIVKILINNSNAQTLEVL 179
DB 120 AAEIRKHELDERTTERQVARTQGFVINEPQVYGRDYEKDEIVKILINNSNAQTLEVL 179
QY 181 ILGNGIGKTTLAQWVNDQVIEHHPKTIWICVSEDPNEKRLIKEIYESTIEEKSGMD 240
DB 180 ILGNGIGKTTLAQWVNDQVIEHHPKTIWICVSEDPNEKRLIKEIYESTIEEKSGMD 239
QY 241 LAPLOKKLRDLNAGKTYLVLDVWNEDODKMAKLRQVLKVGASGAVLTTTRLEKYSI 300
DB 240 LAPLOKKLRDLNAGKTYLVLDVWNEDODKMAKLRQVLKVGASGAVLTTTRLEKYSI 299
QY 301 MGTLOPYELNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGSI 360
DB 300 MGTLOPYELNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGSI 359
QY 300 MGTLOPYELNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGSI 359
DB 300 MGTLOPYELNLSQEDCMLFMQRAFQHOEININLVAIGKEIVKCGGVPLAKTIGSI 359
QY 361 LRFKREERQWVHVDSEIKVLPQESSILPRLRSTYHLPLDRLQCFYCAVFPKDTME 420
DB 360 LRFKREERQWVHVDSEIKVLPQESSILPRLRSTYHLPLDRLQCFYCAVFPKDTME 419
QY 421 KGNLISLMAHGFILSKGNLEENVGNEVMNELYLRSPFOEIEVKSQTYFKMDLTHDL 480
DB 420 KGNLISLMAHGFILSKGNLEENVGNEVMNELYLRSPFOEIEVKSQTYFKMDLTHDL 479
QY 481 ATSLPESATSSSNIREFI-----IVENYHMSIGFTKVVSYSLSLQKFSYLRV 530
DB 480 ATSLPESATSSSNIREFI-----IVENYHMSIGFTKVVSYSLSLQKFSYLRV 530
QY 531 LNLSDIKLQKPPSSIGDLVHLRYNLISGNISIRSLPQCLQNLQTLDTLHGHSLCLCP 590
DB 530 LNLSDIKLQKPPSSIGDLVHLRYNLISGNISIRSLPQCLQNLQTLDTLHGHSLCLCP 590
QY 540 LNLNSEFEQLPSSVGDVHLRYLIDLSGN-KICSLPKRLCKLQNLQTLDTLHGHSLCLCP 598
DB 540 LNLNSEFEQLPSSVGDVHLRYLIDLSGN-KICSLPKRLCKLQNLQTLDTLHGHSLCLCP 598
QY 591 KETSGLGSLRNILLDGCVGLTCTMPRIISLTCTLSRFVVGIOKKSQCOLGELNINLYG 650
DB 590 KETSGLGSLRNILLDGCVGLTCTMPRIISLTCTLSRFVVGIOKKSQCOLGELNINLYG 650
QY 599 KOTSGLGSLRNILLDGCVGLTCTMPRIISLTCTLSRFVVGIOKKSQCOLGELNINLYG 656
DB 599 KOTSGLGSLRNILLDGCVGLTCTMPRIISLTCTLSRFVVGIOKKSQCOLGELNINLYG 656
QY 651 SIEITHLERVKNDMDAKEANISAKENIHSLSMKWDDDERPRIYSEKYEVLKALKPHSNL 710
DB 650 SIEITHLERVKNDMDAKEANISAKENIHSLSMKWDDDERPRIYSEKYEVLKALKPHSNL 710
QY 657 AISITHLERVKNDMDAKEANISAKENIHSLSMKWDDDERPRIYSEKYEVLKALKPHSNL 713
DB 657 AISITHLERVKNDMDAKEANISAKENIHSLSMKWDDDERPRIYSEKYEVLKALKPHSNL 713
QY 711 TCTLTIGFRGRLRDPMMNHSVLKNNVSIIEISCKNCSGLPPRGELPCIKSLIEMRGSAE 770
DB 710 TCTLTIGFRGRLRDPMMNHSVLKNNVSIIEISCKNCSGLPPRGELPCIKSLIEMRGSAE 770
QY 771 EYV-DGPTRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLS 829
DB 770 EYV-DGPTRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLS 829
QY 774 EYVDSGFTLTKRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLS 833
DB 774 EYVDSGFTLTKRRRPPSLRKINIREFGNLIKGLKKEGEGOCVLEIEIKCCPMVPIITLS 833
QY 830 SVKKLIVVSGDKDAIGFSSISNIMALTSLQIRYNKEDASLPEEMFKSIANKIYNISFY 889
DB 830 SVKKLIVVSGDKDAIGFSSISNIMALTSLQIRYNKEDASLPEEMFKSIANKIYNISFY 889
QY 834 SVKKLIVVSGDKDAIGFSSISNIMALTSLQIRYNKEDASLPEEMFKSIANKIYNISFY 892
DB 834 SVKKLIVVSGDKDAIGFSSISNIMALTSLQIRYNKEDASLPEEMFKSIANKIYNISFY 892
QY 890 NUKELPISLAINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQ 949
DB 890 NUKELPISLAINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQ 949
QY 893 NUKELPISLAINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQ 952
DB 893 NUKELPISLAINALKHLEIHSCTALSSLPREGVKGLISLTQLSITYCEMIQCLPEGLQ 952

QY 950 LTAATNLNLSVEFCPTLAKRCCKGIGEDWYKIAHIPRVIY 988
DB 953 LTTLTSLKIRGCPOLIKRCCKGIGEDWYKISHIPRVIY 991

RESULT 12
ADFI17767 standard; protein; 992 AA.

AC ADFI17767;
XX 12-FEB-2004 (first entry)
XX Solanum bulbocastanum RGCI-blb protein sequence.
XX RGCI-blb, Rpi-blb gene cluster; growth regulant; oomycete infection;
XX introgression breeding; plant; late blight.
XX Solanum bulbocastanum.
XX Key Location/Qualifiers
FT Misc-difference 143 /note= "Encoded by GT"
XX EPI334979-A1.
XX 13-AUG-2003.
XX 08-FEB-2002; 2002EP-00075565.
XX 08-FEB-2002; 2002EP-00075565.
XX 08-FEB-2002; 2002EP-00075565.
XX (KWEK-) KWEK EN RESEARCHBEDRIJF AGRICO BV.
XX Van Der Vossen BAG, Allefa JHM;
XX WPI: 2003-714439/68.
XX DR N-PSDB: ADFI17762.
XX New resistance gene conferring resistance against an oomycete pathogen,
XX useful for producing plants, especially potatoes and tomatoes, resistant
XX against oomycete pathogens such as Phytophthora infestans.
XX Example 5; SEQ ID NO 43; 86bp; English.
XX This invention relates to novel isolated polynucleotides that confer
XX resistance against late blight caused by the oomycete pathogen
XX Phytophthora infestans, which threatens both tomato and potato crops.
XX Specifically, it refers to a gene cluster (namely Rpi-blb) that encodes
XX leucine-rich repeat (LRR) proteins identified in Solanum bulbocastanum,
XX and which cause disease resistance to bacteria, fungi, nematodes etc.
XX These R genes, namely Rpi-blb, RGCI-blb, RGCI-blb and RGCI-blb, can be
XX described as plant growth regulators. They are useful in providing
XX resistance to Phytophthora infestans, especially in Solanum tuberosum
XX (potato) plants to protect against oomycete infection or to demonstrate
XX disease susceptibility. Resistance can be conferred by transformation of
XX existing potato and tomato cultivars with the gene, a procedure that is
XX more straightforward and faster than conventional introgression breeding.
XX This polypeptide sequence is the Solanum bulbocastanum RGCI-blb protein
XX of the invention.

QY 992 AA;
SQ Sequence 992 AA;

Query Match 72.8%; Score 3730.5; DB 7; Length 992;
Best Local Similarity 74.7%; Pred. No. 7.4e-299;
Matches 746; Conservative 92; Mismatches 142; Indels 19; Gaps 8;

QY 1 MAAEAPLOVLNLTGFCIGELIGFDEFEKQSTTTTQAVLEDAQKQKQDKAKIEN 60
DB 1 MAAEAPLOVLNLTGFCIGELIGFDEFEKQSTTTTQAVLEDAQKQKQDKAKIEN 60
QY 61 WLQKLNAAYEADDLIDCKTEAPIRQKKNKYGCYHNVITFRHKIGKMKIMEKLDVI 120

DB 61 WLQKLNAAYEADDLIDCKTEA-ARFQAVLGHYHPTITFCYKVGKRMKMEKLDVI 119
QY 121 AAERIKFHLDERTEROVAATPOTGFVLINEPOVYARDKEDIEIVILINNVAQTLPTLP 180
DB 120 AAEERNPHLDERIERQARRQIGFVLEPRVYREKREDEIVKILINNVSIEEVPPLP 179
QY 181 ILGNGGLGKTTLAQMFVNDQREVIHFPKIKVICSEDFENRKLIAKIEVSEIEKSLGMD 240
DB 180 ILGNGGLGKTTLAQMFVNDQREVIHFPKIKVICSEDFENRKLIAKIEVSEIEKSLGMD 239
QY 241 LAPLOKTLRDILNKKTLVLVDVWNEEDQKMAKROVLKVGASGVLTTRLEKNGSI 300
DB 240 LAPLOKTLRDILNKKTLVLVDVWNEEDQKMAKROVLKVGASGVLTTRLEKNGSI 299
QY 301 MGLTQPELNSLQGECDMLFMORAFOHOBELINLVAIGEIVYKKGSGVLAKTGGI 360
DB 300 MGLTQPELNSLQGECDMLFMORAFOHOBELINLVAIGEIVYKKGSGVLAKTGGI 359
QY 361 LRFGREROMEHVADSEIWKLPQESSILPALRLSYHHLPLDLRQCFYCAVFPKDTME 420
DB 360 LRFGREROMEHVADSEIWKLPQESSILPALRLSYHHLPLDLRQCFYCAVFPKDTME 419
QY 421 KGNLISLMAHGFLLSKGNILELVNGNEVWNELYLSFPQEIYVKSQTYFKMDLIDL 480
DB 420 KEYLIALMAHGFLLSKGNILELVNGNEVWNELYLSFPQEIYVKSQTYFKMDLIDL 479
QY 481 ATSLFASSTSSNTRF-----IYENVYHMSIGFTKVVSSVSLSLQKFPVSLRV 530
DB 480 ATSLFASSTSSNTRF-----IYENVYHMSIGFTKVVSSVSLSLQKFPVSLRV 539
QY 531 LNLSDIKLKOLPSSIGLVHLRYLNLGNTSIRSLPOLCQNLQTLIDLHGCSLCLP 590
DB 530 LNLSDIKLKOLPSSIGLVHLRYLNLGNTSIRSLPOLCQNLQTLIDLHGCSLCLP 598
QY 591 KETSGLSLRNLIDGCGYGLTCLMPRIIGSLTCLTSLRFPVVGIOKSCQGLGELRNLVY 650
DB 590 KETSGLSLRNLIDGCGYGLTCLMPRIIGSLTCLTSLRFPVVGIOKSCQGLGELRNLVY 656
QY 651 SIETTHLERKYNMDAKEANLSAKENHSLSMKRDDDERPRIYSEKVEVLEALKPHSNL 710
DB 657 AISTTHLERKYNMDAKEANLSAKENHSLSMKRDDDERPRIYSEKVEVLEALKPHSNL 713
QY 711 TCLTIRGPRGIRLDPDMNHSVLKNVSEIISCSNCSCLPPGELPCLKSLRLRGSABV 770
DB 714 KYLEIIDFCGFCPLDMNHSVLKNVSEIISCSNCSCLPPGELPCLKSLRLRGSABV 773
QY 771 EYV-DSGFPTRRRPPSLRKINIREFGNLKGLLKKEGECCVLEIEIKCCPMFVPIPLS 829
DB 774 EYVDSGFTLRRRPPSLRKINIREFGNLKGLLKKEGECCVLEIEIKCCPMFVPIPLS 833
QY 830 SVKLVVSGDKSADIGSSISNLMALTSLOIRYNKEDASLPDEMFKLANLKYINISFYF 889
DB 834 SVKLVVSGDKSADIGSSISNLMALTSLOIRYNKEDASLPDEMFKLANLKYINISFYF 892
QY 890 NLKELPTSLASLNLKLEIHSYALSLPEEGYKGLISTOLSTYCEMLQCLPEGLQH 949
DB 893 NLKELPTSLASLNLKLEIHSYALSLPEEGYKGLISTOLSTYCEMLQCLPEGLQH 952
QY 950 LTAATNLNLSVEFCPTLAKRCCKGIGEDWYKIAHIPRVIY 988
DB 953 LTTLTSLKIRGCPOLIKRCCKGIGEDWYKISHIPRVIY 991

RESULT 13
ADH51539 standard; protein; 992 AA.
ID ADH51539
XX ADH51539;
XX 25-MAR-2004 (first entry)
XX Plant infection-related protein sequence SeqID56.


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Db 1 MAEAFIVLIDNLSFPLKGBLVLLPFGONEROLSSIFSTIQAVLEDAQOKLNDKPLEN 60
QY 61 WLOKLNAAAYEADDILDECKTEAPIROKNKYCYHPNVITFRHKIGRMKIMEKLDVI 120
Db 61 WLOKLNAAAYEADDILDECKTEAPIROKNKYCYHPNVITFRHKIGRMKIMEKLDVI 119
QY 121 AAEIRIKHLDERTIERQVATROGTVLANEPQVYGRDKKEDEIVKILINNVSNAOTLPVLP 180
Db 120 AAEIRIKHLDERTIERQVATROGTVLANEPQVYGRDKKEDEIVKILINNVSNAOTLPVLP 179
QY 181 ILGWSGKTKTIAQWVFNDQZVIEHHPFKIWCYSEDENEKRLIKEIYESIEEKS-LGSM 239
Db 180 ILGWSGKTKTIAQWVFNDQZVIEHHPFKIWCYSEDENEKRLIKEIYESIEEKS-LGSM 239
QY 240 DIAPIOKKLDLNGKXYLLVLDVWNEODQMAKROVLKVGASGASVLTTRLEKVG 299
Db 240 DIAPIOKKLDLNGKXYLLVLDVWNEODQMAKRAVLKVGASGAFVLTTRLEKVG 299
QY 300 IMGTLOPYELSNLSOEDCWLPMQAPGHQREINLVAIGKEIVKKGCVPLAKTLGG 359
Db 300 IMGTLOPYELSNLSOEDCWLPMQAPGHQREINLVAIGKEIVKKGCVPLAKTLGG 359
QY 360 ILRFKREEROMEHYVDEIWMKLPQESSILPALRLSYHHLPLDLROCFYCAVPKOTEM 419
Db 360 ILRFKREEROMEHYVDEIWMKLPQESSILPALRLSYHHLPLDLROCFYCAVPKOTEM 419
QY 420 EKGNIISLMAHGFILSKNLELENVGNEVWNELYLRSFQOIEVKSQTYFKWHDLIHD 479
Db 420 EKGNIISLMAHGFILSKNLELENVGNEVWNELYLRSFQOIEVKSQTYFKWHDLIHD 479
QY 480 IATSLFASASTSSNREITVENYTHMSIGTKVVSYSLSHLQKVSILRYLANSDIKLK 539
Db 480 IATSLFASASTSSNREITVENYTHMSIGTKVVSYSLSHLQKVSILRYLANSDIKLK 539
QY 540 QLPSSIGLVHLRYLANSGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGL 599
Db 540 QLPSSIGLVHLRYLANSGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGL 599
QY 540 ELSSSIGLVHMRCLDLSENGSIRSLPKQLCKLQNLQTLDLHNCYSLSCLPREPSKGL 599
Db 540 ELSSSIGLVHMRCLDLSENGSIRSLPKQLCKLQNLQTLDLHNCYSLSCLPREPSKGL 599
QY 600 RNLLIDGCGYLTCPMPRIIGSLTCLKTLRSFVVGIOKSCQUGELRNLMYGSIEITHLER 659
Db 600 RNLLIDGCGYLTCPMPRIIGSLTCLKTLRSFVVGIOKSCQUGELRNLMYGSIEITHLER 659
QY 660 VKNMDACEANISAKENHSLSMKWDDEPRIVSEKVEVLEALKPHSNLTCLTIRGFR 719
Db 659 VKNMDACEANISAKENHSLSMKWDDEPRIVSEKVEVLEALKPHSNLTCLTIRGFR 719
QY 720 GIRLEPDMNHSVLAQVNSIEIISCHNCSCLPPFGEIPLCKLSLELWRSAAVEYVDSGFP 779
Db 718 GIRLEPDMNHSVLAQVNSIEIISCHNCSCLPPFGEIPLCKLSLELWRSAAVEYVDSGFP 777
QY 780 RRRPFSIKLNIREFGNTKGLIKKGEBOCPVLEIEIKCCPMFVIFTLSSVYKLVVSGD 839
Db 778 RRRPFSIKLNIREFGNTKGLIKKGEBOCPVLEIEIKCCPMFVIFTLSSVYKLVVSGD 839
QY 840 KSDAIGFSSISLMLTSLQIRYNKEDASLPEEMFSLANLKYLNISFYFNKELPTSLA 899
Db 823 KSDAIGFSSISLMLTSLQIRYNKEDASLPEEMFSLANLKYLNISFYFNKELPTSLA 899
QY 900 SINALKHLEIHSQVLESIPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNLSVE 959
Db 877 SINALKHLEIHSQVLESIPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNLSVE 959
QY 960 FCPPLAKRC 968
Db 937 RCPOLIKRC 945

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 01:07:49 ; Search time 45 Seconds
(without alignments)
1638.962 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEFLQVLNDLNTFCFIGE.....EKIGEDWYKIAHPRVFIV 988

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1240	24.2	1240	3	US-08-930-996A-4
2	1198	23.4	1220	3	US-08-930-996A-2
3	1041	20.3	1402	3	US-09-004-838-11
4	969.5	18.9	784	3	US-09-004-838-12
5	729.5	14.2	553	3	US-09-004-838-16
6	609.5	11.9	1255	3	US-08-947-823-3
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11	571.5	11.1	1257	3	US-08-947-823-5
12	550.5	10.7	905	3	US-09-360-166-3
13	550.5	10.7	905	4	US-09-864-680A-3
14	528	10.3	234	4	US-09-803-286A-8
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16	521	10.2	1247	4	US-09-803-286A-2
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18	512.5	10.0	909	2	US-08-310-912A-142
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21	510	9.9	885	2	US-08-310-912A-2
22	510	9.9	885	3	US-08-841-089-2
23	510	9.9	885	3	US-09-301-085-2
24	510	9.9	885	5	PCT-US95-04589-2
25	510	9.9	885	5	PCT-US95-04589-2
26	505.5	9.9	907	3	US-08-930-996A-7
27	473.5	9.2	1824	2	US-08-680-327-3

28	473.5	9.2	1824	3	US-09-228-246-2	Sequence 2, Appli
29	454	8.9	412	2	US-08-414-938A-4	Sequence 4, Appli
30	436.5	8.5	345	3	US-09-004-838-13	Sequence 13, Appli
31	436.5	8.5	928	4	US-09-336-946B-2	Sequence 2, Appli
32	436.5	8.5	928	4	US-09-993-170-58	Sequence 58, Appli
33	431.5	8.4	928	4	US-09-336-946B-4	Sequence 4, Appli
34	394	7.7	1890	3	US-09-004-838-88	Sequence 88, Appli
35	386	7.5	1074	3	US-09-004-838-111	Sequence 111, App
36	385	7.5	1366	3	US-09-004-838-82	Sequence 22, Appli
37	378	7.4	1144	3	US-08-930-996A-9	Sequence 9, Appli
38	377	7.4	1854	3	US-09-004-838-108	Sequence 108, App
39	374	7.3	1805	3	US-09-004-838-92	Sequence 92, Appli
40	373	7.3	1222	3	US-09-004-838-119	Sequence 119, App
41	367	7.2	1143	2	US-08-310-912A-108	Sequence 108, App
42	367	7.2	1143	3	US-09-301-085-108	Sequence 108, App
43	367	7.2	1143	5	PCT-US95-04589-108	Sequence 108, App
44	367	7.2	1144	1	US-08-261-663A-2	Sequence 2, Appli
45	367	7.2	1144	1	US-08-261-663A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-930-996A-4
Sequence 4, Application US/08930996A
Patent No. 6100449
GENERAL INFORMATION:
APPLICANT: FLUOR, Robert
APPLICANT: ESHED, Yuval
APPLICANT: ORI, Naomi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930, 996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-996A-4
Query Match 24.2%; Score 1240; DB 3; Length 1240;
Best Local Similarity 28.6%; Pred. NO. 1.66-100;
Matches 359; Conservative 211; Mismatches 378; Indels 306; Gaps 39;
QY 6 LQVLLNDLNTFCIGFDE---FEKLOSTFTTQAVLEDAQKQKQKALENW 61
DB 16 LNVLFRLA--PNDLLNMFKHKDHYVLLKKLQWTLRGIOIVISDAENKQASNPSPVADW 73


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Dh 251 TDLKADBNLNOQVQLKADBNLNOQVQLKCKENGRFLVLDVWNNDDYPERMDLLRNF 310
Qy 280 KVGASGASVLTTRLEKVGSTMGTLQPELNLNLSQEDCLLPMQAFGHQF-EIUNLVYA 338
Dh 311 LOGDIGSKIIVTRKESVALMWDSCAIY-MGLISEDSKALFKRSLBEKDKPEPEEE 369
Qy 339 IGKEIVKCGGVP/LAAKTLGGILRKREERQEHNRDSITWLPOEBSIIIPALSLYH 398
Dh 370 VGGQADCKKGPE/LKALAGMKRSEVDENRILRSTIEPSCNSILPALMISTYD 429
Qy 399 LP/LDRCFTYCAVPPKDTMEKGMILSLMWHGEFLSKGNLELNVGSEVNNELYSF 458
Dh 430 LPAHKKQCLAYCAIPKQYFRKEGVYHIMINGLV-----HQHSGNQYIEIARSL 483
Qy 459 FOEIEVKSQYV--FRKMDLIHDLATSLPSASTSSNIR-----EIVENYIHM-MSIG 509
Dh 484 FEMASEPERDVEEFLAMDVLNDLA-----QLASNNHCRLEDNKGSHMLEQCRHMSYSIG 539
Qy 510 ----FTKVSSKXSLSHLOKV-----SLRVNLSDIKLKQ 540
Dh 540 QDEEEKKSKSLFKSQEQLRLLPIDIQFHYSKSLSKRVLHNLIPTRLSRALSLSHYQIEV 599
Qy 541 LPSISIG-DLVHLRYNLNGNTSIRSLPNOLCKLONLOTLDHGSHLCLPKETKLSL 599
Dh 600 LPNDLFTKILRLFDLS-ETSIYTKLPDSIFVLVYLETLLSSCYBLEPLQMEKTLNL 658
Qy 600 RNLLLDGCGYGLCMPRRIGSLTCLKTL--SRFVGIQKSCCOLGELRYNLNYSIEITHL 657
Dh 659 RHLDISNTRRLK-IFLHLSRLKSLQVLVGAKEFLVGGMWNE-YLGAP-NLYGSLSTIEL 714
Qy 658 ERVKNDMDAKENASAKENLHLSMKWDDDEPRRYESEKVEVLEALKRPHSNLTCLTRG 717
Dh 715 ENVVDREAVAKARMEKNHVEQLSEMSBSISADNSQTER-DIDELPPHKIKAVEITG 773
Qy 718 FRGIRLPMWHNSVYKANVSIEIISCKNCSCLPREGELPCLKSLELMAGSAVEVYDSGF 777
Dh 774 YRGINFPWVADPLPVKLVHLYLRNCKDCYSLPALGQPLCFLEFSI-RMGIRVYTEEF 832
Qy 778 PTR-----RPPSLRKLNIR-----EFGNL 797
Dh 833 YGRLSKKKPFNSLVKLRPEDMPEWKQWHTLIGGEPTLEKSIKNCPELSLEIPQFOSL 892
Qy 798 KGL-----LKKE--GE----- 806
Dh 893 KRLIDCDKSVTSFPFSILPTTLKRKIKISGCPKLLLEAPVGEVFYEYLSVIDCGCVDIS 952
Qy 807 -EQCPVLEIEIKKC--PMFPIPR----- 827
Dh 953 PEPLPTARQSLSENCHNVTFLIPATSLHIRNCEKLSMACGGAQULTSLNIWCKKLIK 1012
Qy 828 ----LSSVKKL-----VSGDKDAIAGFSSISNIMALT 856
Dh 1013 CLPELLEPLSKELRLTYCEISEGELPFPNIQIDIRCKCKLVNRKE-----WHQQLT 1066
Qy 857 SLQIRYNKD-----ASLPEMEKSIANIKYL-----NISFYMLX 892
Dh 1065 ELMTIKHDSDEHIEHWELPSSIQRLFIENLKTLSQHLKSLTSLQFLRIVGNLSQFOSQ 1124
Qy 893 ELPLPSLALNLKHLHISCVALBESLPRGVKGLISLQLSITYEMLQCP-BEQHLT 951
Dh 1125 QL-SSFSHLTSLQTLQINFWNLQSLPSALPS--SLSHLISNCPNLOSPLKMP--S 1179
Qy 952 ALTNISVEFCPTLAKRCEKIGEDMYKIAHPRVI 987
Dh 1180 SLSTLSISKCELTPLLELFDKGEYVTEIAHIFTIQT 1215

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APPLICANT:  Melbourne, Richard W.
APPLICANT:  Shen,Kathy
APPLICANT:  Meyers, Blake
TITLE OF INVENTION:  Procedures and Materials for
TITLE OF INVENTION:  Confering Pest Resistance in Plants
NUMBER OF SEQUENCES:  140
CORRESPONDENCE ADDRESS:
ADDRESS:  Townsend and Townsend and Crew LLP
STREET:  Two Embarcadero Center, Eighth Floor
CITY:  San Francisco
STATE:  California
COUNTRY:  USA
ZIP:  94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE:  Floppy disk
COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/Ms-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/09/004,838
FILING DATE:  09-JAN-1998
CLASSIFICATION:  800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:  US 08/781,734
FILING DATE:  10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME:  Eibhorn, Gregory P.
REGISTRATION NUMBER:  38,440
REFERENCE/DOCKET NUMBER:  023070-078810US
TELECOMMUNICATION INFORMATION:
TELEPHONE:  (415) 576-0200
TELEFAX:  (415) 576-0300
INFORMATION FOR SEQ ID NO.:  11:
SEQUENCE CHARACTERISTICS:
LENGTH:  1402 amino acids
TYPE:  amino acid
STRANDDEDNESS:
TOPOLOGY:  linear
MOLECULE TYPE:  protein
FEATURE:
NAME/KEY:  -
LOCATION:  1..1402
OTHER INFORMATION:  /note= "RLG1A amino acids"
US-09-004-838-11

Query Match      20.3%;   Score 1041;  DB 3;   Length 1402;
Best Local Similarity 29.3%;   Pred. No. 9.6e-83;
Matches 311;  Conservative 180;  Mismatches 395;  Indels 174;  Gaps 28

QY    1 MAE-----AFGLVDLNDLTLCFLIQELGLILGFDPKPEKLSPTFTTLOAVLEDKKQLDKD 56
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QY    57 ALENWLOKLNAAAYEADDIIDECKTEADIRQKNKYGCYNPNV-----ITFRNKI 106
DB    427 AVKSWMLNDIQHLAYDIDDLDXXTEAVXRRELTGEGASSMWVKILPSCCTSFSQSNNM 486
QY    107 GKRRKKIMKEKDVIAAEIKRHLDERTIERQVATQTGFVLNRPVYGRDKDEIVKL 166
DB    487 HAKLDIIATRILQELVEAKNNLGSLVITYEKPKIEFEYSALDSGTYGGEEDKKLLEKL 546
QY    167 I--NNVSNAQTLPLPIFGMGGLGKTTTAQWFNVQNDRYLEHPRKIWCISEDFENKRLL 224
DB    547 LGDDXDESSQNFSIYPIVGMSGVGKTTLARLLDYDKXYKDHELPAWVCVSDSEFSVPNIS 606
QY    225 KEIVESIEEKSUGMDLAPLQKRLDLINGKKYLVLDVNVEDODRKAKLRQVLKVAS 284
DB    607 RVIQSVSYGEEKEFEDNLILQEALEKELRNOLFLIVLDVWSSESYGWEKLVGPFLAGSP 666
QY    285 GASVLITTRLEKVASINGTLOPYELSNLSQSDCWLLFMORAFCQHE-EINLNVAIGKEI 343
DB    667 GSRIIMTRREQQLNRKGISHQDPLEBGSJODDALSLFPAOHFAGVDPNFSSHPTLRPHGELEF 726
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QY	344	VKKCGVPLAKTLIGLIRFREEROMENHADVSTWKLPOESSLIRPATRSTYHNLRLD	403
QY	727	VKKCDGRLRLRTIGRLRLRTDDEOWMELLDSIEWLKGSD-ELVPLRLSTYNDLSAXL	785
QY	404	ROCFYCAVFPKJOTEMEKGNLISLMMAHGFI-TSKGNLELNMGNVNNELYLTSFPOEI	462
Db	786	KLFAYGSLFPKJOTVEPDKBELILLMMEGFLHOFPTKSKRRLGLRYEXELLSFPQ-	843
QY	463	EYKSGQTYFKMDDLHDLATSLFSASTSSSI-----RELIIVENYIHM-----	505
Db	844	HAPYKSLFVWHDLMDLDTAFVAGEFGRLDIEMKCEFRKXSLKHRMSFVCEXYIGYK	903
QY	506	-----MSIGTKVYSSLSLH-----LQFVSLRYLNLSDIKLQOLPS	543
Db	904	XFEFPRGAKNLRTELATSLFSAVGEVBEWMEKFEYLSNKNYLDLQDLPLRLRYLXLIXVYPX	963
QY	544	SIGDLVHLRYLNLSGNLSIRSLPNOLQLOTLDLHGCSLOCLPETSKLASRLYL	603
Db	964	XVSGWMLHRYNLNS-KTYITHLPEXKCNLYLQTLYVSGCYLLXALPFTFSXLKNLHFD	1022
QY	604	LDGCVGLTCEPPIRIGSLTCLTSLRFPVVGIOKKSQCOLDELNLNL-NLYGSIETHLERYKN	662
Db	1023	MRTFPLXKNMPLXIGELKXLOTLF-XNIGI-----AIRELNKNIMNHKKCIGIGAKKEN	1076
QY	663	DMDAKEANLSAKENHLISLW-----KWDDERPRIYSEKEVLEALKPHSNL-T	711
Db	1077	AVGCTLSLVSKYKXXKXNMWXXGXIXCPKXW-----BHLKKXSIMWK	1119
QY	712	CL-----TIRGFRGIRLPPDMNHNHSLKKNVSIETISCNCSCLPFRGSLPCLKSL--	761
Db	1120	CLIMWLAKKPYIMSIGIEFPNWGSLRVSSTRDVFMYEK-XCFYFHOSPQKXMIT	1177
QY	762	-----ELMRGSA-----EVEYV-DGSPFTRRRPFLKRLNREFGNLKL	800
Db	1178	SGXIDEMWKRNGIKGLGAVEEISIHSCNEIRILMSEBAASRYMNLKLDJGECENLYSL	1237
QY	801	LKKEGEE-----QCFVLEIEITKCP-----MFVILPLSSVKVLV	835
Db	1238	GEKKEDNNINSGSLTFRRLNFWRCNSLLEHR--CPDSMENLYMHMCDXSITSFPT	1294
QY	836	VSGDKSDAIGFSSISNLMALTSLOIRYKEDASLPEEMFKSLAN-----LKYINISFTFN	890
Db	1295	GGGQK-----IKSLITTDCKKLSBELGGERETRYVLINSKOMLESVDIRMPN	1343
QY	891	LKELPTSLASLNLKHLIEHSVYALLESPEBGVKGILSL	930
Db	1344	LKSL-SELSCFIHNLRYLINSOPKSESPPDEHLPNULSLT	1382

RESULT 4
US-09-004-838-12
Sequence 12, Application US/09004838
Patent No. 6350933
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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1      APPLICATION NUMBER:  US/09/004,838
2      FILING DATE:  09-JAN-1998
3      CLASSIFICATION:  800
4      PRIOR APPLICATION DATA:
5      APPLICATION NUMBER:  US 08/781,734
6      FILING DATE:  10-JAN-1997
7      ATTORNEY/AGENT INFORMATION:
8      NAME:  Elsborn, Gregory P.
9      REGISTRATION NUMBER:  38,440
10     REFERENCE/DOCKET NUMBER:  023070-078610US
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE:  (415) 576-0200
13     TELEFAX:  (415) 576-0300
14     INFORMATION FOR SEQ ID NO:  12:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH:  784 amino acids
17     TYPE:  amino acid
18     STRANDEDNESS:
19     TOPOLOGY:  linear
20     MOLECULAR TYPE:  protein
21     FEATURE:
22     NAME/KEY:  -
23     LOCATION:  1..784
24     OTHER INFORMATION:  /note= "RUG1B amino acids"
25     US-09-004-838-12

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Query Match	18.9%	Score 969.5;	DB: 3;	Length 784;
Best Local Similarity	34.7%	Pred. No. 8.2e-77;		
Matches 242;	Conservative 131;	Mismatches 265;	Indels 59;	Gaps 12.
QY	1	MABAFLOVLDNLNLCFIGELGILGFKDEBEKLSQSTFTTTQAVLEPDKOKLODKALEN	60	
DB	97	LGSAFFAVPEERKLASBALKRVACSKVLDKELEKLSKXINKALLNDASQISENAVKE	156	
QY	61	WLQKLNAAAYEADDIIDECKTEADIRQKKNY-----CYHNVITFRHKIGK	108	
DB	157	WLNLOHLPVIDDLDGLATKAIHRKFESEYCATINKVRKLIPSCFSSLSST---KVRN	213	
QY	109	RMKIMEKLDVIAERIKFHLDETTIRQVATROTGFALNRP-QYGGDEKKEDEIVKLI	167	
DB	214	KIHNTISKLOELBERNNLIGCEIGESRKLNRRSETSKLDSPSSIVGTDEKALLKLY	273	
QY	168	NNVSNADTOLPLPIITGGGAGKTTLAQWVFNDQVIEHFHPKIMICVSEDFENEKALKEI	227	
DB	274	EPCC--RNFSLPIVGGGDLKTTLGRLLYXMQYKHFEKAVCVSDEDFISSTI	331	
QY	228	VESIERSLGMDLAPLOKKLRDLNNGKRLVLDVNNEDQDKAKLRQYIKVAGSAGAS	287	
DB	332	FESIIEGNGQERKDLNLLQVALKEKISKRRFLVLDVDSSESYTWEILERFELAGAPSGK	391	
QY	288	VLTTRLEKSGSINGTLOPYELSNLSQEDCKMLFMQRAF-GHOEININLVAIGKEIYKK	346	
DB	392	VITTRKSLTNQGHQOPQLSDISHNALSLPCQAHFGVNSFDSHPILKPHGEIYVK	451	
QY	347	CGGVPILAKTILGILFRPREERQWENHVDSEIYKLPQESSILPALRLSYNHLPLDLRQC	406	
DB	452	CDGRLPALIALGRILTRGRDEEKWELINSITWIKGRD-ELIPKRLSYNDLSASLKOL	510	
QY	407	FTYCAVEPKOTEMEKGNLISLMAHGFILSKG-NILEENGVNEYNWELLYRSFQELIEVK	465	
DB	511	FAYCSLPPKOVFNFKKILIMMAEGFLHNENTKSMERLXLEYFDLLSRSPFQ--HAL	568	
QY	466	SGQTFYKMHDLIIDLATLSLSASSTSSNI--REILVEYIIM-----	505	
DB	569	DKSLFVHDIMDLNLSVADGYFLRLDIEMKKALKCYRHSFVCSYMYVKKREPEPK	628	
QY	506	-----MSIGTKVVSYSLSH-----LQKVSRLVNLSDIKKOLPSSIGIDLVA	550	
DB	629	AKKLRTFLAMVGNIKSWTTFYLSNKKVLDLJLHPEPLRLVSLSTLSLKEVPEIIGNLKH	688	
QY	551	LRYLNTSGNTSIRSLPNOLCLQMLQOTLDLHGCHSLCCLPEYTSKLGSLRNLIDGCYGL	610	
DB	689	LRYLNTS--HHSITLHPENVCMLYNLQTLILCGCCCTITFPNNFLKRLRYLRHIDISDTGCL	747	


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QY 5 FLQVLDNLTCFIOGELGLIGFKDFEKLQSTFTTIOAVEDAOQKQDKAIENMLQK 64
D 390 FMHLHLHLNLDLSNAYSIALIKEEILVQKDLKFISSFDVABQGLYKDL-----WAV 445
QY 65 LMAAYEADDLDECKTEAPIRQKNKKGCHPNVITFRNHG-KRMKIKKEDV----- 119
D 446 LD-VAYEKADVIDS-----IIVRN-GLAH-LIISLPITTKIKLIEEISALDEN 493
QY 120 IAAER--IKFHLDEKTERQVATQGFVLINEPOVYGRDKEDIVKLLINNVNAQTLF 177
D 494 IPRKGLIVNAPKPKVPRKSLT-----TDKITVGEFEETNILLRGL-----TSGSADLD 543
QY 178 VLPITGKGLQKTTIAQNVENDQVIEHFHKIMCVSEDFNEKRLKIEYIESIEKSLG 237
D 544 VISITGMGSGKTTIAYKVNDKSVSRFDIRAMCTVQGDCKKLTNTITSQVSDSK 603
QY 238 GMDLAPLOKRLDNLNGKKYLLVLDVWNEODQKAKLROYLVKVGASGASVLTTRLEKV 297
D 604 LSENIDVADKRLKQKFGKRYLVLDVW--DTTWDELTRPPBKSGSRILITTR-EKE 660
QY 298 GSIMGTL--OPEYLSNLSQEDCMLFMQARFGHOEIMINLVAIGKEIVKCGVPLAAK 355
D 661 VALHGNKATDPLDLRLRPDSMELLEKRAFGN-ESCPDELDVGEKIAENCKGLPLVAD 719
QY 356 TLGGILFRREERQ-WEHYRDEIYKLPQEBESSILPALRLSYHNLPLDLROCFYCAVFP 414
D 720 LIAGVIAGREKRSVYLEVQSSLSFINSSEVKNVIELSDHLPHHLKPLCLFYASF 779
QY 415 KOTEMEKNLISLMAHGFILSKNLEENGVENWELYSRF--FOEIEVKSQGYTF 471
D 780 KOTSLITYELNVPFAGSGFVGTBNMSMEVVKITMDLIYSVLVCIENEIYALN--F 836
QY 472 KMHDLIHD-----LATSLFSASTSSNIREIIV--ENYIHMSIGFTVWSSY 517
D 837 QIHDLVHDFCLIKARKENLFDQIRSSAPSDLLPQIITDCBEEHFGNFWFEDSKKH 896
QY 518 SLISHQKFSVLNVLNLSDKLKQLPSSICDVLHLYLN-----LSQNTSI-----RSLPNOL 569
D 897 SKKHL--YSLRITIG-----DOLDSDVADAHHLRLRLVLDLHTSFIMKDSLMEI 947
QY 570 CKLONIQTLDLHGCHSLCCLPKETSKLGSINMLLDGCGYGLTCMPRIGSLTCLTLGRF 629
D 948 CMLNHLRYISID--IQVKLPISFNNIMWLSLFTSTRSILVLLPRILDIKLVLS-- 1003
QY 630 VVGIOKKSQGLGELRNMLNYSIEITHLERKVNMDAKENLSAK--ENHLSMKWD 685
D 1004 ----VDACSF-----FMDADESILIAEDTKLENLRILT----- 1033
QY 686 DDERPRIYSEKVENLELKPHSNLTCLIRGFRGRLPDMWNVSVLKNVSIIEISCKN 745
D 1034 ----ELLISYKOTKNIKFRFPNQL-----LSFELKESND 1065
QY 746 CSCLP-FGELPCLKSLE-LMRGSAEVEYVDSG-----PYRRRPS-LARKLNTREFGN 796
D 1066 YSTEQHMFSELDLFTLELTLSVGFKSSNNDGSSVATRRPMDHPSPULKILMLREFPL 1125
QY 797 LKGLLKEGEOCPVLEIEIKCCPMFVPTLSSVKKLVSGKSDATFSSISNLMALT 856
D 1126 TSDSLSTIA--RLPNLEEL-----SLHTIIGHBENWMEGDEDFENMLKFN 1169
QY 857 SIQIRNKEDASLPEEMFKSIANLKYNISFYFNKLEPTSLASINALKHLIEHSCYALE 916
D 1170 FNOVSIKWEVG--EESF--PMLKCLKRGCHKEIETPPSGDIYSLASIKIVASPOL 1224

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RESULT 7
US-08-930-996A-8
; Sequence 8; Application US/08930996A
; Patent No. 6100449
; GENERAL INFORMATION:
; APPLICANT: FLUHR, Robert
; APPLICANT: ESHED, Yuval

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; APPLICANT: ORI, Naomi
; APPLICANT: PARMAN, Ilan
; APPLICANT: ZAMIR, Daniel
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,996A
; FILING DATE: 09-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05272
; FILING DATE: 15-APR-1996
; APPLICATION NUMBER: IL 113,373
; FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 920 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-930-996A-8

```

```

Query Match 11.8%; Score 606; DB 3; Length 920;
Best Local Similarity 22.8%; Pred. No. 2,1e-44;
Matches 250; Conservative 176; Mismatches 371; Indels 300; Gaps 40;

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QY 1 MAEFLQVLDNLTCFIOGELGLIGFKDFEKLQSTFTTIOAVLEDAQK-----KQLK 54
D 1 MASATVDFGIRILSVLENETLLSGVHGEI-KMKKELLNKSFLBETHKNGSGSTTT 59
QY 55 DKAIENMLQKNAAYEADDLDECKTEAPIRQKNKKGYCYH-----PN 98
D 60 TQLFQTVANTRDALAYQLEIDLDE-----FG-YHIGYRSCKAKIMRAPHPRR 105
QY 99 VITFRHKIGKMKKIMEKLDVIAERIKFH-----LDEKTERQVATROGFPV 146
D 106 YMAARHSIAQGLGVNWNVIGISDSMKRYHSENYQALLPPIIDGDAKWNNTISESLF 165
QY 147 LNEPOVYRDEKDEIYKLLINNVSNQTLFVPLILGAGGKTTLLAQNVENDQVIEHF 206
D 166 FSEKSLVGIDAPKCKLIGRLIS--PEPQRI-VVAVVGSGSGKTTLLSNIFKSGSVRRHF 222
QY 207 HPKLMICVSEDF-----NEKRLKIEYIESIEEK-----SIGMDLAPLOKRLDNLNGKK 256
D 223 ESYAWTISKSYVIEDVRNMIKEFYKADQIAPALYSIGYREL--EKLVEYLOSKR 279
QY 257 YLVLDVWNEODQKAKLROVLKVGASGASVLTTRLEKYGSI--MGTLOPELSNLS 313
D 280 YIVLVLDVWNT--TGLMREISIALPDGIVGSRVMMTTRDMNVASPPYIGGYTK-HEIELLK 336
QY 314 QEDCMLFMQARFGHOE--INLNLVVAIGKIVKCGVPLAAKTLGGILFRKREEROME 371
D 337 BDEAWVLPFSNKAFPASLEQCRQTONLEPIARKLVERC-GLPLAIALSLSGMSMTKTFESNKK 395
QY 372 HYRDESEIKVL--POBESSILPALRLSYHNLPLDLROCFYCAVFPKOTEMEKNLISLM 429
D 396 KYVSTLAMELNHNHKLKIVRSIMPLSPNDLVPPLKRCGLYCSLFPVNVYRMKRLILRMM 455

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QY 430 AHGFLSKGNLELVNGEVENNELYLRSPFOEI-----EYKSGQTYFRMGDLIHDLATS 483
Db 456 AGRFVEPIRGVAAEYADSYLNEVLVYRNMLQVILNMPGRPRXA-----FPMHDIWEIALS 511
QY 484 -----LFSASTSSNIREIIVENY-----IHMSIGTFKVYS--Y 517
Db 512 VSKLERFCDVYVDDDDGDAE--TWENYGSRLCTQKEMTPSIRATNINSHSLVCSAKH 570
QY 518 SLSHLQKFSVLNMLSDIKLQOLPSSIGDLVHLRYLNSGNTSIRSLPNOLCKLQNT 577
Db 571 KWEILLPSLNLRLALDLBSSISKLPDLCTVMENLKNLINS--KTQVKEIPKXNHKLVNLET 629
QY 578 LDHCHGS--LCLPKEYSKLSRLNLDGCGYGLTQMPRIGSLTCLKTLRS----- 628
Db 630 LNTK--HSHKIEBLPLGMMWKLKKLRYLI-----TFRRNEGHDSNW 666
QY 629 -FVVG--LOKSCOLGELRNMLVGSIEI-----THLERYKNDMAKE-----ANLS 672
Db 667 NYVLGTRVVPKTMQKLDQWDCNEDELKMLGCMTQLTRISLVMRERHGRDLCDSL 726
QY 673 AKENLHSLMKWDDERPRIYSEKEVEVLKPKHSNLTCLTRNGRIGRLPDMNHSVL 732
Db 727 KIKRIFSLTSLSDIEEPLLEIDLATASIEKTLFLAGLE-----RVPSWEN----- 772
QY 733 KNVVSIEIISCKNCSCLPPGELPCLKSLLEWRGSAEVEYVDSGFPTRRRPPLKKNIR 792
Db 773 ----- 772
QY 793 EFGNLKGLKKEGEBOCYVLEIEIKCCPMFVPTLSSVKLVSGDSDAIGFSSISNL 852
Db 773 -----TLOMLTYLGLGSQLQENALISIOTL 798
QY 853 MALTSIQIRYNKEDASLPEEMF--KSLANIKYLNISFYFNLEKLPSTLSLNLKLEIHS 911
Db 799 PRVLWLS--YANMG--FRLRPAQGFQNLKILEIYQMGHLBEVLEDAAMELOLQLYRA 855
QY 912 CYALESPEEGVKGLISLTQUSTYCEMLQCLPBGLOHLTALTNLSVEFCPTLAKRCEKG 971
Db 856 CRGLEEYV--RGIEMLINLQEL-----HLIHVSQNLVERI-----RG 890
QY 972 IGEDMYKIAHPRVITY 988
Db 891 EGSVDSRV-HIPLAKHY 906

RESULT 8
US-09-245-928A-19

; Sequence 19, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1206
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: ORF2 encoded
; OTHER INFORMATION: polypeptide
US-09-245-928A-19

Query Match 11.2%; Score 575.5; DB 4; Length 1206;

Best Local Similarity 26.3%; Pred. No. 1.7e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;

QY 5 FLOYLDLNLGCEIQLGELIIGKDFEPEKLTSTFTTQAVLEDDOKQL--DOKAIENMLQ 63
Db 339 FPHLLHMLNDLNSNAYSISLKEIEIYVSGEELFISFGDAEQLYD-----IYAR 394
QY 64 KLNAAVEADDLDECKTEAPIRQKNKYGCYHPNVITFRHIG--KRMKKIMEKLDV--- 119
Db 395 VLD--VAEAKVIDS-----IIVRDN--GLLH--LIFSPLITIKIKLKEISALDE 442
QY 120 -IAER--IKFHLDERITEROVATRGTFVINEPQVYGRDKEKEIYKILINNVSNAQT 176
Db 443 NIPDRGLIVNSPKVEKRSILT-----TDKIIYGFEEETMLIRKL---TSGPADL 492
QY 177 FVLPLIGGLGKTTIAQMVNDQVIEHFPKIMICSEDFENKRIKIEIVSEIEEKSL 236
Db 493 DVISITMPGSKTTLIAKYVNDKSVSRHFDLRAMCTVDQGYDQKLDLDTIFSGVSGSDS 552
QY 237 GAMDAPLOKKLRDLNGKTYLVLDDVNMEDODKMAKLRLQVLKVGASGASVLTTRLEK 296
Db 553 NLSNIDVADKLARKQLGKRLIYLDVW--DTTLDELTRPPEAKKGSRIILITTR--EK 609
QY 297 VGSIMGTI--OPELSNISQEDCWLFMQRAFGHQBENINLVAIGKIVKCGVPLAA 354
Db 610 EVALHGKINTDPLRLRLRPDESWELEKRTFGN--ESCPDELDVGEIAENCKGLPLVA 668
QY 355 KITGLIARFKREEQ--WEHRDSEIWLPOEESILALRLSTHYHLPLDLRQCTYCAVF 413
Db 669 DLINGVIAGREKRSWLEVOSSLSFSLNSEVMKVETLSYHLPHLKPLCHLFPWSW 728
QY 414 PKOTEMERKNLISLMAHGFILSKNLELVNGEVENNELYLRSP-----FOEIEVKSQTY 470
Db 729 PKOTFPLIYLLTVLGLGEGFEKTEKMGIEBVYKIMDDLSSLVICFNEI---GDILN 785
QY 471 FKMDLIHDLA-----TSLF-----SASTSSNIREIIV-----ENYIHMSIGFTKVS 515
Db 786 FOIHDVLVDFCLIKARKENLFDRISSAPSDLRQRTIDVDEEHEHGFALFVFDNSKK 845
QY 516 SYSLSHLQKFSVLNMLSDIKLQOLPSSIGDLVHLRYLNSGNTSIR-----SLPN 567
Db 846 RHSGKHL--YSLN-----INGQDDSVSDAFLHRLIRVLDLEPSLIWVNDILN 896
QY 568 QLCQLONLQTLDLHGCHSLCCLPKETSKLSRLNLDGCGYGLTQMPRIGSLTCLKTL 627
Db 897 EICMLNHLRYLRIR--TQVKYLPSPSNLWNLBSLFPVSNKGSILVLLPRILDLVKLYLS 954
QY 628 RFVVGIOKKSQOLGELRNMLVGSIEITHLERYKNDMAKCANLSAK-----ENLHSLMK 683
Db 955 ---VG-----ACSF-----FMDADDESILIAQDTLENRLIG-- 984
QY 684 WDDDERPRIYSEKEVEVLKPKHSNLTCTTRNGRIGRLPDMNHSVLKNVVSIEIISC 743
Db 985 -----ELISYSKQDMNIFKFPNLOVQO-----FELKESWDYSTEDHW----- 1023
QY 744 KNSGCLPPFGLPLKSLK--LMBG--SAEVEYVDSGFPTR---RPSLRKLNIREFGN 796
Db 1024 -----FKLDCLTELETLVGFKSSNTNHGSSVATNRPMDFHFPSS-----N 1065
QY 797 LKGLKKEGEBOCYVLEIEIKCCPMFVPTLSSVKL-----VSGDKSDAIGFSSISN 851
Db 1066 LKELL-----LYDFPLTSDSLSTARLNLNLSLYDTLIOGEBNMGBEDTFEN 1115
QY 852 LMAITSIQIRYNKEDASLPEEMFKSLANLYLNISFYFNLEKLPSTLSLNLKLEIHS 911
Db 1116 LKFLNLRLLTSLKWEVG--EESFPNLEKLIQBCG--KLEIIPSPGDIYSIKFIKIVK 1170
QY 912 CYALE 916
Db 1171 SPOLE 1175

RESULT 9

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US-09-245-928A-17
; Sequence 17, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1243
; TYPE: PRT
; ORGANISM: M1 resistance gene deduced amino acid
US-09-245-928A-17

Query Match      11.2%; Score 575.5; DB 4; Length 1243;
Best Local Similarity 26.3%; Pred. No. 1.8e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;

5 FLOVLLDNLTCTFIOGELGLIGFQDEFEKLOSTTTTQAVLEDAQKOL-KDKALENWLQ 63
Db FVHLHMLNDLSDNAYSISLKEIEIIVSQLEFIRSFEGDAEQQLYKD---IWAR 431
QY KLNAAAYRADDLIDCKTEAPIRQKKNKYGCVHPIVIFRKHIG-KRMKKIMEKLDV--- 119
Db 432 VLD-VAYEKQVIDS-----IIVRDN--GLIH---LIFSPLITTKIKLKEEISALDE 479
QY 120 -IAAER--IKFHLDERTIERQVATROGTFVINEPQVYGRDKDEIYKILINNVSNAQTL 176
Db 480 NIPKRGILVNSPKKPYERKSLT-----TDKIIVGFEEETNLIIRKL---TSGPADL 529
QY 177 PVLPIILMGIGIKTTLAQVFNQDQVIEHFRPKIWCISEDNEKRLLKEIVESIIEEKS 236
Db 530 DIVSITGMFGSGKTTLAKYVNDKSVSRHFDLRACVTDQGDGDKLDTTFSQVSGSDS 589
QY 237 GGMIDLAPLOKKLRDLNKGKTYLVLDVWNEEDQDKMAKLRQVLAKYGASGASVLTTRLEK 296
Db 590 NUSENIDVADKLRKOLFGRKYLIIVLDVW--DTTLDLDELTRFPFAKKGSRIILITTR-EK 646
QY 297 VGSIMGTL--QPYELSNLSQEDCWLIFMQRAFQHOEINLNLVAIGKEIVKKGCVPLAA 354
Db 647 EYALHGKLTNDPLDLRLRPDSWELERKTFGN-ESCPDELIDVGEIENCKGLPLVA 705
QY 355 KTLGGILRFKREERO-WEHVRDSEIWKLPQESSIIPALRLSYHNLPLDLRQCFYCAVF 413
Db 706 DLIAGIAGREKKRSYWEVOSLSFSFIINSEVEWVYELSYDLPHILKPCLLHFAFSW 765
QY 414 PROTMEKENLNLISWMAHGFILSKGNLEENYGENEWNELYSRF---FOEIEVKSQTY 470
Db 766 PNOTPFTTYLLVYIGAGSFEVETEMKKGIEEYVAKYIMDLISSLVICNEL---GDILN 822
QY 471 FPGHDLIHDLA-----TSLF---SASTSSSNIREIIV-----ENYTHMMSIGFTKVS 515
Db 823 FQIHDLVHDFCLIKARKENLFPDIRSSAPSDLLPRQITIDYDEBEHFGILNFMFDSNKK 882
QY 516 SYSLSHLOQFVSLRVNLSDIKKLPSSIGDLVHRYNLNGNSIR-----SLPN 567
Db 883 RHSGKTL---YSLR-----INGDQDDSVSDAFHRLRLRLRVLDLEPSLIMVNDSLN 933
QY 568 QLCCKLONLTDLHGCHSLCPKETSQKLSRLNLLDGCYGLTQMPRIIGSLTCLIKTIS 627
Db 934 ETCMLNHLVYLAIR--TQYKYLPRFSNLMNLESFVSNKSGSLVLLPRLIDLVKLRVLS 991
QY 628 RRVVGIQKSKCOLGELRNINLYGSIEITHLERVKNMDMAKANLSAK---ENLHSLSNK 683

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Db 992 ---VG-----ACSF-----FMDADESILLIAKOTKLENLRLIG-- 1021
QY 684 WDDDERPRIYSEKVEVLEALKPHSNLTCTIRGFRIGRLPDMWNHSLVKNVYSIEIISC 743
Db 1022 -----ELLISYSKDTWNIIFKRPENLQVIO-----FELKESMDYSTEGHW----- 1060
QY 744 KNCSCLPPEGLPCLKSLE-LWRG--SAEVEYDGSFPYTR---RPSLRKLNIREFGN 796
Db 1061 -----FKDCLDTLELTLCVGFKSNTHHGOSSVATNRPMDFHPPS-----N 1102
QY 797 LKGLLKEGBEQCVLEIEIKCCPMFVPIITLSVKL-----VSGDKGDAIGFSSISN 851
Db 1103 LKEEL-----LYDFPLTSDLSSTIRLPLNLESLSYDTLIIQGEWMMGSEDTFEN 1152
QY 852 LMAITSQIRYKNKEDASLPREMFKSLANLYKLNISFENIKELPTSLASINALKHEIHS 911
Db 1153 LKFLNRLTLTSKWEVG--BSFNPNEKLIKQECG--KLEIIPPSGDIYSLKFIKIYK 1207
QY 912 CYALE 916
Db 1208 SPQLE 1212

RESULT 10
US-09-245-928A-18
; Sequence 18, Application US/09245928A
; Patent No. 6613962
; GENERAL INFORMATION:
; APPLICANT: KEYGENE N.V.
; TITLE OF INVENTION: RESISTANCE AGAINST NEMATODES AND/OR APHIDS
; FILE REFERENCE: 960-35
; CURRENT APPLICATION NUMBER: US/09/245, 928A
; CURRENT FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/EP97/04340
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: EP96401764.4
; PRIOR FILING DATE: 1996-08-09
; PRIOR APPLICATION NUMBER: EP97401101.7
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF1 encoded
; OTHER INFORMATION: polypeptide
US-09-245-928A-18

Query Match      11.2%; Score 575.5; DB 4; Length 1257;
Best Local Similarity 26.3%; Pred. No. 1.8e-41;
Matches 254; Conservative 145; Mismatches 385; Indels 181; Gaps 40;

5 FLOVLLDNLTCTFIOGELGLIGFQDEFEKLOSTTTTQAVLEDAQKOL-KDKALENWLQ 63
Db 390 FVHLHMLNDLSDNAYSISLKEIEIIVSQLEFIRSFEGDAEQQLYKD---IWAR 445
QY KLNAAAYRADDLIDCKTEAPIRQKKNKYGCVHPIVIFRKHIG-KRMKKIMEKLDV--- 119
Db 64 KLNAAAYRADDLIDCKTEAPIRQKKNKYGCVHPIVIFRKHIG-KRMKKIMEKLDV--- 119
QY 446 VLD-VAYEKQVIDS-----IIVRDN--GLIH---LIFSPLITTKIKLKEEISALDE 493
Db 494 NIPKRGILVNSPKKPYERKSLT-----TDKIIVGFEEETNLIIRKL---TSGPADL 543
QY 120 -IAAER--IKFHLDERTIERQVATROGTFVINEPQVYGRDKDEIYKILINNVSNAQTL 176
Db 494 NIPKRGILVNSPKKPYERKSLT-----TDKIIVGFEEETNLIIRKL---TSGPADL 543
QY 177 PVLPIILMGIGIKTTLAQVFNQDQVIEHFRPKIWCISEDNEKRLLKEIVESIIEEKS 236
Db 544 DIVSITGMFGSGKTTLAKYVNDKSVSRHFDLRACVTDQGDGDKLDTTFSQVSGSDS 603
QY 237 GGMIDLAPLOKKLRDLNKGKTYLVLDVWNEEDQDKMAKLRQVLAKYGASGASVLTTRLEK 296
Db 604 NUSENIDVADKLRKOLFGRKYLIIVLDVW--DTTLDLDELTRFPFAKKGSRIILITTR-EK 660

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QY 297 VGSIMGTU--OPEYELSNLSOEDCMLFMORAFGHOEINLNLVAIGEIVKKGCVPLAA 354
D6 661 EVALHGKLNTPDLRLRRLRPESEWELKRTFGN--ESCPDELDVYKGEIENCKGLPLVA 719
QY 355 KTLGGILRFRKBERO--WEHVRDSEIWKLPQEBSSILPALRLSYHNLPLDLROCFYCAVF 413
D6 720 DLINGVIGREKKSVLEVOSSLSFINSVEVWKVIELSYDHLPHLKLPHFASW 779
QY 414 PKOTEMEGNLSLMMAHGLISKGNLELVNGVNEVLYRSF---FOEIEVSGQTY 470
D6 780 PKOTPLTYLLTVYKAGFEVTEKEMKGBEEVVKIYMDLSSSLVICFNEI---GDILN 836
QY 471 FKMDLHDLA-----TSLF---SASTSSNIREIIV---ENYIHMMSIGFTKYVS 515
D6 837 FOIHDLVHDFCLIKARKENLFDRISSAPSDLPQGITIDYDEEBEHGALFWFMSDKK 896
QY 516 SYSLSHLOKFSVLRVNLSDIKLQLPSSIGDLVHLRYNLSGNTSIR-----SLPN 567
D6 897 RHSGKHL---YSLR-----INGDQLDSDVSDAFHLRLRLRVLDLPSLIMVNDSLN 947
QY 568 OLCKLONLQTLDHGCHSLCCLPKETSKLGSRLNLLDCCGGLTCMPRIGSLTCLTKLS 627
D6 948 EICMLNHLRYLRIR--TQVKYLPSPFSNLMNLESLFVSNKGSILVLRILLDLVLRVLS 1005
QY 628 RFVVGIOKKSFCOLGELRMLNLYGSIETHLERVKNDMAKESANLSAK---ENLHLSMK 683
D6 1006 ---VQ---ACSF-----FDMADBSILAKOTKLENLRILG-- 1035
QY 684 WDDERPRIYSEKVEVLEALKPHSNLCTLRGFRGRLPDMNMHSLKXNVSIETISC 743
D6 1036 ---ELIYSKDTYNIIFRFPNLQVLO---FELKESMDYSTEGHW----- 1074
QY 744 KNCSCLPFGSLPLCKSLLE--LMRG--SAEVEYVDSGFTRR---RPSLAKNIRERGN 796
D6 1075 ---FPLDCTLELETLCVGFSSNTNHCSSVATNRPWDFHPS-----N 1116
QY 797 LKGLLKEGEGOCPLVEIEIKCCPMFYIPLTSVYKL---VVSGBDASIGRSSIN 851
D6 1117 LKELL-----LYDFPLTSDSLSTIARLPNLENLSYDTIIQGEEMNGEEDTEN 1166
QY 852 LMAITSLQIRYNKEDASLPBEMFKSLANLKYINISFYENKELPTSLASLNAKRLHIS 911
D6 1167 LKPLNLRLLTSLKNEVG--EESFPLBETKLQEGC--KLEIIPSPFSDIYSLKFIKIVK 1221
QY 912 CYALE 916
D6 1222 SPOLE 1226

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RESULT 11
US-08-947-823-5
; Sequence 5, Application US/08947823
; Patent No. 6114605
; GENERAL INFORMATION:
; APPLICANT: Williamson, Valerie M.
; APPLICANT: Kaloehian, Isgouhi
; APPLICANT: Yaghoubi, Jafar
; APPLICANT: Bodeau, John
; APPLICANT: Milligan, Stephen
; TITLE OF INVENTION: Procedures and Materials for Confering
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1257 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-947-823-5
Query Match 11.1%; Score 571.5; DB 3; Length 1257;
Best Local Similarity 26.3%; Pred. No. 4.1e-41;
Matches 254; Conservative 149; Mismatches 380; Indels 183; Gaps 42;
5 FLOVLDNLNFCFIGELGLILGFPOEFKLOSTFTTIOAVLEDAOKQL--KDKAIENWLQ 63
390 FMHLHLHNDLDSNAXYSLIEIEIVSGELFIRSPFGDAEGCLYND----IWAR 445
64 KLNAAVEADDIIDECKTEAPIRQKNKYGCPHPNVITFRHKIG--KRMKKIMEKLV-- 119
446 VLD--VAVEAKVIDS-----IYRDN--GLH--LIFSILPIYIKIKIKEISALDE 493
120 -IAER--IKFHDERTIERQVATROGFGVINEQVYGRDKEKEIYKILINNVSMAQT 176
494 NIPDRGLIVNSPKKVERKSLT-----TDKIIYGFEEETULIRKL--TSGPADL 543
177 PVLPIILGGLGKTLTQMFNDQVIEHFHPKIMICVSEDFNKRRLIKEIVSIEEKS 236
544 DVISITGPPSGKTLTKYKYINDKSVSRHFDLRMCCTVDOGCTDDKLLDITIFSQVSGSDS 603
237 GMDIAPLOKKLRDLNGLKTYLVLDVWNEDDQMKAKLRQVLKVGASGASVLTTRLEK 296
604 NLSNIDVADKLARKQLGKRLIVLDDVW--DTTLDLRLRPPPEAKGSRILITTR--EK 660
297 VGSIMGTU--OPEYELSNLSOEDCMLFMORAFGHOEINLNLVAIGEIVKKGCVPLAA 354
D6 661 EVALHGKLNTPDLRLRRLRPESEWELDKRTFGN--ESCPDELDVYKGEIENCKGLPLVA 719
QY 355 KTLGGILRFRKBERO--WEHVRDSEIWKLPQEBSSILPALRLSYHNLPLDLROCFYCAVF 413
D6 720 DLINGVIGREKKSVLEVOSSLSFINSVEVWKVIELSYDHLPHLKLPHFASW 779
QY 414 PKOTEMEGNLSLMMAHGLISKGNLELVNGVNEVLYRSF---FOEIEVSGQTY 469
D6 780 PKOTPLTYLLTVYKAGFEVTEKEMKGBEEVVKIYMDLSSSLVICFNEI---GDILN 835
QY 470 YFKMDLHDLA-----TSLF---SASTSSNIREIIV---ENYIHMMSIGFTKYV 514
D6 836 NFQIHDLVHDFCLIKARKENLFDRISSAPSDLPQGITIDYDEEBEHGALFWFMSDKK 895
QY 515 SYSLSHLOKFSVLRVNLSDIKLQLPSSIGDLVHLRYNLSGNTSIR-----SLPN 566
D6 896 KRHSKHL---YSLR-----INGDQLDSDVSDAFHLRLRLRVLDLPSLIMVNDSLN 946
QY 567 NOLCKLONLQTLDHGCHSLCCLPKETSKLGSRLNLLDCCGGLTCMPRIGSLTCLTKL 626

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Db 7 ASLMTIESLTFENSPMOSLSCDREELCALREKVSLEFVFNKKNVFGEMTDFEVE 66
Qy 60 NMLQRLNAAVE-----ADILDECKTEAPRQKKNKYGCYHPNITFRHKGKMKIM 114
Db 67 -VRVASAAYETIQRLTGTIVGENKS-----QKKA-----RRRROSLQOVA 109
Qy 115 EKLIVIAERIKFHLDERTEREQVATROTGVLANE-----POVGRDKKEIYKILINN 169
Db 110 EDMOHIMKESFTIQDKQVSKESLVHDFSSSTNDILKKNMVMGRDQKQLDLRLRS 169
Qy 170 VSNMOTLEVLPIILGSGIKTTLAOMVFRDQVIEHFNPKIWCISDFENKRLIKEIVE 229
Db 170 YSGEP--KPIPVGVGIGIKTTLAEVYNDESILCRFVMAWATISQHNKEIILGLIH 227
Qy 220 SI-----BEKSLGMDLAP-LOKRLDILNGKCYLLVLDVWNEDQDKMAKRLQVLA-K-G 282
Db 228 STIKRDDVKMIGELMADMLQSLK-----KKYIIVADDIIS--CEWWDGRRCPPEED 281
Qy 283 ASGASVLTTRLEKVSIMGTIQ--PYELSNLSQEDCMLFMQARFQHOEINLNLVAIGK 341
Db 282 NAGSRILITTRNDEVACYAVENFSLRMSFMDQBSWSLFSKAFS--SEALPYEPETVGK 340
Qy 342 EIVKCGGVPLAKTLGGLRPKREERQENYR--DEIWKLPQESSILPALRLSTHH 398
Db 341 QIABECHGLPLTIVVAGILSKRTIEDMKTVAKDVKSFTVNDPDERCS--RVLGLSYDH 398
Qy 399 LPLDROCFYCAVFPKOTEMEKNLISLMAHGFILSKNLELNVGNENVELYLSF 458
Db 399 LTRSDKTLHLFGITPEEDSDIPVKNLMSWMAEGKLKENDEGH-----VEKC 447
Qy 459 FOEI-----BVKSGQTYFKMHLIHLATSLFSASTSSNIREIYENY 502
Db 448 LQELVDRCLVSKSRDGTIRS---CKVHDLTYDC-----VREVGREN 491
Qy 503 IHMSIGF----- 510
Db 492 FIMNDIVLVSYPECSYLCMYKMPFKRVTGDEINVCYGLYRALLTEVNRQLRDHNN 551
Qy 511 ----TKVVSYSYL-----SHLOKFSVLRVNLSDIKLQLPSSIGDVLHRLVNL- 556
Db 552 LKRTHSVFSFHLBELVYVLSSEVHFYKLVLELRHROIDGFPREILSLTWKRLTSLPS 611
Qy 557 SGNTSIRSLPNQLCQNLQTLDLHGHS--LCCLPKETSRLGSLRNLLDGCYGLTQMP 615
Db 612 YGNPQV---PPEICLKMVLQTFIVQRPFSDIIFAEELMELQRLHLPLRFLYLPDCSG 668
Qy 616 RIG-----SLTCLKLS-----RNVVGIOKSCQGLBELRNILYGSIEITHLERVK 661
Db 669 SVDKGRHLDPENLQITISLSPRCTKEVIMGIONVK--KLGISGNKDDYKSPRDSGLPN-- 725
Qy 662 NDMAKKANLAKENLHSLM--KXDDDERPRIYSEKVELEALKPHENLCTITRRRG 720
Db 726 ----NLVYLQLEILSLISVYSLPVIISAKAPRATLKLKLERLYLS----- 771
Qy 721 IRLPDMAHNSVLKONVSIIEISCKNCS-----LPPFGLPCL-----KSLMLRSGA 768
Db 772 ----WVLDIIAEIENLEVLKMDACCGEEMHIVMGFRLKLLIKYGFELKWKKA-- 824
Qy 769 EREVYDSGFPTRRRPRLKLNIREFGLKGLLKEGEGQCV-----LEEIRIKCCP 821
Db 825 ----TNDNFPVLERLIRKIRCKMLK-----EIPIEPADIHITLQILRLRCP 865

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RESULT 14
US-09-803-286A-8
; Sequence 8, Application US/09803286A
; Patent No. 6664447
; GENERAL INFORMATION:
; APPLICANT: Tankeley, Steven D.
; APPLICANT: Brommonschenkel, Sergio H.
; TITLE OF INVENTION: PLANT GENE CONFERRING RESISTANCE TO TOSPOVIRUSES
; FILE REFERENCE: 1960313201
; CURRENT APPLICATION NUMBER: US/09/803,286A

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; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/188,356
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Lycopersicon var.
; US-09-803-286A-8

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Query Match 10.3%; Score 528; DB 4; Length 234;
Best Local Similarity 45.6%; Pred. No. 1.8e-38;
Matches 110; Conservative 42; Mismatches 75; Indels 14; Gaps 4;

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Qy 176 LPLVPIIIMGGLGKTTTLAOMVFRDQVIEHFNPKIWCISDFENKRLIKEIVESIEEKS 235
Db 2 LTVPIPVGVGIGIKTTLAEVYNDESILCRFVMAWATISQHNKEIILGLIH 227
Qy 236 LSGMDLAPLOKRLDILNGKCYLLVLDVWNEDQDKMAKRLQVLA-KVSGASVLTTRLE 295
Db 62 LVNDNLNQLQVTKERLKEKKEFLVLDVWNEDNENMDELANVFQGDIGSKIITTRKD 121
Qy 296 RVGSIIMGTLPYELSNLSQEDCMLFMQARF-----GHOEINLNLVAIGKEIYKCGG 349
Db 122 SVALLMGNBQ--ISMGNLSTEASWSLFRHAFENMDPMGHSE-----LEEVGRQIANKCG 175
Qy 350 VPLAKTLGGLRPKREERQENYRDEIWKLPQESSILPALRLSTHHLPLDROCFY 409
Db 176 LPLAKTLGMLRKSSEVEWKCILRSEIWL--RNDILPALMSVNDLPAHLFRCSF 233
Qy 410 C 410
Db 234 C 234

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RESULT 15
US-09-330-330-1
; Sequence 1, Application US/09330330
; Patent No. 6274789
; GENERAL INFORMATION:
; APPLICANT: Yano, Masahiro
; APPLICANT: Iwamoto, Masao
; APPLICANT: Katayose, Yuichi
; APPLICANT: Sasaki, Takuji
; APPLICANT: Wang, Zi-Xuan
; APPLICANT: Yamanouchi, Ueako
; TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FaastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,330
; FILING DATE: 11-JUN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 10-181455
; FILING DATE: 12-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06501/032001
; TELECOMMUNICATION INFORMATION:

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? TELEPHONE: 617/542-5070
? TELEFAX: 617/542-8906
? INFORMATION FOR SEQ ID NO: 1
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1205 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FRAGMENT TYPE: internal
US-09-330-330-1

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Query Match 10.3%; Score 526.5; DB 3; Length 1205;
Best Local Similarity 23.8%; Pred. No. 3.8e-37;
Matches 208; Conservative 139; Mismatches 325; Indels 203; Gaps 31.

Qy	130	DEFTIEHQVARRQGFV--LNEPQYGGDKDEKDEIVKLINNVSNAQCLPVLPIIGMGL	187
Db	333	DEKVARKSLRIRTSVGBASESOLIGREKEISELTHILINN--DSQQOYVISMWGMGL	390
Qy	188	GKTLAOMVENDQRYIEHFHPKIWICVEDFENEKELIKEIVEST-----	231
Db	391	GKTLVSGVYOSPRLSDCFDKVFTVIMRPFVILBELSLAEQLHKGSKEELLENVYS	450
Qy	232	EKSLGGMDLAPLOKULBDLNGKKYLLVLDVWMBDDQKAKYRQVL--XVAGASAVLT	290
Db	451	SKKSLASHEDELTGQULKRLLEKSSCLVLDPF--SDPSEMOQIRPTLPLEKTSRLTV	508
Qy	291	TTTRELKV-----GSIMGTLOPEYLSNLSOEDCMLTFMORAFGH--OBEINMLNVA	338
Db	509	TTRENTIANHSGKNQNV-----HNKLVLKHNDAJCLLSKRVFEATYVLDQNNPELYK	562
Qy	339	IGKEIVKCGGVPLAAKTUGGILRFK--REEROMEHVRD--SEWKLPOEBSIIPALRL	394
Db	563	EAKOILKKCDLPLAIVIGGFANRPKTPBEBWRKLANINAAEL--EMNPBELCMIRTVLEK	621
Qy	395	SYHHLPLDLRQCFYCAVFRKPDTEMEKNLISIMAHGFILSKGULELBNGENEWNELY	454
Db	622	SYDGLPFLHKSCLPYLSLFPEDQITSRRLVHRMAABGISTAHGSALEIANGFYMEBK	681
Qy	455	LRS-----FFOEIEVYSGQTYFKMDLHDLATSL-----	484
Db	682	NRSWILPRQSGSSRSKSIDSCVDHMDIAISXSTEENIVRVBEGSAYIHGAILRHA	741
Qy	485	-----FSASTSSSNIREITIV-----ENYIHMSIGFTKVVSYSLSH	521
Db	742	ISSNWGDKSFEFEGIVLSDIRLSLSLFGDMKPFYFGHRRFIRVLDFFEGTRGLBYHHLDQ	801
Qy	522	LQKRVSLRYNLSD--IKYKQJPSISGDIYHLRYNLSGNTSIRSLPNOLQYONQTL--	578
Db	802	IWKJNHLKFLSLRGCYRIDLLPDLGNROLQMDLIRG--TYVKALPKYTIKLOKQYIHA	860
Qy	579	-----DLH-----GC-HSLCCLPKETSISLNLNLL--DGCYGLTC-----	612
Db	861	GKRTDYWEEHGSLMQRCKYGCICATCCLPILCEMYRPLKALARRAMYPACCVKPPS	920
Qy	613	-----MPRIGSLTCLKTLSRFVVVGIQKSCQ--IGELRNLYGSIEITHLER	659
Db	921	IMTVGHEEBGAMVPSGIRKLKDLHTLRININVRGNAILRIDGMLTGLHKLGAAGIN----	976
Qy	660	VKNDMDAKENLSAKENLHLSMK-----WDDERPRIYSEKAVYLEALKPHSN	709
Db	977	-KKNGRFRLAISNKLKTESLVSAGMPGLCGCLDITSSP-----PENIQSLTKGS	1028
Qy	710	LTCLTIRGFRIRLIPDMWNHSLVKVVISIEITSC--NCSCLPFGELPCLKSLEMR--	765
Db	1029	LK-----TLPEWIKL--LOHVLVKLVSTRLEHDVAMELGSLPKEVILVISPF	1076
Qy	766	GSAAVEYVDSGFPTRRRPPLSRKLNIREBGNLKGLLKKEGBEQCVLEEBIKCCPMVI	825
Db	1077	KSEIHFKEP--QKGTAFVSLRYLKLADLGMGKISYKVEEG-----	1114
Qy	826	PTLSYVKLVVSGDKSDAIGSSISNLMALTSLOI	860

Db 1115 -TMPKLERLQVQGR IENEIGSGLEFLQNI NEVQL 1148

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Search completed: April 16, 2005, 01:24:10
Job time : 52 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2005, 01:19:25 ; Search time 150 Seconds
(without alignments)
2189.215 Million cell updates/sec

Title: US-10-647-268-2
5127
Perfect score: 1 MAEAFLOVLDNLTCTFIOGE.....EKGIGEDWYKIAHPRVEIY 988
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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 - 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep:*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3798	74.1	979 15	US-10-360-522-55 Sequence 55, Appl
2	3787	73.9	979 15	US-10-360-522-58 Sequence 58, Appl
3	3766.5	73.5	970 15	US-10-360-522-54 Sequence 54, Appl
4	3752.5	73.2	945 15	US-10-360-522-63 Sequence 63, Appl
5	3736.5	72.9	992 15	US-10-360-522-60 Sequence 60, Appl
6	3730.5	72.8	992 15	US-10-360-522-56 Sequence 56, Appl
7	3708.5	72.3	945 15	US-10-360-522-62 Sequence 62, Appl
8	3654.5	71.3	945 15	US-10-360-522-59 Sequence 59, Appl
9	3625	70.7	972 15	US-10-360-522-61 Sequence 61, Appl
10	3542	69.1	1040 15	US-10-360-522-57 Sequence 57, Appl
11	1517	29.6	1110 16	US-10-437-963-182454 Sequence 182454,
12	1516	29.6	1222 16	US-10-437-963-153490 Sequence 153490,
13	1477.5	28.8	1108 16	US-10-437-963-136142 Sequence 136142,

14	1442.5	28.1	1401 16	US-10-437-963-199180 Sequence 199180,
15	1362	26.6	1230 15	US-10-425-114-55552 Sequence 55552, A
16	1355.5	26.4	1210 16	US-10-437-963-131764 Sequence 131764,
17	1339	26.1	1285 16	US-10-437-963-160278 Sequence 160278,
18	1333.5	26.0	1332 16	US-10-437-963-190417 Sequence 190417,
19	1312.5	25.6	1274 16	US-10-437-963-196165 Sequence 196165,
20	1307	25.5	1322 16	US-10-437-963-108252 Sequence 108252,
21	1283	25.0	1007 16	US-10-437-963-136109 Sequence 136109,
22	1278.5	24.9	1273 15	US-10-437-963-202960 Sequence 202960,
23	1272.5	24.8	2001 16	US-10-437-963-132295 Sequence 132295,
24	1256	24.5	982 16	US-10-437-963-182482 Sequence 182482,
25	1234	24.1	932 16	US-10-437-963-132300 Sequence 132300,
26	1199.5	23.4	1121 16	US-10-437-963-132509 Sequence 159959,
27	1179	23.0	989 15	US-10-424-599-167505 Sequence 167505,
28	1143.5	22.3	1218 15	US-10-424-599-167509 Sequence 167509,
29	1129	22.0	960 16	US-10-437-963-129061 Sequence 129061,
30	1122	21.9	1070 16	US-10-437-963-153488 Sequence 153488,
31	1112.5	21.7	1110 16	US-10-437-963-142830 Sequence 142830,
32	1108	21.6	854 16	US-10-437-963-159362 Sequence 159362,
33	1104.5	21.5	1090 16	US-10-437-963-122130 Sequence 122130,
34	1093	21.3	1058 16	US-10-437-963-131272 Sequence 131272,
35	1080	21.1	1335 16	US-10-437-963-149948 Sequence 149948,
36	1075.5	21.0	1415 16	US-10-437-963-165107 Sequence 165107,
37	1070.5	20.9	804 16	US-10-437-963-127236 Sequence 127236,
38	1066	20.8	994 16	US-10-437-963-129064 Sequence 129064,
39	1065	20.8	961 16	US-10-437-963-163590 Sequence 163590,
40	1059	20.7	1439 16	US-10-437-963-202010 Sequence 202010,
41	1053	20.5	802 16	US-10-437-963-170362 Sequence 170362,
42	1046	20.4	1101 16	US-10-437-963-106891 Sequence 106891,
43	1040.5	20.3	1317 16	US-10-437-963-131841 Sequence 131841,
44	1038	20.2	1012 16	US-10-437-963-113343 Sequence 113343,
45	1035	20.2	986 16	US-10-437-963-203873 Sequence 203873,

ALIGNMENTS

RESULT 1
US-10-360-522-55
Sequence 55, Application US/10360522
Publication No. US200302215A1
GENERAL INFORMATION:
APPLICANT: Vossen v.d., Edwin A.G.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT FILING DATE: 2003-02-07
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: EP 02075565.8
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 979
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: alignment
FEATURE:
OTHER INFORMATION: RGC3-dlb
NAME/KEY: SITE
LOCATION: (1) .. (979)
US-10-360-522-55
Query Match 74.1% Score 3798; DB 15; Length 979;
Best Local Similarity 77.1%; Pred. No. 6e-2877; Indels 12; Gaps 8;
Matches 763; Conservative 75; Mismatches 139;

1 MAEAFLOVLDNLTCTFIOGELGILGFDEFEKQSTFTTIOAVLEDAOKKOLKRAIEN 60
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Oy      61 WLOKLNAAAYEADIDLECKTEAPIRQKKNYGCCHPNVITFRHKGKRMKIKMDLVI 120
Db      61 WLOKLNAAAYEADIDLECKTEAPIRQKKNYGCCHPNVITFRHKGKRMKIKMDLVI 119
Oy      121 AAEIKFHLDBERTTERQVATQGTGFLNEPQVYGRHKEKDEIVKILNNVNAQTLTPVLP 180
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Oy      181 ILGWSGIGKTTLAQMVFNDOVIEHFKPMI CVSEDENEKRLKEIYESIEEKSIGMD 240
Db      180 ILGWSGIGKTTLAQMVFNDOVIEHFKPMI CVSEDENEKRLKEIYESIEEKSIGMD 239
Oy      241 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKYGASGASVLTTRLEKYSI 300
Db      240 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKYGASGASVLTTRLEKYSI 299
Oy      301 MGTLOPYELSNLSOEDCMLFMQRAFGHQBENLNLVAIGKEIVKKGCGVPLAAKTLGGI 360
Db      300 MGTLOPYELSNLSOEDCMLFMQRAFGHQBENLNLVAIGKEIVKKGCGVPLAAKTLGGI 359
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Db      360 LRFREEROMEHVDSEIWKLPQDESSILPALRSYHHLPLDLROCFYCAVFPKOTEMA 419
Oy      421 KGNLISLMAHGFILSKNLELVNGNEVNMELVRSFQELVESGKTYFRMDLHDL 480
Db      420 KENLIAMAGFLSKNLELVNGNEVNMELVRSFQELVESGKTYFRMDLHDL 479
Oy      481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSJRVNLNSDILKQ 540
Db      480 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSJRVNLNSDILKQ 539
Oy      541 LPSISGIDLVIHRYNLNGNTSIRSLPNOLCKLQNTQTDLHGCHSLCCLPKETSKLSLR 600
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Oy      721 RLDPWMAHSHVILKNVYSIBISCKVSCCLPPGELPCLKSLFWMGSAERYV-DSGFPT 779
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Oy      779 RRRPESLAKNIRERGNLKGILLKEGEOCPVLEIEIKCCPMFYITLTSVYKLVSGD 839
Db      778 RRRPESLAKNIRERGNLKGILLKEGEOCPVLEIEIKCCPMFYITLTSVYKLVSGD 830
Oy      839 KSDAIGFESSISNLMATSLQIRYNKEDASLPEEMFKSLANLKYLNISFYFNKLKLPJSLA 899
Db      831 TDPAVALSISNLRALSLDISNNVEATSLPEEMFKSLANLKYLNISFYFNKLKLPJSLA 889
Oy      900 SLNALKHEIHSICALLESIPBEGVKGILSLTOLSTTYCBMLQCLPBGIOHLTALNLSVE 959
Db      899 SLNALKHEIHSICALLESIPBEGVKGILSLTOLSTTYCBMLQCLPBGIOHLTALNLSVE 949
Oy      960 FCPPLAKRCEKIGEDWYKIAHIPPVFY 988
Db      950 FCPPLAKRCEKIGEDWYKIAHIPPVFY 978

```

RESULT 2
 US-10-360-522-58
 ; Sequence 58, Application US/10360522
 ; Publication No. US20030221215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ailefs, Josephus J.H.M.

```

; APPLICANT: Vossen v. d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT FILING DATE: 2003-02-07
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 58
; LENGTH: 979
; TYPE: PR
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(979)
; US-10-360-522-58

Query Match      73.9%; Score 3787; DB 15; Length 979;
Best Local Similarity 76.9%; Pred. No. 4.3e-286;
Matches 761; Conservative 76; Mismatches 140; Indels 12; Gaps 8;

Oy      1 MAEAFIQVLDNLNLSFLKGEVLVLFQDEFORLSMSFSTIQAVALDAQEKQKQNDKPLEN 60
Db      1 MAEAFIQVLDNLNLSFLKGEVLVLFQDEFORLSMSFSTIQAVALDAQEKQKQNDKPLEN 60
Oy      61 WLOKLNAAAYEADIDLECKTEAPIRQKKNYGCCHPNVITFRHKGKRMKIKMDLVI 120
Db      61 WLOKLNAAAYEADIDLECKTEAPIRQKKNYGCCHPNVITFRHKGKRMKIKMDLVI 119
Oy      121 AAEIKFHLDBERTTERQVATQGTGFLNEPQVYGRHKEKDEIVKILNNVNAQTLTPVLP 180
Db      120 AAEIKFHLDBERTTERQVATQGTGFLNEPQVYGRHKEKDEIVKILNNVNAQTLTPVLP 179
Oy      181 ILGWSGIGKTTLAQMVFNDOVIEHFKPMI CVSEDENEKRLKEIYESIEEKSIGMD 240
Db      180 ILGWSGIGKTTLAQMVFNDOVIEHFKPMI CVSEDENEKRLKEIYESIEEKSIGMD 239
Oy      241 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKYGASGASVLTTRLEKYSI 300
Db      240 LAPLOKRLDLNGKKYLLVLDVWNEODKMAKLRQVLKYGASGASVLTTRLEKYSI 299
Oy      301 MGTLOPYELSNLSOEDCMLFMQRAFGHQBENLNLVAIGKEIVKKGCGVPLAAKTLGGI 360
Db      300 MGTLOPYELSNLSOEDCMLFMQRAFGHQBENLNLVAIGKEIVKKGCGVPLAAKTLGGI 359
Oy      361 LRFREEROMEHVDSEIWKLPQDESSILPALRSYHHLPLDLROCFYCAVFPKOTEME 420
Db      360 LRFREEROMEHVDSEIWKLPQDESSILPALRSYHHLPLDLROCFYCAVFPKOTEMA 419
Oy      421 KGNLISLMAHGFILSKNLELVNGNEVNMELVRSFQELVESGKTYFRMDLHDL 480
Db      420 KENLIAMAGFLSKNLELVNGNEVNMELVRSFQELVESGKTYFRMDLHDL 479
Oy      481 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSJRVNLNSDILKQ 540
Db      480 ATSLFSASTSSNIREIIVENYIHMSIGFTKVSSYSLSHLQKFSJRVNLNSDILKQ 539
Oy      541 LPSISGIDLVIHRYNLNGNTSIRSLPNOLCKLQNTQTDLHGCHSLCCLPKETSKLSLR 600
Db      540 LPSISGIDLVIHRYNLNGNTSIRSLPNOLCKLQNTQTDLHGCHSLCCLPKETSKLSLR 599
Oy      601 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQGLRNLNLYGSIETIHLERV 660
Db      600 NLLDGCYGLTCMPRIGSLTCLKTLRSFVVGIOKSCQGLRNLNLYGSIETIHLERV 657
Oy      661 KNDMDAKEANLSAKENLHSLSMKMDDDRPRITYESKEVLEALKPHSNLTCLTIRGRG 720

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Db 658 KKDSDAKANLSAKANLHSLCISWDLGKHR-YDS--EVLKALPHSNLKYLETINGGG 713
Qy 721 IRLPDMNHSVLYKANVSIIEISCKNCSCLPPEGEIPCLKSLJELMRGSAVEYV-DSGPT 779
Db 714 IRLPDMNHSVLYKANVSIIRINGCENCSCLPPEGEIPCLKSLJELMRGSAVEYV-772
Qy 780 RRRPFLKLNIRREFGNLKGILKKEGEOCPVLEIEIKCEPMFVITLISVYKLVSGD 839
Db 773 -GRFPLSLKLVWDPNSNLKGLLKEGEOFPVLEEMTFWCMFVITLISVYKLVIA- 830
Qy 840 KSDAIGFSSISWMLTSLQIRYNKEDASLPPEMKSILANKYINISFYNLKEPLSLA 899
Db 831 -TDAVLRSISNLRALTSIDISNNVEATSLPEEMKSLANKYINISFPRNLKEPLSLA 889
Qy 900 SLNALKLEHISCYALLESIPBEVGKGLISTOLSTTYCEMLQCPGLOHLTALTNLSVE 959
Db 890 SLNALKSLKFEFCNALLESIPBEVGKGLISTELSVSNCKMLKCLPBGLOHLTALTTLTIT 949
Qy 960 FCPFLAKCEKGIKEDWYKIAHIPPVFTY 988
Db 950 QCPVFKKCEKGIKEDWYKIAHIPPVFTLY 978

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RESULT 3

```

US-10-360-522-54
; Sequence 54, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: deduced
; OTHER INFORMATION: Rpl-d1b protein sequence domain A, B and C
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(970)
US-10-360-522-54

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Query Match 73.5%; Score 3766.5; DB 15; Length 970;
Best Local Similarity 75.6%; Pred. No. 1.7e-284;
Matches 753; Conservative 78; Mismatches 130; Indels 35; Gaps 8;
Qy 1 MAEFLOYLDNLTCFIOGELGLIGFODEBKLOSTTTTQAVLEDAQKQKQKAKEN 60
Db 1 MAEFLOYLDNLTCFIOGELGLIGFODEBKLOSTTTTQAVLEDAQKQKQKAKEN 60
Qy 61 WLOGLNAAVYADDIIDECCTEAPIRQKNKYGCCHPVVIFPRHKGKMKKIKKIDVI 120
Db 61 WLOGLNAAVYADDIIDECCTEAPIRQKNKYGCCHPVVIFPRHKGKMKKIKKIDVI 120
Qy 121 AAEIRKFLDERTIERQVATQGTGFLVNEPOVYGRDKKDEIVKILINNVSNAQTLPVLP 180
Db 121 AAEIRKFLDERTIERQVATQGTGFLVNEPOVYGRDKKDEIVKILINNVSNAQTLPVLP 180
Qy 120 AAEIRKFLDERTIERQVATQGTGFLVNEPOVYGRDKKDEIVKILINNVSNAQTLPVLP 179
Db 120 AAEIRKFLDERTIERQVATQGTGFLVNEPOVYGRDKKDEIVKILINNVSNAQTLPVLP 179
Qy 181 ILGNGGIGKTTLAQVAFNDQVIVHFHFKIIVCSSEDFNKKLKEIYESIIEKVS-LGGM 239
Db 181 ILGNGGIGKTTLAQVAFNDQVIVHFHFKIIVCSSEDFNKKLKEIYESIIEKVS-LGGM 239

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Qy 240 DLAPLOKKRLDLNGKTYLLVLDVWVNEDDQKMAKLRQVLKVGASGASVLTTRLEKVS 299
Db 240 DLAPLOKKRLDLNGKTYLLVLDVWVNEDDQKMAKLRQVLKVGASGASVLTTRLEKVS 299
Qy 300 IMGLTQPELNSLQOEDCMLFMQARQHOEINLNLVAIKEIYKKGCGVPLAKTIGG 359
Db 300 IMGLTQPELNSLQOEDCMLFMQARQHOEINLNLVAIKEIYKKGCGVPLAKTIGG 359
Qy 360 ILRFREERQEHVRSDEIMKLPOESSILPALRLSYHHLPLDROCTTCYCAVPPKOTEM 419
Db 360 ILRFREERQEHVRSDEIMKLPOESSILPALRLSYHHLPLDROCTTCYCAVPPKOTEM 419
Qy 420 EKNGLISLMAHGFILSKNLELVNAGNEVNNELYLSFPOEIEYKSGQTYFKMHLIHD 479
Db 420 EKNGLISLMAHGFILSKNLELVNAGNEVNNELYLSFPOEIEYKSGQTYFKMHLIHD 479
Qy 480 LATSLFASSTSSNIREIYENYTHMNSIGFTKXVSSYSLSHLOKFPVSLRYLNSDIKX 539
Db 480 LATSLFASSTSSNIREIYENYTHMNSIGFTKXVSSYSLSHLOKFPVSLRYLNSDIKX 539
Qy 540 QLPSSIGDLYHLRYLNLSGNLSIRSLPNOCLQNLQTLDLHGSHLCCLPKETSGLSL 599
Db 540 QLPSSIGDLYHLRYLNLSGNLSIRSLPNOCLQNLQTLDLHGSHLCCLPKETSGLSL 599
Qy 599 RNLDDSGSLTQCPPRIGSLTCLKTLSPFVVGIOKKSQGLRNLNLVGSIBITHLER 659
Db 599 RNLDDSGSLTQCPPRIGSLTCLKTLSPFVVGIOKKSQGLRNLNLVGSIBITHLER 659
Qy 660 VKNDMAKLANLAKENHLSISMKDDERPRIYESSKEVYELAKPHSNLTCTLTNGFR 719
Db 660 VKNDMAKLANLAKENHLSISMKDDERPRIYESSKEVYELAKPHSNLTCTLTNGFR 719
Qy 720 GIRPDMNHSVLYKANVSIIEISCKNCSCLPPEGEIPCLKSLJELMRGSAVEYV-774
Db 720 GIRPDMNHSVLYKANVSIIEISCKNCSCLPPEGEIPCLKSLJELMRGSAVEYV-774
Qy 775 --SGPFRRRPPLSLKLNIRREFGNLKGILKKEGEOCPVLEIEIKCEPMFVITLISVYK 832
Db 775 --SGPFRRRPPLSLKLNIRREFGNLKGILKKEGEOCPVLEIEIKCEPMFVITLISVYK 832
Qy 777 VHSGFPRIRPPLSLKLNIRREFGNLKGILKKEGEOCPVLEIEIKCEPMFVITLISVYK 830
Db 777 VHSGFPRIRPPLSLKLNIRREFGNLKGILKKEGEOCPVLEIEIKCEPMFVITLISVYK 830
Qy 833 KLVVSGKSDAIGFSSISNLMALTSIQIRYNKEDASLPPEMKSILANKYINISFYENLK 892
Db 833 KLVVSGKSDAIGFSSISNLMALTSIQIRYNKEDASLPPEMKSILANKYINISFYENLK 892
Qy 893 ELPTSLASLNAKLEHISCYALLESIPBEVGKGLISTOLSTTYCEMLQCPGLOHLTA 952
Db 893 ELPTSLASLNAKLEHISCYALLESIPBEVGKGLISTOLSTTYCEMLQCPGLOHLTA 952
Qy 953 LTNLSVEFCPLAKCEKGIKEDWYKIAHIPPVFTY 988
Db 953 LTNLSVEFCPLAKCEKGIKEDWYKIAHIPPVFTY 988

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RESULT 4

```

US-10-360-522-63
; Sequence 63, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allele, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63

```

```

; LENGTH: 945
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; OTHER INFORMATION: T118-tar
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(945)
; US-10-360-522-63

```

```

Query Match      73.2%; Score 3752.5; DB 15; Length 945;
Best Local Similarity 76.6%; Pred. No. 2e-283;
Matches 745; Conservative 82; Mismatches 113; Indels 33; Gaps 7;

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OY 1 MAEAFLOVLDNLTCFIOGELGLIFGFDEBEKLOSTTTTIOAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFIOVLENTITFFIOGELGLIFGFENEFENISSRSTTIOAVLEDAQKQKLDKAIEN 60
OY 61 WLOKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 120
DB 61 WLOKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 117
OY 121 AAERIKFHLDBERTTERQVATQGTGVLNEPQVYGRDKEDEIVKLLINNVSAQTLPLVP 180
DB 118 AKERTDFHLHEKILIERQVAREPETGPVLEPQVYGRDKEDEIVKLLINNVSALESLVLP 177
OY 181 ILGMGGLCKTTLAQWVENDQVITEHFPKTIWCVSEDENEKRLKEIYESIEEKSLSGMD 240
DB 178 ILGMGGLCKTTLAQWVENDQVITEHFPKTIWCVSDDEDEKRLKEIYESIEEKSLSGMD 237
OY 241 LAPLOKRLDLNGKKYLLVLDVWNEEDQKMAKROYLAKYGASGYLTTTRLEKYSI 300
DB 238 LASFQKLIQOLNGKRYLLVLDVWNEEDQKMDNIRAVLAKYGASGYLTTTRLEKYSI 297
OY 301 MGTLOPYELISLNSQEDCWLLEWQAFGHOEININLVAIGKEIYKCGGVPLAAKTLGSI 360
DB 298 MGTLOPYOLSLNSQEDCWLLEFQRAYRHOEISPLVVAIGKEIYKCGGVPLAAKTLGSI 357
OY 361 LRFKREKQWHEVHDSEIWKLPQOESSILPALRLSYHHLPLDLNQCFTYCAVFPDQTEME 420
DB 358 LRFKREKQWHEVHDSEIWKLPQOESSILPALRLSYHHLPLDLNQCFTYCAVFPDQTEME 417
OY 421 KGNLISLWMAHGFILSKNLELVNGEYVWELIYRSFQOIEVSGQTYFPMHDLIDL 480
DB 418 KKKVLSLWMAHGFILSKNLELVNGEYVWELIYRSFQOIEVSGQTYFPMHDLIDL 477
OY 481 ATSLPSASTSSNIREIIVENYINMMSIGFTYVSSYSLSHLQKFVSLRVINLSDIKLKQ 540
DB 478 ATSLPSASTSSNIREIIVENYINMMSIGFTYVSSYSLSHLQKFVSLRVINLSDIKLKQ 537
OY 541 LPSSIGDVLHRLYMLSGNTSIRSLPNQCKQONQTLDHGCHSLCCLPRETSLSLSLR 600
DB 538 LPSSIGDVLHRLYMLSGNTSIRSLPNQCKQONQTLDHGCHSLCCLPRETSLSLSLR 597
OY 601 NLLLDGCGKLTGMPPRIGSLTCLKTLSPRVGSIQKSCCOLGELRMINLTYGSIETHLERY 660
DB 598 NLLLDGCHLTLTPPRIGSLTCLKTLGQPVVG-RKKGYOLGELSLNLYGSIKISHLERY 656
OY 661 KNDMDAKEANTSAKENLHSLSMKWDDEPRRIYSEKYEVLBALRPHSNLTCLTRGPRG 720
DB 657 KNDMDAKEANTSAKENLHSLSMKWDDE-PRHYESEVEVLBALRPHSNLTCLTRISGFRG 715
OY 721 IRLPDMWNSVTKANVSTIISCKKNCCLPPRGELPCLKSLLELMGSAE-VXY----VDS 775
DB 716 IRLPDMWNSVTKANVSTIISCKKNCCLPPRGELPCLKSLLELMGSAE-VXY----VDS 775
OY 776 GPPTRRRPPLSKLNIREFGNLKGILLKKGEGOCPLAEIIEIKCPMFVITPLTSYKVLV 835
DB 776 GPPTRRRPPLSKLNIREFGNLKGILLKKGEGOCPLAEIIEIKCPMFVITPLTSYKVLV 835
OY 836 VSGDSDAIGFSSISNLMAITSLQIRYNKEDASLPREMFKSLANTKYLINISFYFNILKELP 895
DB 836 VSGDSDAIGFSSISNLMAITSLQIRYNKEDASLPREMFKSLANTKYLINISFYFNILKELP 895

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DB 827 -----SNKALTSINISDNKEATSPREMFKSLANTKYLINISHERNKLKP 872
OY 896 TSLASINALKHLEIHSQYALESPREGVKGLISITQSTITYCEMLQCLPGLQHTLATN 955
DB 873 TSLASINALKSLKIQWCMALSIPEBSVKGLTSLTELIVFCMLKCLPGLQHTLATN 932
OY 956 LSVFCEPTLAKRC 968
DB 933 VKIWCPCQLIKRC 945

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RESULT 5
US-10-360-522-60
; Sequence 60, Application US/10360522
; Publication No. US20030221215A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT FILING DATE: US/10/360,522
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 992
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(992)
; US-10-360-522-60

```

```

Query Match      72.9%; Score 3736.5; DB 15; Length 992;
Best Local Similarity 74.8%; Pred. No. 3.9e-282;
Matches 747; Conservative 92; Mismatches 141; Indels 19; Gaps 8;

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OY 1 MAEAFLOVLDNLTCFIOGELGLIFGFDEBEKLOSTTTTIOAVLEDAQKQKLDKAIEN 60
DB 1 MAEAFIOVLENTITFFIOGELGLIFGFENEFENISSRSTTIOAVLEDAQKQKLDKAIEN 60
OY 61 WLOKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 120
DB 61 WLOKLNAAAYEADTILDECKTEADPIROKKNKYGCVHPVITFRHKIGRMMKMEKLDVI 119
OY 121 AAERIKFHLDBERTTERQVATQGTGVLNEPQVYGRDKEDEIVKLLINNVSAQTLPLVP 180
DB 118 AKERTDFHLHEKILIERQVAREPETGPVLEPQVYGRDKEDEIVKLLINNVSALESLVLP 179
OY 181 ILGMGGLCKTTLAQWVENDQVITEHFPKTIWCVSEDENEKRLKEIYESIEEKSLSGMD 240
DB 178 ILGMGGLCKTTLAQWVENDQVITEHFPKTIWCVSDDEDEKRLKEIYESIEEKSLSGMD 239
OY 241 LAPLOKRLDLNGKKYLLVLDVWNEEDQKMAKROYLAKYGASGYLTTTRLEKYSI 300
DB 238 LASFQKLIQOLNGKRYLLVLDVWNEEDQKMDNIRAVLAKYGASGYLTTTRLEKYSI 299
OY 301 MGTLOPYELISLNSQEDCWLLEWQAFGHOEININLVAIGKEIYKCGGVPLAAKTLGSI 360
DB 298 MGTLOPYOLSLNSQEDCWLLEFQRAYRHOEISPLVVAIGKEIYKCGGVPLAAKTLGSI 359
OY 361 LRFKREKQWHEVHDSEIWKLPQOESSILPALRLSYHHLPLDLNQCFTYCAVFPDQTEME 420
DB 358 LRFKREKQWHEVHDSEIWKLPQOESSILPALRLSYHHLPLDLNQCFTYCAVFPDQTEME 419

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Qy 421 KGNLSLMAHGFLLSKGNLELVNGEVMNELYLRSFQEIYKSGQTYFKMDLJHDL 480
Db 420 KEYLIALMAMHAFLLSKGNMELEVDGNEVMNELYLRSFQEIYKSGQTYFKMDLJHDL 479
Qy 481 ATSLFSASTSSNIREI-----IVENYIHMSIGFTKVVSSYSLSLQKRVSLRV 530
Db 480 ATSMFSASASRSIRQINVKDEDMFIVTNYKDMMSIGFSEVSSYSPLSFKRVSRLRV 539
Qy 531 LNLSDIKLKOLPSSIGDLVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 590
Db 540 LNLNSERFQLPSSVGDVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 598
Qy 591 KETSKLGSRLNLLDGCYGLTCMPPRIGSLTCLKTLSPFVVGIOKKSQOLGELRNLYG 650
Db 599 KQTSKLGSLRNLYVDHC-PLTSMRPRIQLTLCTKLTGFFVVG-ERKGYQLGELRNLYRG 656
Qy 651 SIEITHLERVKNDMAKANAISAKENHLSLSMKWDDERPRIYSEKYEVLALKPHSNL 710
Db 657 AISITHLERVKNDMAKANAISAKENHLSLSMSWD---RPRRYSEEVKVEALKPHNLT 713
Qy 711 TCLTIRGFRGRLPDMNMHSHVKNVSVIEISCKNCSCLPPFGELPCLKSLRLMRSALV 770
Db 714 KYLEIITDFCGCLPDMNMHSHVKNVSVIISGCNCSCLPFGELPCLSLSELQDGSVEV 773
Qy 771 EYV-DSGFPTRRRPPSLRKLNIREFGNLKGLKKEGEOCVLEIEIKCCPMFVPTLS 829
Db 774 EYVEDSGFLTRRRPPSLRKLNIGFCNLKGLQRMKGEOQFVLEEMKISDCPMFVPTLS 833
Qy 830 SVKKLVVSGKSDAIGFSSISNLMAITSLQIRYNKEDASLPEEMFKSLANKYINISYF 889
Db 834 SVKLEIWMGE-ADAGGLSSISNLSLTLSKTFNSHTVTSLEEMFKNLENLIYLSVSFLE 892
Qy 890 NLKELPTSLASLNKLEIHSYALSLPBEVKGILSLTOLSTYCEMLQCLPEGIQH 949
Db 893 NLKELPTSLASLNKLEIHSYALSLPBEVKGILSLTOLSTYCEMLQCLPEGIQH 952
Qy 950 LTLATNLVSEFCPTLAKRCEKIGEDWYKIAHPRVFIY 988
Db 953 LTTITLSLKIRGCPOLIKRCEKIGEDWYKISHIPVNIY 991

```

RESULT 6
US-10-360-522-56
Sequence 56, Application US/10360522
Publication No. US20030221215A1

```

GENERAL INFORMATION:
APPLICANT: Allele, Josephus J.H.M.
APPLICANT: Vossen v.d., Edwin A.G.
TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
FILE REFERENCE: U 014413-9
CURRENT APPLICATION NUMBER: US/10/360, 522
PRIOR FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02075565, 8
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/NL03/00091
PRIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 992
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: alignment
FEATURE:
NAME/KEY: SITE
LOCATION: (1)..(992)
US-10-360-522-56

```

Query Match Best Local Similarity 72.8%; Score 3730.5; DB 15; Length 992;
74.7%; Pred. No. 1.1e-281;

Matches 746; Conservative 92; Mismatches 142; Indels 19; Gaps 8;

```

Qy 1 MAEAFLOVLDTNLTFCFIOGELGLILGFQDEBEKLOSTFTTIOAVLEDAQKKOLKDAIEN 60
Db 1 MAEAFLOVLDTNLTFFIOGELGLVFGPEKEPKLSMSMTQAVLEDEQKOLKAKAKN 60
Qy 61 WLQKLNAAVYBADDILDECKTEADIRQKKNYGCYHPNVITFRHKIGRMMKMEKLDVI 120
Db 61 WLQKLNAAVYBADDILDDCKTEA-ARFKQAVLGRYHPRTITFCYKVGGRMEKMEKDAI 119
Qy 121 AAEIKPHLDEKTERQVATQGTGVLANEPQVYGRDKEDIVKILINNVSNAQTLPLP 180
Db 120 AAEERNFHLDERIIRERQARQGTGVLEPRKYREKEDIEIVILINNVSSEKVPALP 179
Qy 181 ILGNGGLGKTTLAQMVFPDORVIEHPFKIWCYSEDPENRRLIKEIYESIEEKSLSGMD 240
Db 180 ILGNGGLGKTTLAQMVFPDORITHFNFKIWCYSDPDERKLLKAIYESIEGSLGMD 239
Qy 241 LAPLOKCLRDLNKGKYLVLVDVWNEBQDKMAKLROYLKYVAGASVLTTRLEKVGSI 300
Db 240 LAPLOKCLRDLNKGKYLVLVDVWNEBQDKMDLRAVLKIGASGASILITTRLEKIGSI 299
Qy 301 MGTLOPYELNSLQEDCMLFMQRAFGHQBENLNVAIGKEIYKCGGVPLAAKTLGCI 360
Db 300 MGTLOPYELNSLQEDCMLFMQRAFGHQBENLNVAIGKEIYKCGGVPLAAKTLGCI 359
Qy 361 LRFREEROMEHVADSEIWMKPOESSITLPAIRLSYHHLPLDLNOCFTYCAVPPDTEME 420
Db 360 LRFRESEMEHVADSEIWMKPODENSVLPAIRLSYHHLPLDLNOCFTYCAVPPDTEME 419
Qy 421 KGNLSLMAHGFLLSKGNLELVNGEVMNELYLRSFQEIYKSGQTYFKMDLJHDL 480
Db 420 KEYLIALMAMHAFLLSKGNMELEVDGNEVMNELYLRSFQEIYKSGQTYFKMDLJHDL 479
Qy 481 ATSLFSASTSSNIREI-----IVENYIHMSIGFTKVVSSYSLSLQKRVSLRV 530
Db 480 ATSMFSASASRSIRQINVKDEDMFIVTNYKDMMSIGFSEVSSYSPLSFKRVSRLRV 539
Qy 531 LNLSDIKLKOLPSSIGDLVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 590
Db 540 LNLNSERFQLPSSVGDVHLRYLNLGNTSIRSLPNOLCKLQNLQTLDLGCHSLCCLP 598
Qy 591 KETSKLGSRLNLLDGCYGLTCMPPRIGSLTCLKTLSPFVVGIOKKSQOLGELRNLYG 650
Db 599 KQTSKLGSLRNLYVDHC-PLTSMRPRIQLTLCTKLTGFFVVG-ERKGYQLGELRNLYRG 656
Qy 651 SIEITHLERVKNDMAKANAISAKENHLSLSMKWDDERPRIYSEKYEVLALKPHSNL 710
Db 657 AISITHLERVKNDMAKANAISAKENHLSLSMSWD---RPRRYSEEVKVEALKPHNLT 713
Qy 711 TCLTIRGFRGRLPDMNMHSHVKNVSVIEISCKNCSCLPPFGELPCLKSLRLMRSALV 770
Db 714 KYLEIITDFCGCLPDMNMHSHVKNVSVIISGCNCSCLPFGELPCLSLSELQDGSVEV 773
Qy 771 EYV-DSGFPTRRRPPSLRKLNIREFGNLKGLKKEGEOCVLEIEIKCCPMFVPTLS 829
Db 774 EYVEDSGFLTRRRPPSLRKLNIGFCNLKGLQRMKGEOQFVLEEMKISDCPMFVPTLS 833
Qy 830 SVKKLVVSGKSDAIGFSSISNLMAITSLQIRYNKEDASLPEEMFKSLANKYINISYF 889
Db 834 SVKLEIWMGE-ADAGGLSSISNLSLTLSKTFNSHTVTSLEEMFKNLENLIYLSVSFLE 892
Qy 890 NLKELPTSLASLNKLEIHSYALSLPBEVKGILSLTOLSTYCEMLQCLPEGIQH 949
Db 893 NLKELPTSLASLNKLEIHSYALSLPBEVKGILSLTOLSTYCEMLQCLPEGIQH 952
Qy 950 LTLATNLVSEFCPTLAKRCEKIGEDWYKIAHPRVFIY 988
Db 953 LTTITLSLKIRGCPOLIKRCEKIGEDWYKISHIPVNIY 991

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RESULT 7
US-10-360-522-62

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; Sequence 62, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Vossen v.d.; Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 945
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(945)
; US-10-360-522-62

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Query Match      72.3%; Score 3708.5; DB 15; Length 945;
Best Local Similarity 75.8%; Pred. No. 5,5e+280;
Matches 738; Conservative 82; Mismatches 120; Indels 33; Gaps 7;

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QY 1 MAEAFLOVLNLTCTFIOGELGLILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
DB 1 MAEAFIOVLNLTCTFIOGELGLILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
QY 61 WLOKNAAYEADDLDECKTEAPTRQKKNKYGCYHPVITFRHKGKMKIMEKLDVI 120
DB 61 WLOKNAAYEADDLDECKTEAPTRQKKNKYGCYHPVITFRHKGKMKIMEKLDVI 117
QY 121 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 180
DB 121 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 177
QY 118 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 177
DB 118 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 177
QY 181 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 240
DB 181 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 240
QY 178 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 237
DB 178 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 237
QY 241 LAPLQKJRLDNLGKKYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 300
DB 241 LAPLQKJRLDNLGKKYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 300
QY 238 IASFOKQLQOLNGKRYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 297
DB 238 IASFOKQLQOLNGKRYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 297
QY 301 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 360
DB 301 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
QY 298 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
DB 298 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
QY 361 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 420
DB 361 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
QY 358 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
DB 358 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
QY 421 KNLISLMAAHGFIISKGNILENVNGEVENNELYLSPFOEIEVSGQTYFPQMDLIHDL 480
DB 421 KNLISLMAAHGFIISKGNILENVNGEVENNELYLSPFOEIEVSGQTYFPQMDLIHDL 477
QY 481 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 540
DB 481 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 478 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
DB 478 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 541 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 600
DB 541 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 600
QY 538 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 597
DB 538 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 597
QY 601 NLLDGCYGLTGWPPRIGSLTCLKTLSPRVVGIQKSCOLGELRLNMLVGSIEITHLERV 660
DB 601 NLLDGCYGLTGWPPRIGSLTCLKTLSPRVVGIQKSCOLGELRLNMLVGSIEITHLERV 660

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DB 598 NLLDGHCHRLTRTPRIGSLTCLKTLGQSVK-RKKGYQGEIGSLINLXGSIKISHLERY 656
QY 661 KNDMDAKENALSAKENLHSMKWDDEPRRIYESKEVLEALXPHSNLTCLTIGFPG 720
DB 661 KNDMDAKENALSAKENLHSMKWDDEPRRIYESKEVLEALXPHSNLTCLTIGFPG 715
QY 657 KNDMDAKENALSAKENLHSMKWDDEPRRIYESKEVLEALXPHSNLTCLTIGFPG 715
DB 657 KNDMDAKENALSAKENLHSMKWDDEPRRIYESKEVLEALXPHSNLTCLTIGFPG 715
QY 721 IRLPDMNHSVLKNVSIETISCKNCSCLPPFEGELPCLSLBMRGAS-VEX-----VDS 775
DB 721 IRLPDMNHSVLKNVSIETISCKNCSCLPPFEGELPCLSLBMRGAS-VEX-----VDS 775
QY 776 GPTTRRRPRLKRLNIREPNLKLKKGEGECVPLEIEIKCCPMFVPTLSVYKLV 835
DB 776 GPTTRRRPRLKRLNIREPNLKLKKGEGECVPLEIEIKCCPMFVPTLSVYKLV 835
QY 776 GPTTRRRPRLKRLNIREPNLKLKKGEGECVPLEIEIKCCPMFVPTLSVYKLV 826
DB 776 GPTTRRRPRLKRLNIREPNLKLKKGEGECVPLEIEIKCCPMFVPTLSVYKLV 826
QY 836 VSGDKSAIGFSSISNMLTSLQIRNKEBASLPEEMFSLANLKYINISFYFNKELP 895
DB 836 VSGDKSAIGFSSISNMLTSLQIRNKEBASLPEEMFSLANLKYINISFYFNKELP 895
QY 827 -----PINKALTSINISDNKEATSPPEEMFSLANLKYINISFYFNKELP 872
DB 827 -----PINKALTSINISDNKEATSPPEEMFSLANLKYINISFYFNKELP 872
QY 896 TSLASLALKHLHSCYALLESIPBEGVGLISLTOASTYCEMLQCLPBGLOHTALTN 955
DB 896 TSLASLALKHLHSCYALLESIPBEGVGLISLTOASTYCEMLQCLPBGLOHTALTN 955
QY 873 TSLASLALKHLHSCYALLESIPBEGVGLISLTOASTYCEMLQCLPBGLOHTALTN 932
DB 873 TSLASLALKHLHSCYALLESIPBEGVGLISLTOASTYCEMLQCLPBGLOHTALTN 932
QY 956 LSVFECPTLAKC 968
DB 956 LSVFECPTLAKC 945
QY 933 LKINGCPQLIKRC 945
DB 933 LKINGCPQLIKRC 945

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RESULT 8
US-10-360-522-59
; Sequence 59, Application US/10360522
; Publication No. US20030221215A1

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; GENERAL INFORMATION:
; APPLICANT: Vossen v.d.; Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; TITLE OF INVENTION: FUNGAL RESISTANCE AND RELATED METHODS
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 945
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(945)
; US-10-360-522-59

```

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Query Match      71.3%; Score 3654.5; DB 15; Length 945;
Best Local Similarity 75.3%; Pred. No. 9e+276;
Matches 730; Conservative 72; Mismatches 142; Indels 25; Gaps 5;

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QY 1 MAEAFLOVLNLTCTFIOGELGLILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
DB 1 MAEAFIOVLNLTCTFIOGELGLILGFDEFEKLOSTFTTIOAVLEDAOKQKDAIEN 60
QY 61 WLOKNAAYEADDLDECKTEAPTRQKKNKYGCYHPVITFRHKGKMKIMEKLDVI 120
DB 61 WLOKNAAYEADDLDECKTEAPTRQKKNKYGCYHPVITFRHKGKMKIMEKLDVI 119
QY 121 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 180
DB 121 AAEIKFHLDEKTERIOVATROTGFVLNEPQVYGRDKDEKDEIVKILINNVSNAQTLPLYLP 179
QY 178 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 240
DB 178 IIGMGLGKTTTAAQVAVNDQVITENHPRKIWTCSVEDPFRKLIKEIVESTIEKSLGMD 237
QY 241 LAPLQKJRLDNLGKKYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 300
DB 241 LAPLQKJRLDNLGKKYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 300
QY 238 IASFOKQLQOLNGKRYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 297
DB 238 IASFOKQLQOLNGKRYLLVLDVNNEDQDKWAKLROVLKVGASGASVLTTRLEKVGSI 297
QY 301 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 360
DB 301 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
QY 298 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
DB 298 MGTLOPYELSNLSQEDCWLLFMQARFGHQBESILPALRLSTHNLPLRLRCFTYCAVFPDTEME 357
QY 361 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 420
DB 361 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
QY 358 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
DB 358 IAPKREKREWEHVRSEIKLQOEBSILPALRLSTHNLPLRLRCFTYCAVFPDTEME 417
QY 421 KNLISLMAAHGFIISKGNILENVNGEVENNELYLSPFOEIEVSGQTYFPQMDLIHDL 480
DB 421 KNLISLMAAHGFIISKGNILENVNGEVENNELYLSPFOEIEVSGQTYFPQMDLIHDL 477
QY 481 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 540
DB 481 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 478 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
DB 478 ATSLFSASTSSNIREIIVENTYIHMSIGFTKYVSSYSLSHLOKQVSLAVNLSDIKLQ 537
QY 541 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 600
DB 541 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 600
QY 538 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 597
DB 538 LBSISGIDLVLHLYNLSTGTSRSLPNOICXKQONOTLHLGHSLCCLPKETSXLGSLR 597
QY 601 NLLDGCYGLTGWPPRIGSLTCLKTLSPRVVGIQKSCOLGELRLNMLVGSIEITHLERV 660
DB 601 NLLDGCYGLTGWPPRIGSLTCLKTLSPRVVGIQKSCOLGELRLNMLVGSIEITHLERV 660

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Qy 181 ILGNGGKTTLAQVFNDOQVIEHFPKINI CVSEDENERKLIKEIYESIEEKS-IGGM 239
Db 180 ILGNGGKTTLAQVFNDOQVIEHFPKINI CVSEDENERKLIKEIYESIEEKS-IGGM 239
Qy 240 DLAPLOKKRLDLNGKRYFLVLDVWNEQDQKAKLROVLKVGASGASVLTTRLEKVS 299
Db 240 DLAPLOKKRLDLNGKRYFLVLDVWNEQDQKAKLROVLKVGASGASVLTTRLEKVS 299
Qy 300 IMGTLOPELISNLGOEDCWLPMORAFGHOEINLVAIGKEIYKKGQVPLAKTLG 359
Db 300 IMGTLOPELISNLGOEDCWLPMORAFGHOEINLVAIGKEIYKKGQVPLAKTLG 359
Qy 360 ILRFREROMEHVDSEIMWLPOESSILPALRLSYHNLPLDLRQCFTYCAVFPKOTEM 419
Db 360 ILRFREROMEHVDSEIMWLPOESSILPALRLSYHNLPLDLRQCFTYCAVFPKOTEM 419
Qy 420 EKEKLISSIMAHGFLLEKGLQPEVGNVSKELCLRSFPOEIEAKCGTYFKMHDLDHD 479
Db 420 EKEKLISSIMAHGFLLEKGLQPEVGNVSKELCLRSFPOEIEAKCGTYFKMHDLDHD 479
Qy 480 LATSLFASSTSSSNIREINVKGYPRKMSIGFTEVSSYSPSLSQFVSLRVNLNSLHFE 539
Db 480 LATSLFASSTSSSNIREINVKGYPRKMSIGFTEVSSYSPSLSQFVSLRVNLNSLHFE 539
Qy 540 QLPSSIGDLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Db 540 QLPSSIGDLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Qy 600 RNLILDCGYGLTQMPRIISLTCLKTLSRFVVGIOKSCQJGELRNMLYGSIEITHLER 659
Db 600 RNLILDCGYGLTQMPRIISLTCLKTLSRFVVGIOKSCQJGELRNMLYGSIEITHLER 659
Qy 660 VKNMDAKEANLSAKENHSHSMKDDERPRIYSESEVLEALPKPSNLTCTITGRFR 719
Db 660 VKNMDAKEANLSAKENHSHSMKDDERPRIYSESEVLEALPKPSNLTCTITGRFR 719
Qy 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLIELMRGSAEYVDSGFP 779
Db 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLIELMRGSAEYVDSGFP 779
Qy 748 RRRPPLRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCMPFVITPLSSVKLVVSGD 839
Db 748 RRRPPLRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCMPFVITPLSSVKLVVSGD 839
Qy 840 KSDAIGSSSISNMLTSLQIRYNKEDASLPBEMFKSIANKYINISPYNKLPLPSLA 899
Db 840 KSDAIGSSSISNMLTSLQIRYNKEDASLPBEMFKSIANKYINISPYNKLPLPSLA 899
Qy 900 SLNALKHLEIHSYALBSLPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNSVE 959
Db 900 SLNALKHLEIHSYALBSLPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNSVE 959
Qy 960 FCPTLAKRC 968
Db 960 FCPTLAKRC 968
Qy 937 RCPQLIKRC 945
Db 937 RCPQLIKRC 945

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; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; NAME/KEY: SITE
; LOCATION: (1)..(972)
; US-10-360-522-61

Query Match 70.7%; Score 3625; DB 15; Length 972;
Best Local Similarity 74.2%; Pred. No. 1.9e-273;
Matches 726; Conservative 92; Mismatches 143; Indels 18; Gaps 7;

Qy 1 MAEAFQVLNDNLTCFIOGELIGLGFEDPEKLOSTFTTIOAVLEDAQKKQLDKAIEN 60
Db 1 MAEAFQVLNDNLTCFIOGELIGLGFEDPEKLOSTFTTIOAVLEDAQKKQLDKAIEN 60
Qy 61 WLQKLNAAVEADDIIDECKTEADIRQKKNGCYHPNVITFRHKIGRKKIKEDLVI 120
Db 61 WLQKLNAAVEADDIIDECKTEADIRQKKNGCYHPNVITFRHKIGRKKIKEDLVI 120
Qy 121 AAEIKTHLDEBTERBOVATROGCVLNEPOVGRDKEKEIVKILNNVNAQTLPVLP 180
Db 121 AAEIKTHLDEBTERBOVATROGCVLNEPOVGRDKEKEIVKILNNVNAQTLPVLP 180
Qy 120 AAEIRNHLDEBTERBOVATROGCVLNEPOVGRDKEKEIVKILNNVNAQTLPVLP 179
Db 120 AAEIRNHLDEBTERBOVATROGCVLNEPOVGRDKEKEIVKILNNVNAQTLPVLP 179
Qy 181 ILGNGGKTTLAQVFNDOQVIEHFPKINI CVSEDENERKLIKEIYESIEEKSIGMD 240
Db 181 ILGNGGKTTLAQVFNDOQVIEHFPKINI CVSEDENERKLIKEIYESIEEKSIGMD 240
Qy 240 DLAPLOKKRLDLNGKRYFLVLDVWNEQDQKAKLROVLKVGASGASVLTTRLEKVS 300
Db 240 DLAPLOKKRLDLNGKRYFLVLDVWNEQDQKAKLROVLKVGASGASVLTTRLEKVS 300
Qy 300 IMGTLOPELISNLGOEDCWLPMORAFGHOEINLVAIGKEIYKKGQVPLAKTLG 359
Db 300 IMGTLOPELISNLGOEDCWLPMORAFGHOEINLVAIGKEIYKKGQVPLAKTLG 359
Qy 360 ILRFREROMEHVDSEIMWLPOESSILPALRLSYHNLPLDLRQCFTYCAVFPKOTEM 420
Db 360 ILRFREROMEHVDSEIMWLPOESSILPALRLSYHNLPLDLRQCFTYCAVFPKOTEM 420
Qy 420 EKEKLISSIMAHGFLLEKGLQPEVGNVSKELCLRSFPOEIEAKCGTYFKMHDLDHD 479
Db 420 EKEKLISSIMAHGFLLEKGLQPEVGNVSKELCLRSFPOEIEAKCGTYFKMHDLDHD 479
Qy 480 LATSLFASSTSSSNIREINVKGYPRKMSIGFTEVSSYSPSLSQFVSLRVNLNSLHFE 539
Db 480 LATSLFASSTSSSNIREINVKGYPRKMSIGFTEVSSYSPSLSQFVSLRVNLNSLHFE 539
Qy 540 QLPSSIGDLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Db 540 QLPSSIGDLVHLRYNLISGNTSIRSLPNOLCKLQNLQTLDLHGCHSLCCLPKETSGLSL 599
Qy 600 RNLILDCGYGLTQMPRIISLTCLKTLSRFVVGIOKSCQJGELRNMLYGSIEITHLER 659
Db 600 RNLILDCGYGLTQMPRIISLTCLKTLSRFVVGIOKSCQJGELRNMLYGSIEITHLER 659
Qy 660 VKNMDAKEANLSAKENHSHSMKDDERPRIYSESEVLEALPKPSNLTCTITGRFR 719
Db 660 VKNMDAKEANLSAKENHSHSMKDDERPRIYSESEVLEALPKPSNLTCTITGRFR 719
Qy 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLIELMRGSAEYVDSGFP 779
Db 720 GIRLPMWNNHSHVLRNVVSIIEIISCKNCSCLPPFGELPCLKSLIELMRGSAEYVDSGFP 779
Qy 748 RRRPPLRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCMPFVITPLSSVKLVVSGD 839
Db 748 RRRPPLRKLNIREFNGNLKGLLKKGEBOCPVLEIEIKCCMPFVITPLSSVKLVVSGD 839
Qy 840 KSDAIGSSSISNMLTSLQIRYNKEDASLPBEMFKSIANKYINISPYNKLPLPSLA 899
Db 840 KSDAIGSSSISNMLTSLQIRYNKEDASLPBEMFKSIANKYINISPYNKLPLPSLA 899
Qy 900 SLNALKHLEIHSYALBSLPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNSVE 959
Db 900 SLNALKHLEIHSYALBSLPBEGVKGILSLTQLSITYCEMLQCLPEGLQHLTALTNSVE 959
Qy 960 FCPTLAKRC 968
Db 960 FCPTLAKRC 968
Qy 937 RCPQLIKRC 945
Db 937 RCPQLIKRC 945

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Db      775 EYEDSGTTRRRPPLAKHIGFCNKLQKQKGAQFPVLJEMKISDCPMFVPTLS 834
Oy      830 SVKTLVSGDXSDAIGFSSISNLMALTSIQIRYNKEDASLEPEMFKSIANKYINISFYF 889
Db      835 SVKLEIIGE-ADAGGLSSISNLTSLTKIFSNHTVSLJEMFNKINENIYISVSYLE 893
Oy      890 NLKELPTSLASINAKLHEISCVYALSELPBGVWGLISLQOLSTYCEMQLCEGLOH 949
Db      894 NLKELPTSLASINAKLHEISCVYALSELPBGVWGLISLQOLSTYCEMQLCEGLOH 953
Oy      950 LTALNLSVERPCPTLAKRC 968
Db      954 LTLTSLKIRGCPOLIKRC 972

RESULT 10
US-10-360-522-57
; Sequence 57, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 1040
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: alignment
; NAME/KEY: SITE
; LOCATION: (1)..(1040)
US-10-360-522-57

Query Match      69.1%; Score 3542; DB 15; Length 1040;
Best Local Similarity 68.4%; Pred. No. 6,2e-267;
Matches 716; Conservative 105; Mismatches 160; Indels 66; Gaps 10;

```

```

Oy      307 YELSNLSOEDCWLLFNQRAFQHOEINLNLVAIGKEIVKCGGVPLAAKTLGILFRKRE 366
Db      360 YHLSNLSPHDSLLFPQRAFGQOKKANPNLVAIGKEIVKCGGVPLAAKTLGILFRKRE 419
Oy      367 ERMWEHVRSEIYKLPQESSILPARLSYHNLPLRCCFTYCAVPPDTEKKNLIS 426
Db      420 ESEWEHVRDEIYSLPQESSILPARLSYHNLPLRCCFTYCAVPPDTEKKNLIT 479
Oy      427 LMAHGFILSKNLELVNENEVWNLVLSFQSEIVKSGQGYFFROMDLIHDLSLPS 486
Db      480 LMAHGFILSKNLELVNENEVWNLVLSFQSEIVKSGQGYFFROMDLIHDLSLPS 539
Oy      487 ASTSSNIREIYENYTHMMSIGFTKVSSYSLSHOKFVSLVNLSDIKQLQSSSIG 546
Db      540 ASASCGNIREINVDYKHVTSIGFAAVSSSPSLKKFVSLVNLVLSYKQLQSSSIG 599
Oy      547 DLYHRLNLSGNTSIRSLPNOCLQNLQTLHDGHSICLPKESKGLSLRNLLDQ 606
Db      600 DLHLRLNLSGNTSIRSLPNOCLQNLQTLHDGHSICLPKESKGLSLRNLLDQ 658
Oy      607 CYGLTCMPRIISLTCLTSRFVVGIOKSCQJGELRNILYGSIEITHLEKKNMDMA 666
Db      659 C-PLTSTPPIGILTLCTKTIQGFIVG-SKKGYQJGELRNILYGSIEITHLEKKNMDMA 716
Oy      667 KEANLSAKENLSHLSMKWDDERPRIYESKRYVLEALXKHSNLTCLTIRGFGILPDW 726
Db      717 -EANLSAKENLSHLSMKWDDERPRIYESKRYVLEALXKHSNLTCLTIRGFGILPDW 774
Oy      727 MNHSLVKNVSIETISCKNCSCLPPFGEPLCLSLLEMRSAEVEVD-----SGEPTTR 781
Db      775 INHSLVKNVSIETISCKNCSCLPPFGEPLCLSLLEMRSAEVEVD-----SGEPTTR 834
Oy      782 RFPSLRKINIREFNLKGLKKEGEOCVLEIEIKCEPMVYIPILSYKLVSGDKS 841
Db      835 SFPSLRKINIREFNLKGLKKEGEOCVLEIEIKCEPMVYIPILSYKLVSGDKS 893
Oy      842 DAIPSSISNLMALTSIQIRYNKEDASLEPEMFKSIANKYINISFYFNLKELPTSLAS 901
Db      894 NTRGLSSISNLTSLTKIFSNHTVSLJEMFNKINENIYISVSYLENLKELPTSLAS 953
Oy      902 NALHRLHSCVYALSELPBGVWGLISLQOLSTYCEMQLCEGLOHLTALTNLSVEFC 961
Db      954 NALHRLHSCVYALSELPBGVWGLISLQOLSTYCEMQLCEGLOHLTALTNLSVEFC 1013
Oy      962 PTLAKRCGIGEDWYKIAHPRVFIY 988
Db      1014 PEVEKRCDEIGEDWYKIAHPRVFIY 1040

RESULT 11
US-10-437-182454
; Sequence 182454, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 182454
; LENGTH: 1110
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:

```

OTHER INFORMATION: Clone ID: PAT_MRT4530_79641C.1.pep
us-10-437-963-182454

Query Match 29.6%; Score 1517; DB 16; Length 1110;
Best Local Similarity 34.9%; Pred. No. 7e-109;
Matches 396; Conservative 189; Mismatches 345; Indels 206; Gaps 35;

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4 AFLQVLLDNLTCFIOGELGLIL---GPKDFEKLQSTFTTIOAVLEDAQKQKQKAIEN 60
9 AFMQLFQPLS---EATLDHFISWGHGKLESSTLSQAPFLDDAEKQLTASARG 65
61 WLQKNAAYEADTILDECKTEAPTRQKKKYGCHPNVITF-----RHKIGR 109
66 WLAKIKDIAVDLDDLDSDYSKAS-WRMKQRC-VIFPTVASFLSSPLSLNLYQHRIRK 122
110 MKKIKEXDVIABERIKFHLDBRTIERQVATF---QTGVLINEPQVGRDKKDKITV-I 165
123 INITLERDCKIAQEDDTTGLQMICENRRYDTSERQSSSLVDSAVFGEREREMVRLV 182
166 LINVSNQOTLEPVLPILGWGIGAKTTTLAQMVFNDDRVIEHFHPKIMICVSEDFNEKRLIK 225
183 LSDNHNCSNLCVIVVGWGGIGKTTLMQVYHDRVENHFDLRITVYSEFDERKLTQ 242
226 EIVSEIE-EKSGMDLAPLQKKLRLDNLGKKYLLVDDVNNEDQKNAKLQVILKVAS 284
243 ETLASDYDQSVASTNMNMLQETLSRVLRGKRYLLVDDVNNEDLDKMSYRAALISGAF 302
285 GASVLTTRLEKVGSIKGTLOPYELSNLSQEDCMLLFQORAF-----GHQEIYMLNVA 338
303 GSKIVVTSRNENVGIRMGIEIPYKLOKLSDDSVSFSGHARDDCSAHPF-----LEA 357
339 IGKEIVKKGCGVPLAAKTLGGILRFKREERQWEHNRDEIMWLPOESSILPALRLSYH 398
358 IGMEIVKGLKGLPLASKLGLSILFCKTBEEKKQILDIMELPKADKNILPALRLSYH 417
399 LPDLRQCFYCAVFPKOTEMEKGNLISLMAHGFILSKNLELVNENVEWNNELYLRSF 458
418 LPPLHKQCFACSVYPKDYFRREKLVKIMLALGFIQSRKKRMDGTGNAYFNELLSRF 477
459 FOEIVKSGQGYFKKHDLIDLATSL----- 484
478 FQPYE---NNYVMDAMHDLAKSISMEDCDHLDYGRHDNALIKTRHLPFCKDAKCMH 532
485 FSASTSSNIREIYENYIHMMSIGFTKVSSYSLSHLOKFSKLVNLSIDIKLQPLSS 544
533 FNPLYGFKRLTLT---IH---GYKSMQLPBGLFMKLEYLRLVLDHAGQGLKEPES 585
545 IGDVHLRLVYLSGNTSIRSLPNQCLQNTQTLDLHGCHSLCCLPKETSKLGSIRNL-- 602
586 IGNLKQALFLDLS-STEIEITLPASLVKLYNQILKSDCNFLREVPOGITRILINRHLA 644
603 ---LIDGCTGLCMPRIIGSLTCLTSLRFVVGIOKKS-CQLGEIRNLN-LYGSIEITHL 657
645 STRLSLRHIG-----IGSLVCLQLEEFVY--QKRGSHVNTBELNDELQGLSIRGL 695
658 ERYKNDMAKEANLSAKENLHLSMKMDD--ERPRIESEKVEYLEALKHSHNLTCTLI 715
696 NNVPFGDVAQCKANKKELKTLHLIMBEDCESNP---SEQOEVLBGLPDLDELKELVI 751
716 RGFRIQLPDMWNHSLKVVSIIEISCKNSCLPPFGLPCLKSLIELMRSAEVEYDS 775
752 KGFGEVRFPMSLASFPLKLOTIHCNCRS--TRLPALQOLPFLAKLVA-AGVTETVQJSS 809
776 ---GPTTRRRPPLSKLNIREFGNLKGILKKEGEGOCVLEIEIKCCPMF-VIPTLSS 830
810 EFTGGQKQKGPALDELLELDMPLSEWIPVADQLFPOLTELGLIKCPOLKPPPIST 869
831 VKKLVSGDKSADIFSSISNLM-----ALPSL 858
870 LRTLVTSSES-----GLESLPELONNSCPSSPTSLYINDCPNLTSLRVGLLAVRPALKSL 924
899 QIRYNKEDASLPEEMFKSLANLKYLNISFY-----FNLKE---LPTS----- 897

```

```

DB 925 TIANCEGLVSLPEECFRELISLSRIHT--YECPLVPWTALGGLLPTSIEDIRINSCPT 982
QY 898 -----IASIANLKHLEIHS CYALBESLPEEGVKGILSTQLSITVCEMQLCEGHQ 949
DB 983 IASVINGLSTLPHLRHREIADCPDINNFRAGLPH--TLQPLFISCCDDICLPPGLH 1040
QY 950 LTA-----LTNLSVEFCPTLAKCEKGIKGDWYKIAHI 982
DB 1041 ISSLETLRISNCPGVESLPKEGLPMGLNELYIKGCPQIKQCCQSG-GEYHAKIAHI 1095

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RESULT 12
US-10-437-963-153490
; Sequence 153490, Application US/10437963
; Publication No. US20040123343A1

```

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David R.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 153490
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_53440C.1.pep
US-10-437-963-153490

```

Query Match 29.6%; Score 1516; DB 16; Length 1222;
Best Local Similarity 32.9%; Pred. No. 9.7e-109;
Matches 408; Conservative 194; Mismatches 355; Indels 284; Gaps 35;

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QY 1 MAE---AFLQVLLDNLTCFIOGELGLILGPKDFEKLQSTFTTIOAVLEDAQKQKQK 57
DB 1 MAELSLALPLRLKKKABESLSTERSFIGIERRSELYTLLANQVINDADQASKPA 60
QY 58 IENVLQKNAAYEADTILDECKTEAPTRQKKKYGCHPNVITFRHKIG 107
DB 61 VKSWIAXLKLAAACADALDELHAYEELRCEALRGHKNITGVRAFSSHYVPLFKYRIG 120
QY 108 KRMKIMEKDVIAAEIKF-----HDBERTIERQVATRQTFVANEPOVGRDKED 160
DB 121 KRLQOIVERIDQVLSQNRFGFLNCSMPVDER-----MOTYSYVDEBEVIGRDKERD 172
QY 161 EIVKLINNVSNAOTLEPVLPILGWGIGAKTTTLAQMVFNDDRVIEHFHPKIMICVSEDFNE 220
DB 173 EIVMMLS--AETBELILPVGIGSLKTTIADLVNDVAKVHFGKMMVVCSENFVS 230
QY 221 KRLIKEIVESI-EKSGMDLAPLQKKLRLDNLGKKYLLVDDVNNEDQKNAKLQV 278
DB 231 PVIKGIIDVATIGNDCLKFDNLELLQORLREELGQKRYLLVDDVNNEDQKNGALRTL 290
QY 279 LKVASGASVLTTRLEKVGSIKGTLOPYELSNLSQEDCMLLFQORAFGHQOEINLNUVA 338
DB 291 LQSGCMASAVVTVTRNVKVASIMESISPLCLENINPDSWIVFSRRAFGTGVETPELVE 350
QY 339 IGKEIVKKGCGVPLAAKTLGGILRFKREERQWEHNRDEIMWLPOESSILPALRLSYH 398
DB 351 VGRKIVKCGGLPLATISMGALSTKQETDMLSTILESNTN---DESSQLPLASLQYK 407
QY 399 LPDLRQCFYCAVFPKOTEMEKGNLISLMAHGFILSKNLELVNENVEWNNELYLRSF 458
DB 408 LPSHMQCFACVAFVPDYVEIDKODLIHLWVSNQFISPKKMSDIEBGNHVFMELVRSF 467

```

[illegible][illegible]

Db 859 LBPSTLVEIKIS-----EAGFSVLPVPAHPRFLPSLTRLOIHKCPNLTSLQOGLISQOLS 913
Qy 870 -----PEEMFKSLANKXNLNISPYNKELPTS----- 897
Db 914 ALQOLTTNCPDELHPPEGKRTLTALQSLHI---YDCPRLATVAMHRLGLPRMIEDLRIT 970
Qy 898 -----LASLNLKHLHISCYALSLPEE-----GVKGLIS----- 928
Db 971 SCSTNINPLDELNELPRLKVLADCVSLNTPPEKLPATLKLEIFNCSNLASLPACLO 1030
Qy 929 ---LTLSTICYCMLQCLP-EGLOHTALTNLVSFPCPTLAKRCEKIGEDWYKIANI 982
Db 1031 EASCLTWTITNVCYSIKCLPAHGLP--LSLELYIKCECPFLAERCQENSGSDWPKISHI 1087

RESULT 14
US-10-437-963-199180
; Sequence 199180, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 199180
; LENGTH: 1401
; TYPE: PR
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_9476C.1.pep
US-10-437-963-199180

Query Match 28.1%; Score 1442.5; DB 16; Length 1401;
Best Local Similarity 31.6%; Pred. No. 6.5e-103;
Matches 394; Conservative 189; Mismatches 375; Indels 287; Gaps 32;

Qy 1 MAE---AFLQVLNLTNCFIQGBELGLILGFYDEFEKLOSTFTTIOAVLEDAQKQKDKA 57
Db 1 MAELSLALPRLKKAAGSLSTBPSFIGIEHRESELVTLALINQVYGAEBQASKKPA 60
Qy 58 IENNLQKINAAAYEADLDLDECKTEAPTRQKKKNG-----CYHNNVITFRKI 106
Db 61 VKSWITTKKLKACADADLDLHLYEA-LRSEALRGRHKINGVRAFPSSHNPLLFKYRI 119
Qy 107 GKRMKKIMEXKDVLAERIKFHL-----DERTIERQVATRQGFVNEPOVGRDCK 159
Db 120 GKRIQOIVEQIDQLVSQMGFPLNCPMBEDR-----MQTYSYDEBGIGRHKER 171
Qy 160 DEIVKILINNVSNQQTLPVLPIILGWGLGKTTLAQMVNDORVIEHFPKIMICVSEDPN 219
Db 172 DEFTHMLS--AKSDKLLIPVIGIGGKTTLAQVLVNDVKVKAHFGKHMVVCSENF 229
Qy 220 EKRLIKEIVESI--EKSLSGMDLAPLQKLRDLNKGKLYLVLDVNNEDQKRAKLRQ 277
Db 230 VPDIVKGIIDALIGDCIKSDNLELQOORLEESIQKRYLLVLDVNNEDQKREALRT 289
Qy 278 VLKYGASGASVLTTRLEKVSIGWTLQPYELSNLSQDCMLFQORAFQOBEINILVY 337
Db 290 LKCGSKMGSAVAVTTTRNSVAVSGMTVPPLALEQSLQSDSTLFEKRAFRGVAKSCFV 349
Qy 338 AIGKEIVKCGVPLAAKTLGILFKEERQMEHVRSEIWKLPQESSILPALRLSYH 397

Db 350 EIGTKIVQKSGVPLAINSNGGLISRKHSVRDWLAIIONTW----EENNLTVLISLYK 405
Qy 398 HLPDLRQCFYCAVFPDTEMENGNLISLMAHGFILSKGNLELVNENVELYLR 457
Db 406 HLPSPMQCFACFCAVFPDYEIDDKDLHMLINSGLFIPSKETSDIEEGNVLPLELMRS 465
Qy 458 FFOEIEVKSQ-----TYFKXHDLIHDLATS-----LBSASTSSNIR 495
Db 466 FFOKQKRSRKEEYIVGYKDVTTCKIHDLHMDLAVSISGDECYTLQVLVINKPKNVH 525
Qy 496 EIIYENTHMSIGFTK-----VVSYSYL--SHIQKPSL-----RYNLSDIKQL 541
Db 526 HLV--FPHPKIGFVQRCPIIRSLFSLKHNHNSKMDVEMVSPCCALGLHICDNRF 582
Qy 542 PSSIGDLVHLRYNLNGTSIRSLPNOLCKLONQTLDLHCHSLCCPKETSKLSIRN 601
Db 583 SVEPAMKHLRYLDLS--SSDKITLPEAVSALYNQILMLNCRGLTHLPDGMKFMISLRH 641
Qy 602 LLLDGCYGLTCMPBRIGSLTCLKTLSPRVVGIQKKSQGLRLNUNLYGSIETHLERVK 661
Db 642 VYLDGCSLQMPRGLQSLRTLTVMVYG--NESDCRHLKDLGKRLQIHNLKVT 700
Qy 662 NDMAKKANLSAKNMSLSMKMD-----DERPRIYSEKVEVLEAKPHSNL 710
Db 701 NPLQAKENLENKKNLQOLALCWDSRNFTCSHCSADEYQLCRPE--EVDALKPPNGL 758
Qy 711 TCLTRGPRGIRLDDMMHNSV-LKNVYSIEIISCKNSCLPPFGLPCLKSLRLMSAE 769
Db 759 KVLKLRQMGSNFPMHEDGYTLQNIYKLSRGSVMCYKLPVWQLPLEVYLRKR-MER 817
Qy 770 VEYVDSGFPTRRR-----PSSLRKINIREFGNIKGLKKEGE--QCPVLEIEIK 818
Db 818 LKVCYRPRPDBEYGNQVVFQKLTSLBEMESLEMHXYDQVTSVTPPKDAMEII 877
Qy 819 CCP-MFVITPITSSVKYLVSDSKDALGSSISNMLL-----TSIQIR-----YKXE 865
Db 878 DCPKLTALPNVPIILKSLTGNKVLGLVSGISNLSYVLGASQSSRRVTLYYINGE 937
Qy 866 -----DAST----- 869
Db 938 REGSTDKEHILPDHLMSWGLTKLHLQGPNTAPENVKISGHHMSVQDLVLSGCCFC 997
Qy 870 -----PEEMFKSL----- 877
Db 998 IQHGLQSPWFWSFGLOQLLEIWCDSLTFMPEEBERSLSEKLFIVDCNFTGVP 1057
Qy 878 -----ANLKINLSIFENL----- 891
Db 1058 DRLSARSTDGGPCNLEVLQIDRCPNLVFPPTNFCILRILVITDSNVLEGLPGGFCOGT 1117
Qy 892 -----KELPTSLASLNLKHLHISCYALSLPEGVKGLISTQLSTIYCEM 939
Db 1118 LTTVLIGCSFSSLPASIRCLSNLKSDELTSNNSLSLP-EGMQLNLATLTHPIKCPG 1176
Qy 940 LQCLPEGL-CHLTALTNLVSFPCPTLAKRCEKIGEDWYKIANI 983
Db 1177 ITALPBGLOQLHGLQFTTVEDCPALARRCRG--GDVWEKXKDP 1220

RESULT 15
US-10-425-114-55552
; Sequence 55552, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 01:06:28 / Search time 52 seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-647-268-2
Perfect score: 5127
Sequence: 1 MAAEPLQVLDNLTCFLQGE.....EKIGEDMYKIAHPRVFY 988

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240	24.2	1240	2 T06404	resistance complex
2	1212	23.6	1220	2 T06403	resistance complex
3	1020.5	19.9	571	2 T02213	NBS-LRR type resist
4	904	17.6	1802	2 T00020	bacterial blight-r
5	763.5	14.9	852	2 T08416	disease resistance
6	716	14.0	847	2 T12977	hypothetical prote
7	694	13.5	908	2 T48899	disease resistance
8	676.5	13.2	1584	2 F96573	protein F12M16.25
9	671	13.1	906	2 T48898	disease resistance
10	660	12.9	835	2 T45590	hypothetical prote
11	655.5	12.8	389	2 T04390	NBS-LRR type resist
12	655	12.8	906	2 G96621	probable disease r
13	649	12.7	797	2 T06219	probable cyst nema
14	635.5	12.4	831	2 T51185	resistance protein
15	632.5	12.3	847	2 T12979	hypothetical prote
16	632	12.3	926	2 A57072	disease resistance
17	625	12.2	820	2 T51186	resistance protein
18	618	12.1	821	2 A86243	hypothetical prote
19	618	12.1	907	2 F96617	probable disease r
20	614.5	12.0	839	2 B96538	hypothetical prote
21	609.5	11.9	1255	2 T06267	nematodes resistan
22	585	11.4	269	2 T04394	NBS-LRR type resist
23	573	11.2	900	2 G96617	probable disease r
24	572	11.2	899	2 H96617	probable disease r
25	571.5	11.1	1257	2 T06269	root-knot nematode
26	570.5	11.1	483	2 T02226	NBS-LRR type resist
27	547.5	10.7	695	2 T52429	PRM1 homolog (limp
28	540	10.5	919	2 T05746	hypothetical prote
29	527	10.3	885	2 B86257	NBS/LRR disease re

30	524.5	10.2	898	2 B96659	hypothetical prote
31	516	10.1	967	2 G96637	hypothetical prote
32	514	10.0	889	2 F96637	hypothetical prote
33	512.5	10.0	255	2 T04389	NBS-LRR type resist
34	512.5	10.0	909	1 A54809	disease resistance
35	509.5	9.9	925	2 H96638	protein T1F9.20 [i
36	503	9.8	921	2 D86293	F7H2.22 protein -
37	498.5	9.7	227	2 T07755	disease resistance
38	497.5	9.7	985	2 T06049	hypothetical prote
39	490.5	9.6	892	2 T01899	disease resistance
40	486.5	9.5	613	2 T52465	hypothetical prote
41	480	9.4	263	2 T02227	NBS-LRR type resist
42	475	9.3	889	2 C86257	resistance to Paeu
43	473.5	9.2	1824	2 T07589	disease resistance
44	470.5	9.2	893	2 H96651	protein T3P18.19 [
45	468	9.1	560	2 T52438	PRM1 homolog [limp

ALIGNMENTS

RESULT 1
T06404
Resistance complex protein I2C-2 - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06404
R:Ori, N.; Eshed, Y.; Paran, I.; Presting, G.; Aviv, D.; Tanksley, S.; Zamir, D.; Fluhr,
Plant Cell 9, 521-532, 1997
A:Title: The I2C family from the wilt disease resistance locus I2 belongs to the nucleot
A:Reference number: 215652; MUID:97290204; PMID:9144960
A:Accession: T06404
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1240 <ORI>
A:Cross-references: UNIPROT:O24016; EMBL:AF004879; NID:92258316; PIDN:AAB63275.1; PID:92;
C:Genetics:
A:Gene: I2C-2
A:Map position: 11
C:Function:
A:Description: confers resistance against Fusarium oxysporum
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match 24.2% Score 1240; DB 2; Length 1240;
Best Local Similarity 28.6%; Pred. No. 4.8e-63;
Matches 359; Conservative 211; Mismatches 378; Indels 306; Gaps 39;

QY 6 LOVLDNLTCFLQGE-LGLIGFKDE--PEKLOSTFTTIOAVLEDAQKQLKDKALEW 61
DB 16 LNVLFDRLA--PNQDLNMRKHDYKLLKDKMTLRGIQIVLSDAENKQASPSVRDW 73
QY 62 LQKINAAVAEADTILDECKTBPATROKKKNGCCYHN-----VITRHKIKG 108
DB 74 LNELRDAVDSAEINLEEVNYEA---LRLVGEQGHQNFSETSNQOVDEFLNKDKLED 129
QY 109 RMKIMKELDVIAERIKFHLDEKTEROYATRGTVLNPQVYGGDKDEIVKILIN 168
DB 130 TTEFLKDLQDQIGLGLGKRYFDSTKLTTRTPSTS---LIDSPDIFGQSEIEDLIDRLS 186
QY 169 NVSNAQTLPVLPILIGMGLGKTTLAQVFNFDORIEHFHKIWIQVSEDEFNEKRLKEIV 228
DB 187 EAGSGKRLTVPIVGMGLGKTTLAQVFNDESXKHFIDKAWCVSEAVNAFPIITGLL 246
QY 229 ESTIEKSLGMDLAFLQKLRDLNGKTYLLVDDVNNEDQAKAKRQVYLKVGASGASV 288
DB 247 QEIGSIDLVDDNINQLOVKLKERLKEKKFLIVDDVNDVNNEDLRNFVQGDIGSKI 306
QY 289 LITTRLEKGSINGTQPYELSNLSQEDCWLLFMQRAF-----GHQESINLVVAIGKE 342
DB 307 IVTRKDSVALMGWNEO-ISMGNLSTASWSLQRRHAFEMNDPWGSE-----LEEYGRQ 360
QY 343 IVKCGGVPLAATLTGLILFKREERQWHRDSEIWKLPQEESSILPALRLSYHHLPLD 402

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Db      361  IAAKCGPLALKTLAGMLRSKSEVEEMKCLRSBIMEL--RNDIILPALMLSYNDLPAH 418
Qy      403  LRQFTTCVAVPPKOTEMEKGNLISLMAHGFIISKMLEENGVENNELYLSPFOEI 462
      419  LKRCFSFCALPPKQYPRFKEQVILHLMANGLVPEDEI-IDDLGNQFPLELSSSLFERV 477
Qy      463  EVKSG---QYFKMNDLHDATSLFS-----ASTSSNIRELIVNYTHMMSIGFTK 512
      478  PNSEBGNIKELFLMHMDLVNDLAQLASSKLCIRLESQSQSHMLECRHLSYMSMGDGEFK 537
Db      513  VSSVSYSLHLQKPY-----SLRYNLSDIKLKOLPSSIG 546
Qy      538  LTPYKLEQLATLLPTGSSVAVFVNPVLTFRVHNLPTLRSLRALSLSHYKMEELPNLF 597
Db      547  -DLVHLRYNLSGNTSIRSLPNQCLONLQTLIDHGHSICCPKETSIGSLRNLLD 605
Qy      598  IKLKLRLPLDIS-PTNIRLPLDISICVLYNLBTLLSSC-KLEELPQMEKILINRHDIS 655
Db      606  GCGYGLTQMPRIGSLTCLKTL--SRFVVGIOKSSQGLGELNMLNLYSIEITHLERYND 663
Qy      656  NTMHLK-MPLHLSTRKSLQVLVGAKEFLVGWRME-DLGEAQ-NLYGSLVVKLENVDR 711
Db      664  MDAKEANLSAKENLSLMSKWDDEPRPIYSEKVEVLEALKPHSNLTCLTTRFGIRL 723
Qy      712  REAVKPKREKNHVEQLSLEWSESISADNSQTER-DILDELPHKNIQEVKLIYRGTFN 770
Db      724  PDMNHSLVKNVSVLEIISCKNCSCLPFGELPCIKSLELRGSAFEVYVDSGF----PT 779
Qy      771  PNWVADPLFLKLVKLSLNCKDCYSLPALQGLPCIKFLSV-KGMHGIRVWVEEFGRUSS 829
Db      780  RRRPSLRK-----INIRFEGNLKGL-----LKEGEE 807
Qy      830  KKPENCLEKLEPEDMTWKOMHALIGFPLLEKLSIINCELSLEIPIQSSSLKRFVVF 889
Db      808  QCPV-----LEELIEIKCC-----PMFVPIPTSSVKKLVSG----- 838
Qy      890  GCPVVFYDAQLRSQLEGMKQIEEYIRDCNSVTSFPFSILPT-TLKTIDISGCPKIKL 947
Db      839  ---MA-----LTSLOIRYKKEDASLPE----- 871
Qy      948  EAPVCENSMFLBESVSECGVSPFLPTARELRIGNCHNVRFILPTATETLHTRNCNV 1007
Db      853  ---MA-----LTSLOIRYKKEDASLPE----- 871
Qy      1008  EKLMACGGAQOLISLDSIGCKKCLKPELPLSKLEQVLTNCPRIEGLPLNLOKLYIRD 1067
Db      872  -----EMF-----KSIAN 879
Qy      1068  CKKLVNGRKEWHLQRLTKLYIYHDSDEIDIEHWELPCSIITRLEVENLITLSSQHLKSLTS 1127
Db      880  LKYNLISYFVNLKELP-----TSLASNALKLELHSCVLESLEPBEVKGILISLOLSI 934
Qy      1128  LQYLCID--GNLSPIQSQGQISFSEHLSLTQTLQWNNHNLQSSSALPS--SLSQLEI 1183
Db      935  TYCEMLQCLP-EGLOHLTALTNLSVEPCPTLAKCEKIGEDWYTIHAPRVI 987
Qy      1184  FHCPLQSLPLANGM--SLSKTLISGCPLLPLLEPRKGEVWPQIAHIIPTILI 1235

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A:Cross-references: UNIPROT:O24015; EMBL:AF004878; NID:g2258314; PIDN:AA63274.1; PID:g22
C:Genetics:
A:Gene: l2c-1
A:Map position: 11
C:Function:
A:Description: confers resistance against Fusarium oxysporum
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match      23.6%; Score 1212; DB 2; Length 1220;
Best local similarity 29.2%; Pred. No. 1,98-61;
Matches 361; Conservative 207; Mismatches 378; Indels 290; Gaps 39;

Qy      6  LQVLLDNLTCFTQGE-LGLILGFKDE--FEKLGSTFTTQAVLEDAQKQKDXAIENW 61
      16  LNVFLFDRLA--PNDLILNMRKHTDVELEFKGLDILSLQIYVLSDAENKKAASQVPSQW 73
Db      62  LQKNAAAAYEADTIDE-----CKTEAPRQKKNKYGCHPVPVITFRHKIGRMMKIM 114
Qy      74  LHKLTQVDAEMLIEOVNVEALRLKVEYSNQVSDNLCLSD--FFLNIRKKLEDTI 130
Db      115  EKLQVIAERIKEHLDERTEROVATR-QTGFVNLSEPOVYGRDKEDKIYKILINVSNA 173
Qy      131  KGLSEVLEKQIGRLGKHEHFTSKQETTPSTSLVDSGIFGRKNIEINLVGRLLSMQTKR 190
Db      174  QTLPEVLPILGNGIGKTTLAQWVFNDQVLEHFRPKIWCVSDEDFNEKRLKEIVSIEE 233
Qy      191  KNLAIVVPIVGGGKGTTLAKAAYVNDERVOGHFGLTAMFCSSEAYDAFRITKGLLOEIGS 250
Db      234  KSLGMD-----LAPLQKLRDLNKGKYLVLVDVNMEDQKAKKROYL 279
Qy      251  TDLKADNLNLOQVLEKADNLNLOQVLEKELNGKRFVLVLDVNMNDPBMWDLNLF 310
Db      280  KVGSAGSVLTTRTLEKYSIMGTLOPELSNLSEQDEWLLFMQARQHOE-EINLNLVA 338
Qy      311  LQDGSIKIIVTRTKESVALMDSGALT-MGILSSESMALFKRHSLEHOPKHEPEEE 369
Db      339  IGKEIVKCGGVPLAAKTLGILIFKREERQWEHVRDSEIWKLPQESSIILPALRLSYH 398
Qy      370  VGQIADCKKGLPLALKALAGMLRSKSEVDEWRNIRSEIWEIPELSCNGIILPALMLSYND 429
Db      399  LPDLRQFTTCVAVPPKOTEMEKGNLISLMAHGFIISKMLEENGVENNELYLSPF 458
Qy      430  LPALHKQCFAYCALPYDQYRKQVILHMTANLV-----HOFHSGNQFIELRSLSL 483
Db      459  FOEIEVNSGQTY--FKMNDLHDATSLFSASTSSNIR-----EIVENYIHM-MSIG 509
Qy      484  FEMASPESEPVVEFLMHDLVNDLA---QIASNNHCIRLEDNKGSHMLECRHMSYSIG 539
Db      510  ---FTVVSYSYSLHLQKPY-----SLRYNLSDIKLKOLPSSIG 540
Qy      540  QDGFEEKLSLFSKSEQRLTLPLPIDIOFHSKLSKRYVLNHLPTLRSLRALSLSHYQIEV 599
Db      541  LPSSIG-DLVHLRYNLSGNTSIRSLPNQCLONLQTLIDHGHSICCPKETSIGSL 599
Qy      600  LPNLIPLIKLRLPLDIS-FTSITKLPDSIFVLNLELTLSSCYLLEELPQMEKILINL 658
Db      600  RNLLDGCYGLTQMPRIGSLTCLKTL--SRFVVGIOKSSQGLGELNMLNLYSIEITHL 657
Qy      659  RHLDISNTRRLK-MPLHLSTRKSLQVLVGAKEFLVGWRME-YLGEAH-NLYGSLSLTEL 714
Db      658  ERYNDMDAKEANLSAKENLSLMSKWDDEPRPIYSEKVEVLEALKPHSNLTCLTTRG 717
Qy      715  ENVDREAVVAKKREKNHVEQLSLEWSESISADNSQTER-DILDELPHKNIAVAVELTG 773
Db      718  FRGIRLPRMNHSLVKNVSVLEIISCKNCSCLPFGELPCIKSLELRGSAFEVYVDSGF 777
Qy      774  YRGTFNPWVADPLFVKLVHLYLNCKDCYSLPALQGLPCIEFSLI-RGMHGIRVWVEEF 832
Db      778  PTR-----RRPPLRKLNIR-----EFGNL 797
Qy      833  YGRLSKKPFPNSLVKLAREPDMRWKMHMTLIGFPLETKLSINCELSLEIPIQFSSL 892
Db      798  KGL-----LKEE--GE----- 806

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Db 893 KRLLICDKSVTSFFSILPTLLKRIKISGCPKLTLEAPVGMFEVYLVIDCGCVDDIS 952
Qy 807 -EQGPVLEIEIKKC--PMFVIPT----- 827
Db 953 PEPLPTARQSLIENCHNVTREPLIPATESLHINCEKLSMACGGAOLTSINWGCKK 1012
Qy 828 -----LSSVKKL-----VSGDKSDAIGFSSISNLMALT 856
Db 1013 CLPELLEPLKELRLTYCEIEGELPFPNLIIDIRCKGLVNRKE-----WHLQRLT 1064
Qy 857 SLQIRYNKD-----ASLPEEMKSLANLKYL---NISFYENLK 892
Db 1065 ELWIKHDSDEHIEHWELPSSIORLFIPLNLKTLSSQHLKSLTSLQFLRIVGNLSQFQSG 1124
Qy 893 ELPTSLALNKLKHEHSCALBESLPREGVKGLISLTQLSITVCEMLQCLP-BELQHLT 951
Db 1125 QL-SSFSHLTSLQTLQIWNFNLOSLPESALPS--SLSHLILISNCPNLQSLPLKGM--S 1179
Qy 952 ALTNLSVEFCPTLAKRCEKIGEDWYKIAHPRVPI 987
Db 1180 SLSTLSICKPLPLPEFDKGEWTEIAHIFTIOI 1215

RESULT 3

NBS-IRR type resistance protein - rice (fragment)
C/Species: Oryza sativa (rice)
C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02213
R/Leister, D.; Kutsch, J.; Laurie, D.A.; Yano, M.; Sasaki, T.; Devos, K.; Graner, A.; Sch
Proc. Natl. Acad. Sci. U.S.A. 95, 370-375, 1998
A/Title: Rapid reorganization of resistance gene homologues in cereal genomes.
A/Reference number: Z14623; MUID:98081880; PMID:9419382
A/Accession: T02213
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-571 <LEI>
A/Cross-references: UNIPROT:O48981; EMBL:AF032688; NID:g2792219; PIDN:AA69685.1; PID:g2
C/Genetics:
A/Gene: r1
C/Superfamily: disease resistance protein Rps2; leucine-rich alpha-2-glycoprotein repeat

Query Match 19.9%; Score 1020.5; DB 2; Length 571;
Best Local Similarity 41.1%; Pred. No. 6,1e-51; Indels 81; Gaps 18;
Matches 250; Conservative 98; Mismatches 179;

Qy 105 KIGKMKKIMEKLDVIAERIKFHLDERTIEROVATROTGFEVNLPOYVGHDKEDKDIYK 164
Db 2 RAGPDMSTMR-----EETK-----ERP-----KTSLSIDGSSVFGREEDKENIVK 43
Qy 165 ILIN-NVSNNAOTLPVLPILMGIGKTTLAQWVENDQVIEHFAPKIVCSSEDFNEKRL 223
Db 44 MLTPNNNSHNAVSVLPVIGMGIGKTTLTQLVNDDPVKVEYFQLRVPVCSSEDFNEKRL 103
Qy 224 IKELVESIE---EKSLGMDLAPLOKRLDLNGKKVLLVDDVNEODMOKAKROYLK 280
Db 104 TKETTESVAGSGSVTTMMNL--LDSDLSKLEGGKRLFLVDDVNBDEPKMDRRCALV 161
Qy 281 VGASGASVLTTRLEKVSINGTLOPELNSLQEDCMILFMQAFGH-OEININLVAI 339
Db 162 SGSNGSRVLTTRNNVNGKMGKMPFPLKQISENDCNMLFRSYAFAGDSLSHHEIT 221
Qy 340 GKEIVKCGVPLAKTGLGILRFGRERQWEHVDSEIWKLPQESSILPALRLSYHL 399
Db 222 GKEIVKCKGKPLAKAIGSLCTKOTEDDMKCVLRSEIWEIPLSPKNILPALRLSYHL 281
Qy 400 PLDRQCTYCAVPEKQEMEKGNLSLMAHGFLLSGNLELVNGEVMNELYLRSEF 459
Db 282 PALLRGCAFCGKVDYVFEKETIVQIWMALGFIQSGFRRTIEGLSSYFDELGRSFF 341
Qy 460 QEIEVKSQGTFFKMIDLHDLATSLF-----SASTSSS-----NIREII 498

Db 342 Q-HHKG--VYNHADMHLAQSVMDECLRLDDPNNSSSTSSNRLSFCNHRSTS 396
Qy 499 VENTYHMMSIGFTKYVSSYSLSHLQKFS-----LRYNLNSDLIKLQKLPSSIG 546
Db 397 FEDF-----LGFKARTLLLANGYKSRSPSPDLFLMLRLYHLELNRROTTELPSDIG 451
Qy 547 DLVHLRYNLNSGNTSIRSLPNQCLQNLQTLDLHGCHSLCCLPKETSILGSLRNLL--- 603
Db 452 NLKMLRYNLNSG-TGITVLPSSIGRLFNLTQLKKNCHVLECIP-----GSITLVNMR 504
Qy 604 -LDGCTGTCMPRIAGSLTCKTISRFPVGIQKSCQGLERL-NLNGSIEITLERYK 661
Db 505 WLEARIDLTIGIAGILMLTCLQDLSEFVH-NDKGKXISELKTWMSIGGRICIKNLEAVD 563
Qy 662 NDMADKXA 669
Db 564 SAERNGRA 571

RESULT 4

T00020
bacterial blight-resistance protein Xal - rice
C/Species: Oryza sativa (rice)
C/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C/Accession: T00020
R/Yoshimura, S.; Yamanouchi, U.; Katayose, Y.; Toki, S.; Wang, Z.X.; Kono, I.; Kurata, N.
Proc. Natl. Acad. Sci. U.S.A. 95, 1663-1668, 1998
A/Title: Expression of Xal, a bacterial blight-resistance gene in rice, is induced by bac
A/Reference number: Z14057; MUID:98132648; PMID:9465073
A/Accession: T00020
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1802 <OS>
A/Cross-references: UNIPROT:O49647; EMBL:AB002266; NID:g2943741; PIDN:BA425068.1; PID:g24
A/Experimental source: strain IR-Bel; green leaves inoculated with Xanthomonas oryza pv.c
C/Genetics:
A/Gene: Xal
A/Map position: 4

Query Match 17.6%; Score 904; DB 2; Length 1802;
Best Local Similarity 29.2%; Pred. No. 1.5e-43;
Matches 280; Conservative 138; Mismatches 362; Indels 178; Gaps 27;

Qy 143 TGFVNEPOYGRPEKDEIKILINVSNAQTLPLVPIILMGIGKTTLAQWVENDQV 202
Db 288 TSTVLPETVYGRAHEMETIKQILMSNRNSGIT--VLPVNGGIGKTTLAQVYKDLVI 345
Qy 203 IEHFHPKIMCVSDPNEKRLIKEISIEKSLGK-DLAPLOKRLDLNGKKVLLV 261
Db 346 KSGFNVKIMVYSDKFDVVKITRQILDHVSQSHGINSNLTLOQDLSEOKSKKFLIVL 405
Qy 262 DDVNNEDODKAKROYLAKG-----ASGASVLTTRLEKVSIMGTLOPELNSL 312
Db 406 DDVNEIRTRDKKLLAPLRPDQVNSQGEATGMIIILTTIIGSLGKTVGVSILKEAL 465
Qy 313 SQEDCMILFMQAFGH-OEININLVAIGKEIVKCGVPLAATLGLILPFKEBERQWE 371
Db 466 KDDIIVSLFKYHAAGNDKSDSPGLQVYKQIABELKGNPLAAKTVSGLLTGNLTIDMD 525
Qy 372 HVDSSEIKWLPOEBSILPALRLSYHLPLDRQCTYCAVPEKQEMEKGNLSLMAH 431
Db 526 SIISSEKVSLOQAYGMQALKSLDYHLSNPLQCVSYCSLPKGYSPSKQOLQIOWIAQ 585
Qy 432 GFILSKNLELVNGEVMNELYLRSPFOELE-VKSGQTYRKMDLHDLATSLFS---A 487
Db 586 GFV-EESSEKLEQGMKYLALVNSGFLQVESYRFSSEYFVMDLMDLAQKVSQTEYA 644
Qy 488 STSSSNIREI-----IYENYI-----HMSIGFTKYVSSYSL--- 519
Db 645 TIDSECTELAPSRHLSIVTDSAYRKEKYNISNRYFEKRLKMYRSRSLRSLVLIQ 704
Qy 520 --SHLQKFSLRVLNLSDLIKLQLP-----SSIGDLVHLRYNLNSGNTSIRSLPN 567

648 LYG-----SIEITHLEKYNOMDAKEMANLAKENLHSLSMKMDDEDERPRIYSEKVEYLEA 703
677 LYGHSTHSSVTLDIRM-TKRYLAVALSERKCNFTTS-----SS 715
OY LKPSNLTCLTIRGFRGIRLDPMMNHSVLRKNVSEIISCKNCSCLPPFGLPCIKSLET 763
Db LRELRNLETNLFSLSELYWMDVNGEFLDHFH-----LKQGL 755
OY 764 WRGSAEVEYVDSGPTTTRRRPRLKRNIRBGNLKGILKKEGEOCPYLEIEIKCCMF 823
Db AVMSKI-----PDQHPF-----PRLVHLFLIYCGM- 782
OY 824 VIPLSSVKLVGSGSDAIGFSSISNLMALTSQIRYNKEDASLPREMFKSLANLKYL 883
Db 783 -----EED--PMPILKILHLKSV 799
OY 884 NIS-FYFNKLKLPISLASINLKHLEHSCYALBS-LPBGVKGILSLTOLSTYCEMLQ 941
Db 800 RLAKKAPLGSRMVCSKGGFPQLCVIEISKESELEWYIEBG-SMPCLRITLTDCKKLG 857
OY 942 CLPBGLOHLYALTNLSVEFCPTLAKCKEKG--GEDMYKIAHPRV 985
Db 858 ELPGKLKTYTSLKELKIEGMKREWK-EKLVPGGEDYKVOHIDPV 901

RESULT 8

protein F12M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96573
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Coma, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Autors: Saldeberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1584 <STO>
A:Cross-references: UNIPROT:Q9MAG6; GB:AE005173; NID:g7769860; PIDN:AAF9538.1; GSPDB:GN
C:Genetics:
A:Gene: F12M16.25
A:Map position: 1

Query Match 13.2%; Score 676.5; DB 2; Length 1584;
Best Local Similarity 25.0%; Pred. No. 1.4e-30;
Matches 266; Conservative 183; Mismatches 347; Indels 269; Gaps 44;

OY 10 LDNLTCFIOGELGLGKDEBEKLOSTFTTIOAVLEDAQKOLDKALBNMLOKLNA 69
Db 323 VEKMWELLSRESARLNGDEVDGKGRLOSLKDKADAKTERKRNFLLEVXIV 382
OY 70 YEADDI-----LDECK-TEAPTRQKNKYGCYHNVITFRNK-----IGRMKIMEK 116
Db 383 YDADITISPLNLRKGEKGIKKQVRLTACG-----LVDRKRFASDISGITRRISEVIG 438
OY 117 LDVIAERI-----KFHDEFTIERQVATRTQTVLNEPVOYVGDKEDIVKLLINV 170
Db 439 MOSLIGIHADGGSLQER--QREI--RQTFERNSSSDLVGIDGVEELVDHLVEN- 493
OY 171 SNAQTLPLPLITGMLGCTTTLAOMVENDQRIEHPRIWICVSEDENEKRLIEIYES 230
Db 494 ---DSVQVAVSGMGIKGTTLAROVFNHDIVRRHFDGFSWVCQOFRKQWQRIIAD 550
OY 231 IE--EKSIGMDLAPLOKRLDLNGKTYLVLDVWNVEDODKAKLQVLRVGSASAV 288

Db 551 LRPYDEGIQIMDEYTLQGBLFFELLESGRYLLVLDVWKEED--WDRKAVFP-HKRMKM 607
OY 289 LTTTRLEKVG-SIMGTLQPELNLNISOECMLFMORAFCHOEINLNL-VAIGKEIYVK 346
Db 608 LITSRNGLGIMADPTCFARPRILITPESQWKLPERIVSSRDKTERKVEAMKENVY 667
OY 347 CGGVPLAKTLGGLLRKREERQMEHVRSIEIKL-----DQESSILPALRSTYHL 399
Db 668 CGGLPLAVKVLGGILAKKHVLEMKRVHNSITVHIVGSKGLSDSNSVYRVLSIYEDL 727
OY 400 PLDIRQFTTCAYFPKOTMEKGNLSLMAHGFILS-KNLBLEANVGNVMEIYRSF 458
Db 728 PMOLKHFYLAHPEEDYKIDVXILFFNYVAEGITTFHDGSTIQDTGESYLEEVRNM 787
OY 459 --FOEIEVKSQQYFKKNDLIHDLATS-----LFSASTSSNI-----REI 498
Db 788 VVVEESTYTRIEYCOHDMREVCLSKAEENFIRVVKYPTTSTTNNOFPSRSRLV 847
OY 499 VE--NYIHMSIGFTKVSSYSLSHT-QKFVS-----LRYNLSDIKLK--QLPS 544
Db 848 LHSNALHMLGHDKONKARAVLIFGVEKFKMGFGQLPLRLVLDLSYQFEGGKLPS 907
OY 545 IGDVHLRYNLGNTSIRSLPNOLCTLOQLTLDHGHSLCC-LPKETSKLGSNL 603
Db 908 IGDVHLRYNLGNTSIRSLPNOLCTLOQLTLDHGHSLCC-LPKETSKLGSNL 603
OY 604 LDGCVGLTCMPPR-----IGSLTCLKTLRFRV--GIQKSCQGLERLNLVGSIEITHL 657
Db 967 LP-----RSMPAKTKLELDVNLNLSITNSTKGSTYDILLRMKLSLVAVIBGECT-- 1019
OY 658 ERVKNDAKEMANLAKENLHSLSMKMDDEDERPRIYSEKVEYLEALKPSNLTCLTIRG 717
Db 1020 -----FET-----LILSLRELRNLETTSFHD 1040
OY 718 FRGIRLDPMMNHSVLRKNVSEIISCKNCSCLPPFGLPCIKSLETIRGSAEVEYVDSGF 777
Db 1041 FOKVSV--ANHG--GELVLDVFLHLDLTL-----SMHLPR-----P 1073
OY 778 PTRRPRSLKRNIRBGNLKGILKKEGEOCPYLEIEIKCC-----PMEVITLSSVK 832
Db 1074 PDQTRP-----PHAIHWILGCMEMDPMTLEKHLHK 1108
OY 833 KLVSVDKSDAI-----GFSSISNLMALTSQIRYNKEDASLPREMFKSLANLKY 882
Db 1109 SVYLS--SGAFGLGRMVCSKGGFPQ-----LIALKMSYKCE----- 1142
OY 883 LNTSFYRNKELPISLASINLKHLEHSCYALBSLPBGVKGILSLTOLSTYCEMLQ 942
Db 1143 -----LVEMRVEBG--SMPCLRITLTDCKKLG 1169
OY 943 LPEGLOHLYALTNLSVEFCPTLAKR--CEKGI--GEDMYK-IAHI 982
Db 1170 LPDGLKTYTSLKELKIE--RMKREWTERVIGGEDYKVOHIDPV 1210

RESULT 9

T48898

disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48898
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Dangl,
Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evolution
A:Reference number: Z24999; MUID:9930193; PMID:9811794
A:Accession: T48898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-906 <MCD>
A:Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AA63165.1; PID:g3928862
A:Experimental source: Landberg erecta

A:Gene: RPP8
A:Introns: 293/1; 342/1
C:Function:
A:Description: promotes resistance to *Peronospora parasitica*

Query Match 13.1%; Score 671; DB 2; Length 906;
Best Local Similarity 24.9%; Pred. No. 1.3e-30;
Matches 267; Conservative 173; Mismatches 372; Indels 260; Gaps 38;

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Oy 1 MAAEFLQVLNLNFCIGELGLIGFDEFEKQSTFTTQAVLEDAQKQKQKALEN 60
Db 1 MAEAVSGLEGLMDLRSERLQGVDEQIDGLRQQLSLQSLDKDADAKHGSDRYRN 60
Oy 61 WLQKLNAAAYEADIDDECKTEAPRQKK--NKYGCYHPNVYTFRRHKGKMKIMEKLD 118
Db 61 FLEVDKDLVPDAEDIESYVNLKRGEGKGVKHRRRLRLPDLTDHKAASIDEGTKRIS 120
Oy 119 VIAERIKFHL-----DERTIERQVATRGTFVNLNEPOVYGRDKDEIKYKI 165
Db 121 DVGEMQGFQIQIIDGVRSLSLGRQVOREI--RQTYPPDSBEDLVGEGSVKELVGH 178
Oy 166 LNNVSNAGOTLPVLPILGNGGIGKTTLAQWPNDRVLEHHPKVICVSEDFNEKRLIK 225
Db 179 LVEN---DVHQVVSIAQMGGIGKTTLARQVFNHDLVRHFDGFAMVCVSOQFQKHWO 234
Oy 226 EIVSIE--EKSLSGMDLAPLOKKRLDLNGKKYLLVDVWNEPDQKAKLRQYLKVG 283
Db 235 RILQGLQHDHDDIQLMDERYALQKRLFQLEAGKYLVLDDWKKED--WDVIKAVFP-RK 291
Oy 284 SGASVLTTRLEKVG-SINGTLQPYELSNLSQEDCMLFMORAFGHOEINMLT---VA 338
Db 292 RGMKMLTIRNMGVGIHADPTCLTFRASIINPESWKCERLVFPRDETEVLDEMEWA 351
Oy 339 IGKEIVKCGGVPLAKTLGGLRKREERQWENVRDEIKL-----POEBSILPA 391
Db 352 MGKEWVTHCGGLPLAVKVLGGLANKHTVPEWKRVSNDIGQIVGSGCLDINSINSVRI 411
Oy 392 LRLSYHHLPLDLROCFYCAVFPKOTEMEGNLSLMAAHGF-----ILSKNLELEWVG 446
Db 412 LSLSTEDLPHLKRFLFLAHFPEYSKISAYDLFMYAVGEGYDQSTIQDGEVYILELV 471
Oy 447 NE---VWNLVLRSEFFQIEVKSQGYFQMDLIHDLATS-----LFSASTSSNI 494
Db 472 RRLVIADNRVLSHSSKNCQ-----MEDWMEVCLSKAKEENPLQIHKDPTSTSTI 522
Oy 495 -----REIIVENYIHMSIGF--TKV-----VSSYSLHLOKFTVSLRYLN 532
Db 523 NAQSPSRSRRLSIHSGKAFHLLGHKNNTKVRSLIYWDEDFGIRASAVFH--NLTLRLVLD 580
Oy 533 LSDIKLK--OLPSSTIGDLVHLRYNLISGNTSIRSLPNQLCKLQ-----NLQTLDHGCHS 585
Db 581 LYWKFEBGCKLPSSIGSLIHLRYSLF--LAGVSHLPSTMRNKLKLLYLNLSVNNKEPH-- 638
Oy 586 LCCLPKETSKLSLRLNLLDGCYGLTQMPRIIGSTYCTKLTLSRFVWGIQKXSCQGLBELRN 645
Db 639 ---VPNVLAKEMIQRLY-----SLPLKDD-----DKTKLELGDVLVN 671
Oy 646 LN-LYG-----SIEITHLERVKNDMDAKENLSAKENLSLSKMDDDRPRRIYSEK 697
Db 672 LEFLFGFSTQSHSVYDLHMTKLR---YLAVSISERCNPFETLS----- 711
Oy 698 VEVELEAKPHSNLTCTLRGRGIRLPRMNMHSVLANVSIIEISCRNCSGLPRGELPC 757
Db 712 ---SSLELRNLETLVYLFSPBEIFWVDYMGEFVLDHTI----- 747
Oy 758 LKSLLEMGASAVEVYDGSFPTRRRFPRLKRLNIREFGNLKGLKKEGBOCPVLEIEI 817
Db 748 LKEGLAVRMSKI-----PDQQLP-----PHLAQIYI 775
Oy 818 KCCPMFVYPTLSSVKKLVVSGDKSDAIGSSISNLMALTSIQIRNKEDASIPPEMFSL 877
Db 776 CNGRM-----EBD-----PMPILKEL 791

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Oy 878 ANLKYLNISF-VENIKELPISLASINMLKULEHISCALBS-LPEGVKGLISTQLSIT 935
Db 792 LHLKSVKLTFFKAFGRNVCSSKGGFTQCALEISQSELEFWEIIEG--SNPCLRTLTTH 849
Oy 936 YCEMLQCLPEGLQHLTALTNLSVEFCPTLAKRCEGI--GEDWYKIAHPV 985
Db 850 DCEKLELPDLKLYTSLKEIKIGMKREWK--EKLVPGEEDYKQVHPV 899

RESULT 10

745590
hypothetical protein F12A12.50 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 31-Mar-2000
R:Chotane, N.; Robert, C.; Broctier, P.; Winkler, P.; Catcollco, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223008
A:Accession: T45590
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-835 <CHO>
A:Cross-References: EMBL:AL133314
A:Experimental source: cultivar Columbia; BAC clone F12A12
C:Genetics:
A:Map position: 3
A:Note: F12A12.50

Query Match 12.9%; Score 660; DB 2; Length 835;
Best Local Similarity 26.2%; Pred. No. 4.8e-30;
Matches 230; Conservative 175; Mismatches 302; Indels 170; Gaps 35;
C:Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

```

Oy 9 LLDNLTCIGELG-----LILGFDFEKQSTFTTQAVLEDAQKQKQKALEN 60
Db 1 MVDATFEVFGKIGNVYLIEASMPMAVEDLEELTELCTHGYLKQVBAREREDEVSKE 60
Oy 61 WLQKLNAAAYEADIDDECKTEAPRQKKYGCYHPNVYTFRRHKGKMKIMEKLDV- 119
Db 61 WSKVLDPAVYEDVLDTHYHKLREBSQR-----GLRLTKIKGKMDAYSTVDIR 113
Oy 120 IAAERIKFHLDERTIERQVATRGTFVNLNEPOVY-----RDKEDEIV-- 163
Db 114 ILKRI--LD---ITRRETYGIG-GLKEPQGGNTSLRVQLRRARSVDQEVVGL 166
Oy 164 ---KILNVSNAQOTLP--VLPILGNGGIGKTTLAQWPNDRVLEHHPKVICVSED 217
Db 167 EDDAKILLEKLDVEBKRRFLISIFGNGGLKTLARQLVNSRDVKEFEYRAWTYVSOE 226
Oy 218 FNEKRLIKELIESIEKSLGMDLAPLOK-----KLARDLNGKKYLLVDVWNEPDQ 269
Db 227 YKTGDILKRIIRSLGNTS--GEELKIRKFAEELVYLYGLGKKYLVVVDIIV--ER 282
Oy 270 DKWAKLRQVLKVGASGAVLTTRLEKVG-SINGTLQPYELSNLSQEDCMLFMORAFGH 328
Db 283 EAWDSLKRALPCNHGSRVITITRIKAVAGVDGRFAHKRLRFLPEESWELFGQARRN 342
Oy 329 QEEINLNLVAKGKIVKCGVPLAATLGGLIFRKREERQWENVRDEIKLPOEBS-S 387
Db 343 IQRQDEDLKTKGEMVQKCRPLPLCIIVLAGILS-RKTPSPMNVCNS-LWRRLKDSIH 400
Oy 388 ILP-ALRLSYHHLPLDLROCFYCAVFPKOTEMEGNLSLMAAHGFILSGNLEWVG 446
Db 401 VAPVDFDSFKEHLNESHKLCFLYSLIPPEYETLEKLIHLVABGFIQGBEEMMEDEVA 460
Oy 447 NEVNMELYLRSEFFQIEVKSQGY-FQMDLIHDLA-----TSLFS--ASTSSN 493
Db 461 RYVIEELIDSLBAVVRGKQVMSCRHDLRLVLAIKSKELNFVNVYNDHVAQHSST 520
Oy 494 IREIIVENYIHMSIGTKVSSYSLHLOKFTVSLRYNLSDITLQK-----LBSI 545
Db 521 CRREVVHQFQRYSSEKRRKRRMSFLYGFEBHVLGIDFETLKLRLVLDGSLMLPPI 580

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QY 546 -GDLVHLRYLNLNGNT-----SIRSLPNOCKLONL-----OTLDLHGHSCLCPK 591
 Db 581 NMDLHLRLTLDIGDSINDFDLAIATSKIRFLQTLFVSNVYFEEITDLR----- 630
 QY 592 EYSKSGSLNLLDGCYGTCTMPPRIGSLTCKTYSRFV-----VGIQ 634
 Db 631 ---KLTSLHVIAGNFGGILL-----IGDVANLQTLTSLISFDSMNKLPKELLINLRLDGLS 682
 QY 635 KKS-----COLGELRNLYVGLSLEITHL-----PRVNDMDAKKANLSAKEN 676
 Db 683 EMSRKRERAVHVSMASTYLSLRKVLKATPTPEV--HLSESEAVSRMDVISRSL---ES 738
 QY 677 LHSLSMKDDDERPRIPYSEKXVLEALK-PSHNLTCLTIRGFRGIRLPDMNHSV----- 731
 Db 739 VLVGITEEDPMPLQKWPRLLEDLILLSGVNSGKMSVSEQFGRLRLKLDLMSRLDLQ 798
 QY 732 ----LKNVVSLEI-ISCNCSCLPP-----FGEIPLC 757
 Db 799 IEEBAMPULIELEISVSRRKRLIIPNRLRFGQIYC 835

RESULT 11

T04390
 NBS-IRL type resistance protein - barley (fragment)
 C:Species: Hordeum vulgare (barley)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04390
 R:Leister, D.; Kurth, J.; Laurie, D.A.; Yano, M.; Sasaki, T.; Devos, K.; Graner, A.; Sch
 Proc. Natl. Acad. Sci. U.S.A. 95, 370-375, 1998
 A:Title: Rapid reorganization of resistance gene homologues in cereal genomes.
 A:Reference number: 214623; MUID:96081880; PMID:9419382
 A:Accession: T04390
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-389 <LEI>
 A:Cross-references: UNIPROT:O48976; EMBL:AF032683; NID:92792209; PIND:AA86980.1; PID:92
 A:Genetics:

Query Match 12.8%; Score 655.5; DB 2; Length 389;
 Best Local Similarity 39.1%; Pred. No. 3e-30;
 Matches 145; Conservative 81; Mismatches 122; Indels 23; Gaps 12;
 QY 126 KFHLDERTIERQVATROTGFVINEPQYGRDKEDEIVKILINNVAQTLPLVPLILG 185
 Db 4 RYHLRVNRIISNN--ARLTTSVPVEVKMYGRESERDKIIEILIEGSS--DLNVLPVVGIG 59
 QY 186 GLAKTTLAQMVFNDQVLEHHPKIMICVSDPNEKRLIKEIVAST-----EKSLSGMD 240
 Db 60 GVGNTTLARFVCKQORLRDHFLOMWCSTDFNEVRLTYREILHVENROEYENISFN 119
 QY 241 LAPLOKTLRDILNKKYLLVLDVW--NEDQKNAKLQVLKV--ASGAVLTTRLEKVG 298
 Db 120 V--LQKVLKINIRKRLVLDVDMWEDKDMGWLKFLAPLKGNAOSCMILATTRMDSA 177
 QY 299 SIMWTLQPELSTNSQDCMLFMQAFGHQ--EININLVAIGELVKKCGVPLAAKTL 357
 Db 178 KIITQMDKVLISGNEBEFWLLFVCAFGNENYEGEGISGKIYKALKGCPPLAAQSV 237
 QY 358 GGLRFRGEROMEVHVDSIWKLPQESS--ILPALRLSYHHLPLDRQCFYCAVPPK 416
 Db 238 GALLNTSVSKMRAVVDK--WRSLOEDANDILFVLKSTDYPLVHLQHCFSYCSLPPED 295
 QY 417 TEMEKGNLISLMAHGFILSK--NLELENVGNEMVELYLRSFQELVKSQGYTFMM 475
 Db 296 KHFDTGELVHAWVSQNFVQCEDPTVKLEETGQOYLDRVLQCFQK----GSRVY-MHD 350
 QY 476 LIHDLATSLFS 486
 Db 351 LMHBLAGVSS 361

RESULT 12

G96621
 probable disease resistance protein F23H11.10 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: G96621
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huitzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Razzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: G96621
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-906 <STO>
 A:Cross-references: UNIPROT:Q9XIF0; GB:AE005173; NID:95080812; PIND:AAD39321.1; GSPDB:GN
 A:Genetics:

Query Match 12.8%; Score 655; DB 2; Length 906;
 Best Local Similarity 24.7%; Pred. No. 1e-29;
 Matches 265; Conservative 172; Mismatches 354; Indels 282; Gaps 44;
 QY 1 MAEAFLOVLNLTCTFQIAGLILGFKDFEKLQSTFTTQVLDLDAKQKQKDAIEN 60
 Db 6 MVDIVSFGVEKLMKLSQYERFGVEBQITLDRDLKMLAFSLDADAKQKQTRALAN 65
 QY 61 WLOKMAAAVEADDIIDECTEAPIRQKNKYCY--HNVTTFHKGKRMKATME-- 115
 Db 66 CLEIKETIYDADIIIEFLKGSVNM--SLACFGRREIALQITTSISKRSKYIQA 123
 QY 116 ----KLVIAERIKFHLDETRIERQVATROTGFVINEPQYGRDKEDEIVKILINN 170
 Db 124 QNLGITSIDM--DGVSHQ--LEKRLRHTFSSSSNLVLEKNEVKEIVELVGD 178
 QY 171 SNAQTLPLVPLIIGMGLGKTTLAQMVFNDQVLEHHPKIMICVSDPNEKRLIKEIVS 230
 Db 179 SSHG----VSITGGLGKTTLARQIFDHDKVSHPDGLAWCVSQEPTFKDVMWKTILGN 234
 QY 231 IEKSLGMDLA--PLQKTLRDILNKKYLLVLDVWMDQKNAKLQVLKVAGSASV 288
 Db 235 LSPK-YKSDLPREDIQLKFLQLETKKALIVFDDLMK--REDWRIADMPERRAGMRY 291
 QY 289 LTTTRLEKVSIMGTLOPELSTNSQDCMLFMQAFGHQEE-----INLNLVAIGKEI 343
 Db 292 LITSRNDALHPICVFPK--EL--LTHDECKMLQRLAPSKQITTYGILIDKEMVMAKEM 348
 QY 344 VKKCGVPLAAKTLGILFKEEROMEHVDSIWKL-----POESSILPALRLS 395
 Db 349 TRICRKLPLAVKLLGGILDAKHTLRQMKLISENIIISHIVAGTSSNENDSSVNVHLSIS 408
 QY 396 YHHLPLDRQCFYCAVFPKOTEMEKGNLISLMAHGFILSGNE--LENVGQVWNE 452
 Db 409 FEGLEPYLHCLLYLASYPEDHEIERLISYWAABG--ITYPGNVEGATIRVADALYEE 467
 QY 453 LYLRSEF--QELVKSQGYTFMMDL-----IHDLA--- 481
 Db 468 LVKRNWVISERDALSRFEKQQLHLMELGLKAKENPLQIYVDPITSSSVHSLAASR 527
 QY 482 -----TSLFSAT--SSSNIRIIVENYIHMMSIGFTKYVSSYL-SHLQKVSILRV 530
 Db 528 SRRLVYNTSIFSGENDKNSKLRSL-----FLPVGY--SRFSMGSNVRIELPLRLV 577
 QY 531 LNLSDIKL--QLPSSIGDLVHLRYLNLNGNTSIRSLPNOCKLONLQTLDLHGHSCLC 588
 Db 578 LDLDGAKKRGKTLPSISIGKLIHLKYLISL-QASVYIPLSSLRNLSKSLYLYLNLN----- 628

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Qy 589 LPKETSKLGSIRNLILDCGYLCTCPPRIGSLTCLKTLRFVVGIOKKSQCLGELRLN-N 647
Db 629 -----RINS-----GQLINPN 640
Qy 648 LYGSEITHLERVKNMDAKKANLSAKR-NLHSLSMKDDDERPRIYSEKVENLELK 705
Db 641 VF-----KEMELIRYSLPWE----- 656
Qy 706 PHSNLTCLIRGFRGIRLPLDMNHSVLKNVSIETI---SCNKGSCLPFGELPCLKSL 762
Db 657 -RSLTLKLE-----LGNLAKLETILNIPSTK----- 680
Qy 763 LMRGSAVEYVDGFPPTRRRPPSLKLNIREFGNLKGLLKEGEQCVLEIEIKCPM 822
Db 681 -----DSSVTLDRMTKLRITLQILISG-EGHMETLSALSMLGHL-----DL 723
Qy 823 FVITPLTSVK---KLAVSGDKSDAIGFSSISNMLATLSLOIRYKKEASLPEEFKSLA 878
Db 724 TVTSENSVQPKHPLIYRPMIPVQHPPS-----HLTTISLVY---CPLSEDEMPYLE 774
Qy 879 NLKTLN-ISFYENL---KEPLTSLASLNAHLKHLIHSYALSS-LPEEGVKGISLTQLS 933
Db 775 KTLQKLVSLMYNNAVGRMYCTGGFPPLRLRLEIWMGDALBEMIVEGSMPL-LHTLH 832
Qy 934 ITYCEMLQCLPEGLQHLTALTNLSVEFC-PTLAKRCEKIGEDWYKIAHPRV 985
Db 833 IVDCKKLKEIPDGLRPFISSLKELAIRTEKVFQKKVSKG-GEYDYKMGHVLI 884

```

RESULT 13

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T06219
probable cyto nematode resistance gene - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06219
R:Lagudah, B.S.; Mouillet, O.; Appels, R.; Chandramohan, S.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z15543
A:Accession: T06219
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-797 <LNG>
A:Cross-references: UNIPROT:O65113; EMBL:AF052641; NID:G2367836; PIDN:AA05834.1; PID:92
C:Genetic source: cv. AUS 18913
A:Gene: Cre3
A:Map position: 2DL

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Query Match 12.7%; Score 649; DB 2; Length 797;

Best Local Similarity 25.2%; Pred. No. 1.9e-29;

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Matches 245; Conservative 146; Mismatches 309; Indels 272; Gaps 37;
Qy 105 KIGKRMKK-----IMKLDVIAERIKPHLDERTIRQVATROTGFVINEPOVYG 154
Db 5 KLVSLKKEININEAHQILEKLNLS-----ISDNIRHTVMVNPPTTAVSPQKVF 57
Qy 155 RDKKDEIVKTLIN-----NVSNAOTLPVLPIIIMGSLKKTLLAQVVF-----NDQR-- 201
Db 58 RDNORDKTIAMLHKEGGLDPTSGLCFSVYIGHVSGSGSTLTAQCVVAHEKNDKDN 117
Qy 202 VIEHFPKIWIQVSEDFNEKRLIKEIVSIEKSL---GMDLAPLQCKDLNLNGKYL 258
Db 118 KEDHFDLVMMVHVQDFVWVGIPKELVYASADPRVPCQGFNNNINLEBELRKDGKRF 177
Qy 259 LVLDVW-NED--ODKAKLROVLKVGASVLTITRL-----EKVSGIMGTLOPYELS 310
Db 178 LVLDVWGNADVGNQELPKLSPLKKGKSGKILVITTSKYALPDLCPGVYVYAMP--IT 235
Qy 311 NLSGEDCMLLMQARF--GHOEINLNLVAIGKEIVKCGVAPLAAKTLIGLARKREER 368
Db 236 EVDDTAFELFMHVALEGDQDSMFQN--IGVELAKLKSPSLAARTVGNLRQDQVD 292
Qy 369 QMEHVRSB---IWLQPESSILPALRLSYHNLPLDLQCFYCAVPKDTMEKGNLI 425

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Db 293 HMRVQDULPKVWTGP-----LWMSYQGEQARRCFAVCSIFPRHRLYRDELV 343
Qy 426 SLMAHGFILSKG-NLELVENGVNMLYLRSPFO---EIEVSGQTYFKMHLIDHLLA 481
Db 344 RLMABEGRITBDGADHEDVGLGIPNELLSISFLQPEGQVMYHNGKYYLVHDLVYLA 403
Qy 482 -----TSLFS-----ASTSSNIREIYENV-----IHMM--S 507
Db 404 GAVAGTQCFRINDNMIOKESMAQDVPDVHRLFVQSYDALITGKILVLENLTLVYS 463
Qy 508 IGFTRVSSVSLHQLQFV-SLRVLNLS-----DYLKQLPSPISGLVHLRYNL 556
Db 464 VGGDTVVEEIVIKNILSLPLRVLATLALCLEKQGFICRPNLSVPSISQLKRLRYLAF 523
Qy 557 SGNRSIR-SLPNOCIKONLOTLDLHGCHSLCCLPKETSKLGSIRNLILDCGYLTGMP 615
Db 524 RTDIECRVILPSSLNOLYOMOLDFGVCANL-----VFSCGDLIN-LRHVCSGFGLOPS 576
Qy 616 RIGSLTCLKTLRFVVGIOKKSQCLGELRLN-LYGSIEITHLERVKNMDAKKANLSAK 674
Db 577 NIGRLVSLQITPAFKVS-HEQGHEAKQRLYNRLSGELSIYGLQSVESREBALAFDLAK 635
Qy 675 ENHLSMKWDDEPRPRIYSEKVEVLEALKPHSNLTCLTTRGFRGIRLPLDMNHSVLKN 734
Db 636 KRLAELTSLFSGS-----SEVAEVLGCLPVGVLVTLDRDYDGLVYPRKM----- 682
Qy 735 VVSIEIISCKNCSCLPPRGELPCLKSLLEMRGSAVEYVDGFPPTRRRPSLRKLNIREF 794
Db 683 -----V 683
Qy 795 GNGLKLLKEGEEOCPVLEIEIKCPMFVITLSVVKLVVSGDKSDAIGFSSISNMLA 854
Db 684 GRONGAEK-----LQQLDSGWSQSG----- 705
Qy 855 LTSIQIRYNKEDASLPBEMFGLANLKYLNISFYFNKLEPLTSLASLNAHLKHLIHSCTA 914
Db 706 -----PAPALKAFFNHLCLNL-MHCSMNALPCNNHLSLESTVYIIKCLN 749
Qy 915 LESLPEBVGKLSLTQLSITYCMLQCLPEGLQHLTALTNLSVEFCPTLAKRCEKIGE 974
Db 750 IRLSP-----TLPO-SLTYFWLKC-DUGF-----WESCOTVGH-----P 782
Qy 975 DWYKIAHPRVF 986
Db 783 NMKTIQHICRKY 794

```

RESULT 14

Resistance protein Rpp13 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000

C:Accession: T51185

R:Blitner-Bddy, P.D.; Crute, I.R.; Holub, E.B.; Beynon, J.L.

Plant J. 21, 177-188, 2000

A:Title: Rpp13 is a simple locus in Arabidopsis thaliana for alleles that specify downy n

A:Reference number: Z25333

A:Accession: T51185

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-831 <BIT>

A:Cross-references: EMBL:AF09731; PIDN:AAF42831.1

A:Experimental source: cultivar Rld

C:Genetic source: Rpp13

A:Gene: Rpp13

A:Map position: 3

C:Superfamily: disease resistance protein Rps2; leucine-rich alpha-2-glycoprotein repeat

Query Match 12.4%; Score 635.5; DB 2; Length 831;

Best Local Similarity 26.6%; Pred. No. 1.2e-28;

Matches 239; Conservative 173; Mismatches 335; Indels 153; Gaps 38;

Db 832 DGATKMI 839

Search completed: April 16, 2005, 01:23:21
Job time : 62 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 16, 2005, 01:11:09 ; Search time 188 Seconds

(without alignments)
2691.140 Million cell updates/sec

Title: US-10-647-268-2

Perfect score: 5127
Sequence: 1 MAEAFQVLNDNLTCFIQGE.....EKIGEDMYKXIHPRVFIY 988

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: 1: UniProt_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3766.5	73.5	970	1	RGAA2_SOLBU
2	3753	73.2	1025	1	RGAA1_SOLBU
3	3745	73.0	948	2	OGTA7
4	3687.5	71.9	947	2	OGTA7
5	3669	71.6	948	2	OGTA7
6	3587	70.0	988	1	RGAA3_SOLBU
7	3483.5	67.9	947	1	RGAA3_SOLBU
8	1517	29.6	1110	2	OG4J69
9	1516	29.6	1222	2	OG4J69
10	1479.5	28.9	1035	2	OG4XG0
11	1479	28.8	1024	2	OG4XG0
12	1477.5	28.8	1108	2	OG4XG0
13	1464.5	28.6	1259	2	OG4XG0
14	1463.5	28.5	1259	2	OG4XG0
15	1436	28.0	1048	2	OG4XG0
16	1414	27.6	1081	2	OG4XG0
17	1395	27.2	1124	2	OG4XG0
18	1385	27.0	1124	2	OG4XG0
19	1381	26.9	1129	2	OG4XG0
20	1367.5	26.7	1189	2	OG4XG0
21	1366	26.6	1217	2	OG4XG0
22	1362	26.6	1217	2	OG4XG0
23	1359.5	26.4	1133	2	OG4XG0
24	1355.5	26.4	1210	2	OG4XG0
25	1350.5	26.3	1124	2	OG4XG0
26	1346.5	26.3	1292	2	OG4XG0
27	1331.5	26.0	1066	2	OG4XG0
28	1312.5	25.6	1274	2	OG4XG0
29	1307	25.5	1261	2	OG4XG0
30	1307	25.5	1322	2	OG4XG0
31	1299	25.3	1105	2	OG4XG0

32	1288.5	25.1	1054	1	R131_ARATH
33	1287	25.1	1118	2	OG3V16
34	1284.5	25.1	1211	2	OG8ZF0
35	1277.5	24.9	1315	2	OG8ZD0
36	1251	24.4	1406	2	OG13G4
37	1244	24.3	1266	2	OGXET3
38	1243	24.2	1312	2	OG8ZD5
39	1240	24.2	1240	2	OG4016
40	1234	24.1	1279	2	OG6A87
41	1221.5	23.8	1073	2	OG6A36
42	1212	23.6	1220	2	OG4015
43	1211.5	23.6	1297	2	OG4556
44	1211	23.6	1286	2	OG9A83
45	1197	23.3	1284	2	OG13K6

ALIGNMENTS

RESULT 1	RGAA2_SOLBU	STANDARD	PRT:	970 AA.
ID	RGAA2_SOLBU	STANDARD	PRT:	970 AA.
AC	OGXG09; OGXA18; OGXA41;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Disease resistance protein RGA2 (RGA2-b1b) (Blight resistance protein RPI)			
GN	Name=RGAA2; Synonyms=177013.40, CB3A14.5, RB, RPI-BLB1;			
OS	Solanum bulbocastanum (Wild potato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	lamiales; Solanales; Solanaceae; Solanum.			
CC	NCBI_TaxID=147425;			
CC	[1]			
CC	SEQUENCE FROM N.A. AND VARIANTS.			
CC	PubMed=12872003; DOI=10.1073/pnas.1533501100;			
CC	Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,			
CC	Haberlach G.T., Liu J., Kuang H., Austen-Phillips S., Buell C.R.,			
CC	"Gene RB cloned from Solanum bulbocastanum confers broad spectrum			
CC	resistance to potato late blight."			
CC	Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).			
CC	[2]			
CC	SEQUENCE FROM N.A.			
CC	PubMed=14675451;			
CC	Van Der Vossen E., Sikkema A., Heekert B. B.L., Grog J., Stevens P.,			
CC	Mukens M., Wouters D., Pereira A., Sikkema W., Alfefs S.;			
CC	"An ancient R gene from the wild potato species Solanum bulbocastanum			
CC	confers broad-spectrum resistance to Phytophthora infestans in			
CC	cultivated potato and tomato."			
CC	Plant J. 36:867-882(2003).			
CC	-1- FUNCTION: Disease resistance protein. Resistance proteins guard			
CC	the plant against pathogens that contain an appropriate avirulence			
CC	protein via a direct or indirect interaction with this avirulence			
CC	protein. That triggers a defense system which restricts the			
CC	pathogen growth. Confers a broad resistance to all known races of			
CC	P. infestans.			
CC	-1- INDUCTION: Constitutively expressed.			
CC	-1- BIOTECNOLOGY: Can be introduced into cultivated potato			
CC	(S. tuberosum) or tomato (L. esculentum) to transfer a broad-			
CC	spectrum late blight resistance to cultivated Solanaceae from			
CC	sexually incompatible host species.			
CC	-1- MISCELLANEOUS: Belongs to a four-gene family located at the same			
CC	locus. Although the four genes are expressed in the resistant			
CC	haplotype, only RGA2 confers the resistance to P. infestans. In the			
CC	susceptible haplotype, RGA1 and RGA3 are likely to be pseudogenes			
CC	created by deletions and mutations, while RGA2 contains also			
CC	several modifications.			
CC	-1- SIMILARITY: Belongs to the disease resistance NB-LRR family.			
CC	-1- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.			
CC	-1- CAUTION: Ref.1 (AAP45164) sequence differs from that shown due to			

```

CC      an internal deletion of the corresponding genomic clone.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY336128; AAP6601.1; -
DR      EMBL; AY303170; AAP45164.1; -
DR      EMBL; AY303171; AAP45188.1; -
DR      EMBL; AY426259; AAP29069.1; -
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR002182; NB-ARC.
DR      Pfam; PF00560; LRR; 10.
KW      ATP-binding; Leucine-rich repeat; Plant defense; Repeat.
FT      NP_BIND 182 189      ATP (Potential).
FT      DOMAIN 135 438      NB-ARC.
FT      REPEAT 525 548      LRR 1.
FT      REPEAT 550 571      LRR 2.
FT      REPEAT 573 594      LRR 3.
FT      REPEAT 595 619      LRR 4.
FT      REPEAT 638 662      LRR 5.
FT      REPEAT 672 697      LRR 6.
FT      REPEAT 752 777      LRR 7.
FT      REPEAT 787 811      LRR 8.
FT      REPEAT 813 832      LRR 9.
FT      REPEAT 833 857      LRR 10.
FT      REPEAT 859 882      LRR 11.
FT      REPEAT 884 906      LRR 12.
FT      REPEAT 907 931      LRR 13.
FT      REPEAT 946 970      LRR 14.
FT      VARIANT 22 22      V -> A (in susceptible haplotype).
FT      VARIANT 449 540      Missing (in susceptible haplotype).
FT      VARIANT 889 894      Missing (in susceptible haplotype).
SQ      SEQUENCE 970 AA; 110346 MW; 3727029C3CAD9C47 CRC64;

Query Match 73.5%; Score 3766.5; DB 1; Length 970;
Best Local Similarity 75.6%; Pred. No. 2.1e-205;
Matches 753; Conservative 76; Mismatches 130; Indels 35; Gaps 8;

QY      1 MAEFLDYLDNLTCTFQSGELILGKDEPEKQSTFTTQAVLEDAOKKOLKDKALIN 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 MAEFLDYLDNLTCTFQSGELILGKDEPEKQSTFTTQAVLEDAOKKOLKDKALIN 60
QY      61 WLOKLNAAAEADDIIDECKTEAPIRQKKNKYGCGYHPNVITFRHKGKMKIMEKLDVI 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 WLOKLNAAAEADDIIDECKTEAPIRQKKNKYGCGYHPNVITFRHKGKMKIMEKLDVI 120
QY      121 AAEIRKTHDERTIERQVATROTGTGVINEPQVYGRDKKEIKVILINNVSNAGTLFVLP 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      121 AAEIRKTHDERTIERQVATROTGTGVINEPQVYGRDKKEIKVILINNVSNAGTLFVLP 180
QY      181 ILGMSGGKTKTLQAMVNDQVRIEHPKWTICVSEPNKRLIKELIVESIEEKS-LGSM 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      181 ILGMSGGKTKTLQAMVNDQVRIEHPKWTICVSEPNKRLIKELIVESIEEKS-LGSM 239
QY      240 DLAPLQKRLDLNGKCYLLVLDVNMEDDKMAKLRQVLKVGASGASVLTTRLEKVG 299
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      240 DLAPLQKRLDLNGKCYLLVLDVNMEDDKMAKLRQVLKVGASGASVLTTRLEKVG 299
QY      300 IMGTLOPELSTNSQEDCWLIFMORAFGHOEINLNLVAIGELVKKCGVPLAKTLGG 359
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      300 IMGTLOPELSTNSQEDCWLIFMORAFGHOEINLNLVAIGELVKKCGVPLAKTLGG 359
QY      360 ILAFKREERQWERVRDSEIKVLQSESSILPALRLSTHHPDLRQCFYCAVPPKTEM 419
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      360 ILAFKREERQWERVRDSEIKVLQSESSILPALRLSTHHPDLRQCFYCAVPPKTEM 419
QY      420 EKGNLISLMAHGFILSKNGLLENVNGEWNELYLTSFQETIEVKSQGYTFPKMHLID 479
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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DB      420 EKGNLISLMAHGFILSKNGLLENVNGEWNELYLTSFQETIEVKSQGYTFPKMHLID 479
QY      480 LATSLSFASTSSSSNIREIIVENTYIMMSIGFTKVSSYSLSHLOKPVSLRYNLSDIKLK 539
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      480 LATSLSFASTSSSSNIREIIVENTYIMMSIGFTKVSSYSLSHLOKPVSLRYNLSDIKLK 539
QY      540 QLPESIDVHLRLNLSGNTSIRSLPNQICLONLOTLDLHGHSLLCCPKETSKGSL 599
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      540 QLPESIDVHLRLNLSGNTSIRSLPNQICLONLOTLDLHGHSLLCCPKETSKGSL 599
QY      600 RNLLDSCGYLTCMPPIGSLTCLKTSLRFVYGIQKSCQUGELRNINLVGSEITLER 659
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      600 RNLLDSCGYLTCMPPIGSLTCLKTSLRFVYGIQKSCQUGELRNINLVGSEITLER 659
QY      658 VKNDKDAKEANLSAKGNLHLSLSMSW--NFGPHIYESSEVKVLEALKPHSNLTSIKYGFR 716
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      658 VKNDKDAKEANLSAKGNLHLSLSMSW--NFGPHIYESSEVKVLEALKPHSNLTSIKYGFR 716
QY      720 GIRLPDMANHSVYLNKVISIEISCNCSCLPFGELPLCKSLRLMRSAAVEEYVD 774
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      720 GIRLPDMANHSVYLNKVISIEISCNCSCLPFGELPLCKSLRLMRSAAVEEYVD 774
QY      775 --SGFPTRRRPPSLRKLNIREFGNLKGLKKEGBQCPVLEIEIKCCPMFVITLSVVK 832
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      775 --SGFPTRRRPPSLRKLNIREFGNLKGLKKEGBQCPVLEIEIKCCPMFVITLSVVK 832
QY      777 VHSGFPTRRIRPPSLRKLDIWDPSGLKGLKKEGBQCPVLEIEIKCCPMFVITLSVVK 830
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      777 VHSGFPTRRIRPPSLRKLDIWDPSGLKGLKKEGBQCPVLEIEIKCCPMFVITLSVVK 830
QY      833 KLVVSGDKSDAIGFSSISNLMALTSQIRYNKEDASIPREMPKSLANTKYLISFYENLK 892
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      833 KLVVSGDKSDAIGFSSISNLMALTSQIRYNKEDASIPREMPKSLANTKYLISFYENLK 892
QY      893 ELPTSLASLNAKHLIEHSCYALESLPEBGVKGLISTQISTYCEWLOCLPEGLQHTA 952
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      893 ELPTSLASLNAKHLIEHSCYALESLPEBGVKGLISTQISTYCEWLOCLPEGLQHTA 952
QY      953 LTNLSVFCPTLAKRCCEKIGEDMYKIAHPRFYIY 988
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      953 LTNLSVFCPTLAKRCCEKIGEDMYKIAHPRFYIY 988
QY      934 LTSIKRIGCCQQLIKRCEKIGEDMHKISHIPNNIY 969
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      934 LTSIKRIGCCQQLIKRCEKIGEDMHKISHIPNNIY 969

RESULT 2
RGAL SOLBU STANDARD; PRT; 1025 AA.
ID RGAL SOLBU
AC 07XA42; 07XA21;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative disease resistance protein RGAL (RGAs-b1b).
GN Name=RGAL; Synonyms=17013.37, CB3A14.4;
OS Solanum bulbocastanum (Wild potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=147425;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX PubMed=12872003; DOI=10.1073/pnas.1533501100;
RA Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
RA Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
RA Helgeson J.P., Jiang J.;
RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
RT resistance to potato late blight."
RL Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van Der Vossen E., Sikkema A., Hekkert Bc B.L., Groe J., Stevens P.,
RA Muskens M., Wouters D., Pereira A., Sikkema W., Allefs S.;
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RT cultivated potato and tomato."
RL Plant J. 36:867-882 (2003).
CC -!- FUNCTION: Disease resistance protein. Resistance proteins guard

```

CC	the plant against pathogens that contain an appropriate avirulence
CC	protein via a direct or indirect interaction with this avirulence
CC	protein. That triggers a defense system which restricts the
CC	pathogen growth.
CC	-1- INDUCTION: Constitutively expressed.
CC	-1- MISCELLANEOUS: Belongs to a four-gene family located at the same
CC	locus. Although the four genes are expressed in the resistant
CC	haplotype, only RGA2 confers the resistance to P.intestans. In the
CC	susceptible haplotype, RGA1 and RGA3 are likely to be pseudogenes
CC	created by deletions and mutations, while RGA2 contains also
CC	several modifications.
CC	-1- SIMILARITY: Belongs to the disease resistance NB-LRR family.
CC	-1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC	-1- SIMILARITY: Contains 1 NB-ARC domain.
CC	-----
CC	EMBL; AY303170; AAP4S163.1; -
DR	EMBL; AY303171; AAP4S165.1; -
DR	EMBL; AY426261; AAR29071.1; -
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR002182; NB-ARC.
DR	Pfam; PF00560; LRR; 9.
DR	Pfam; PF00931; NB-ARC; 1.
KW	ATP-binding; Leucine-rich repeat; Plant defense; Repeat.
FT	DOMAIN 181 483 NB-ARC.
FT	NP BIND 228 235 ATP (Potential).
FT	REPEAT 570 593 LRR 1.
FT	REPEAT 595 616 LRR 2.
FT	REPEAT 617 640 LRR 3.
FT	REPEAT 641 665 LRR 4.
FT	REPEAT 683 707 LRR 5.
FT	REPEAT 794 819 LRR 6.
FT	REPEAT 869 887 LRR 7.
FT	REPEAT 888 912 LRR 8.
FT	REPEAT 914 936 LRR 9.
FT	REPEAT 937 961 LRR 10.
FT	REPEAT 963 985 LRR 11.
FT	REPEAT 986 1011 LRR 12.
FT	VARIANT 88 88 Q -> L (in susceptible haplotype).
FT	VARIANT 195 195 P -> S (in susceptible haplotype).
FT	VARIANT 212 212 I -> T (in susceptible haplotype).
FT	VARIANT 605 605 F -> V (in susceptible haplotype).
FT	VARIANT 609 609 N -> S (in susceptible haplotype).
FT	VARIANT 612 612 K -> R (in susceptible haplotype).
FT	VARIANT 639 681 SKGLSRMLLDGCSLTSTPRIGLITCKSLSCVIGRRK
FT	GH -> ISKLCLYQWEKRY (in susceptible
FT	haplotype).
FT	R -> L (in susceptible haplotype).
FT	R -> E (in susceptible haplotype).
FT	Missing (in susceptible haplotype).
FT	A -> S (in susceptible haplotype).
FT	K -> N (in Ref. 2 and susceptible
FT	haplotype).
FT	Missing (in Ref. 2 and susceptible
FT	haplotype).
FT	TA -> NV (in Ref. 2).
FT	I -> V (in Ref. 2 and susceptible
FT	haplotype).
FT	N -> D (in Ref. 2).
FT	M -> V (in Ref. 2 and susceptible
FT	haplotype).
FT	K -> R (in Ref. 2).
FT	H -> Y (in Ref. 2).
FT	T -> S (in Ref. 2).
FT	M -> K (in Ref. 2).
FT	V -> A (in Ref. 2 and susceptible
FT	haplotype).
FT	CONFLICT 264 264
FT	CONFLICT 259 259
FT	CONFLICT 382 382
FT	CONFLICT 616 616
FT	CONFLICT 681 681
FT	CONFLICT 707 707
FT	CONFLICT 841 841
FT	CONFLICT 876 876

FT	CONFLICT	898	898	haplotype	haplotype	
FT	CONFLICT	898	898	D -> N (in Ref. 2 and susceptible haplotype)		
FT	CONFLICT	920	920	K -> N (in Ref. 2 and susceptible haplotype)		
FT	CONFLICT	949	949	D -> N (in Ref. 2)		
FT	SEQUENCE	1025 AA; 116529 MW; B2600A4C34B9C1C6 CRC64;				
Query Match 73.2%; Score 3753; DB 1; Length 1025;						
Best Local Similarity 73.4%; Pred. No. 1.3e-204;						
Matches 760; Conservative 77; Mismatches 140; Indels 58; Gaps 9						
QY		1	MAEAFLVLLNLTCTFOIGELGLIGFDFEEKLGSTFTTQAVLADAKKOLDKDAIEN	60		
DB		1	MAEAFLVLLNLTCTFOIGELGLIGFDFEEKLGSTFTTQAVLADAKKOLDKDAIEN	60		
QY		61	WLQKNAAYEADDLIDCKTEAPIRQKNKCYCHPNVITFRHKIGKMKIMKLDVY	120		
DB		61	WLQKNAAYEADDLIDCKTEAPIRQKNKCYCHPNVITFRHKIGKMKIMKLDVY	120		
QY		121	AAERIKPHLDEETIERQVATROT	143		
DB		120	ABERKKFLQEKTIERQATRETQVSMFSTCSSHPYLFIVQNPSPYVFLPTPEKECUN	179		
QY		144	-----GFLNFPQVYGRDKDELYKLLINNVSNQTLPLYPILOMGIGKTTLQ	194		
DB		180	ILIWTLAPGSVLTPEQVGRDKDELYKLLINNVSNQTLPLYPILOMGIGKTTLQ	239		
QY		195	MYFNQRYIEHHPKIMVCSDFENFKRIKEIVSEIEKSLGDMPLAPLOKLRDLNG	254		
DB		240	MYFNQRYTERPYKIMVCSDFENFKRIKAIYESIEKSLGDMPLAPLOKLRDLNG	259		
QY		255	KKYLVLVDDVNNEDDKAKLRQVLKVGASGAVLTTLTLEKVGSLMGTLQPYELSNLSQ	314		
DB		300	KRYFLVLDVNNEDDKKAVNLAVLVKGASGAVLTTLTLEKVGSLMGTLQPYELSNLSQ	359		
QY		315	EDCMLLPQARAFGHOEINLNLVAIGKEIVKCGGYPLAKTLGGLRFRERQENHR	374		
DB		360	EDCMLLPQARAFGHOEINLNLVAIGKEIVKCGGYPLAKTLGGLRFRERQENHR	419		
QY		375	DSEIMKLEPOESSILPALRLSYHNLPLDIRQCFYCAVPPKOTAKENLILAMMAHGL	434		
DB		420	DSPINLPODESSILPALRLSYHNLPLDIRQCFYCAVPPKOTAKENLILAMMAHGL	479		
QY		435	LSKGNLELVNGVENVNELYLRSFOEIEVKSQGYFKKHDLIHDLATSLFSASTSSNI	494		
DB		480	LSKGNLELVNGVENVNELYLRSFOEIEVKSQGYFKKHDLIHDLATSLFSASTSSNI	539		
QY		495	REIIVENTYIHMSIGFTKYVSSYSLSHLOKFLSKVLNLSDKLQDPSISGLVHLRYL	554		
DB		540	REIINAYGVYMSIGFAEVSSYSLSLQKFVSLRYLNLNRSNLNDLPSSIGLVHLRYL	599		
QY		555	NLSGNTSIRSLPNOICLQNLQTLHLGHSHCCLPKETSXJGSLANLLLDGCGYTCMP	614		
DB		600	NLSGNTSIRSLPNOICLQNLQTLHLGHSHCCLPKETSXJGSLANLLLDGCGYTCMP	658		
QY		615	PRIGSLTCLKTSRFFVVGIOKSCCOLGELRLNLVGSIEITHLERYXNDMDAKEANLSAK	674		
DB		659	PRIGSLTCLKTSRFFVVGIOKSCCOLGELRLNLVGSIEITHLERYXNDMDAKEANLSAK	717		
QY		675	ENLHLSLMSKMDDEPRPIYESKEVEYVLEALKPHSNLTCTLTIRGFRGRLPDMNNHLYLN	734		
DB		718	ANLHLSLMSKMDDEPRPIYESKEVEYVLEALKPHSNLTCTLTIRGFRGRLPDMNNHLYLN	773		
QY		735	VVSIETIICCKNCSCLPFGELPCLKSLLEMRSAVEYV--DSGFPTRRRPSPSLRKNIIR	792		
DB		774	VVSIIRIRGENCSCLPFGELPCLKSLLEMRSAVEYV--GRPSPSLRKNIIR	831		
QY		794	FGNLKGLLKEEEOCPVLEIEIKCCPFFVPLTSSVYKLVVSGDKSDAIGFSSISNLM	853		
DB		832	FSNLKGLLKEEEOCPVLEIEIKCCPFFVPLTSSVYKLVVSGDKSDAIGFSSISNLM	889		
QY		854	ALTSIQIRYNKEDASLPBEMFSLANLKYLNISFFNLKELPTSLASLANLRLLEHSCY	913		

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Db      890 ALTSIDISDNVATSPSEEMFKSLANLKYKISFENLKEPLTSLASNALSLKPEFD 949
QY      914 ALESIPESGVKLLISTOUSTYCEMLQCLPBGLOHLYTLTSLVEFCCTLAKCEKGIG 973
Db      950 ALESIPESGVKLLISTELTSLSVSNCMWLKCLPBGLOHLYTLTTLTQCPYKCEKGIG 1009
QY      974 EDWYKIAHIPRVFIY 988
Db      1010 EDMHKIAHIPVLTLY 1024

RESULT 3
Q6TAF7  PRELIMINARY;  PRT;  948 AA.
AC      Q6TAF7;
DT      05-JUL-2004 (TREMblrel. 27, Created)
DT      05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE      Blight resistance protein 1118 (Fragment).
OS      Solanum tajiense.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      lamids; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxId=257458;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=14675451;
RA      Van Der Vossen E., Sikkema A., Hekkert B.T., Gros J., Stevens P.,
RA      Muskens M., Mouters D., Pereira A., Stiekema W., Allefs S.,
RT      "An ancient R gene from the wild potato species Solanum bulbocastanum
RT      confers broad-spectrum resistance to Phytophthora infestans in
RT      cultivated potato and tomato."
RT      Plant J. 36:867-882(2003).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RA      EMBL; AY426266; AAR29076.1;
RA      GO; GO:0005524; F:ATP binding; IEA.
RA      GO; GO:0006915; P:apoptosis; IEA.
RA      GO; GO:0048229; P:defense response to pathogen; IEA.
RA      InterPro; IPR000767; Disease_resist.
RA      InterPro; IPR006209; EGF_like.
RA      InterPro; IPR001611; LRR.
RA      InterPro; IPR002182; NB-ARC.
RA      InterPro; IPR003058; wing_hlx_DNA_bnd.
RA      Pfam; PF00560; LRR_1; 9.
RA      Pfam; PF00931; NB-ARC; 1.
RA      PRINTS; PR00364; DISEASERIST.
RA      PROSITE; PS01186; EGF_2; UNKNOWN_1.
FT      NON_TER 948
SQ      SEQUENCE 948 AA; 108444 MW; 09E14450231751D5 CRC64;

Query Match      73.0%; Score 3745; DB 2; Length 948;
Best Local Similarity 76.0%; Pred. No. 3.4e-204;
Matches 741; Conservative 84; Mismatches 116; Indels 34; Gaps 6;
QY      1 MAEAFLOVLLDNLTCTFQGEIGLILGFKDEFEKLQSTFTTIOAVLEADOKKOLDKAIEN 60
Db      1 MAEAFLOVLLDNLTCTFQGEIGLILGFKDEFEKLQSTFTTIOAVLEADOKKOLDKAIEN 60
QY      61 WLOKLNAAAYEADLDDECTEAPIRKKNKYGCYHPNVITPRHKGKMKIMKLDVT 120
Db      61 WLOKLNAAAYEADLDDECTEAPIRKKNKYGCYHPNVITPRHKGKMKIMKLDVT 120
QY      61 WLOKLNAAAYKVDLDLECKA---ARLEQRLGHHPKAIWFRHKIGKRILEMMEKLDAL 117
Db      61 WLOKLNAAAYKVDLDLECKA---ARLEQRLGHHPKAIWFRHKIGKRILEMMEKLDAL 117
QY      121 AAEIRKPHLBERTEROVATRONGFVINEPOYGRDKEKDEIKILLINNSMAGTLPLVP 180
Db      121 AAEIRKPHLBERTEROVATRONGFVINEPOYGRDKEKDEIKILLINNSMAGTLPLVP 180
QY      118 AKERTDFHLEKTIEROVAREPTEPVLTPEOVYGRDKEDEIVKILLINNSMAGTLPLVP 177
Db      118 AKERTDFHLEKTIEROVAREPTEPVLTPEOVYGRDKEDEIVKILLINNSMAGTLPLVP 177
QY      181 ILGNGGIGKTTLLAQMVENDQVLEHFPKIMICVSEDFNFKRIKILKIVESIEKSGMD 240
Db      178 ILGNGGIGKTTLLAQMVENDQVLEHFPKIMICVSDPDFDKRIKILKIVESIEKSGMD 237

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QY      241 LAPLOKRLDLNKKYLLVLDVWNEODKALROVLYKVGASGVLTTRILEKYSI 300
Db      238 LASFOKRLQOLNKKRYLLVLDVWNEODKALROVLYKVGASGVLTTRILEKYSI 297
QY      301 MGLTQPYELNSQEDCMLLFMQRAFQHOEININLVAIGKEIYKKGQVPLAKTGGI 360
Db      298 MGLTQPYQLSQDDCMLLFQRAVHQEISNLVAIGKEIYKKGQVPLAKTGGI 357
QY      361 LRFREERQWEHVVDSEIWKLPQESSILPALRISYHLLPDLNQCCTYCAVFPKOTEME 420
Db      358 LRFREERQWEHVVDSEIWKLPQESSILPALRISYHLLPDLNQCCTYCAVFPKOTEME 417
QY      421 KGNLISLMAGFLSKGNLEENYGNVWNELYLRSFPOEIEKSGQTFKXMDLJHDL 480
Db      418 KKVYISLMAGFLSKGNLEENYGNVWNELYLRSFPOEIEKSGQTFKXMDLJHDL 477
QY      481 ATSLFSASTSSNIREIYENYIH-MMSIGFTKVSSYSLSHQKPVSLRVLNLSIDIKL 539
Db      478 ATSLFSAANTSSNIREIYENYIHMMSIGFSEVSSYSLSHQKPVSLRVLNLSYSKFE 537
QY      540 QLPESIDVHAKRYLNSGTSIRSLPNOJCKLQNLQTLDLHGCHSLCCLPKETSKLGS 599
Db      538 ELPSISDLVHLRYMDLSNNIEIRSLPKQCLQNTQTLQYCTRLCCLPKQTSKLGSL 597
QY      600 RNLLDGCYGLTQMPPIRIGSLTCLKTLRSFVVGIOKKSQOLGELRNMLNLSIEITHLER 659
Db      598 RNLLHGHCHLTLTPRIGSLTCLKTLGQFYVA-RKKGYQLGELGSLNLSYKISHLER 656
QY      660 VKNDMAKEANLAKENLHSLMKWDDEPRRIYESKRYEVLBALRPHSNLTCLTTRGFR 719
Db      657 VKNDKEAKEANLAKENLHSLMKWDDEPRPHRYESEVYVLEALRPHSNLTCLTISGRF 716
QY      720 GIRLPMNHSVLYKNVSTIEIISCKNCSCLPPGELPCLKSLMLMGSAE-----VEYV 773
Db      717 GIRLPMNHSVLYKNVSTIEIISCKNCSCLPPGELPCLKSLMLMGSAE-----VEYV 776
QY      774 DSGFTFRRRPRLKINIREFNGILKGLKKEGEGQCPVLEIEIRKCPMFWIPTLSVKK 833
Db      777 DSGFTFRIRPRLKICICFKFDLKGIVKGEQGPVLEEMIRCP---ITLS----- 829
QY      834 LVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPSEMFKSLANLYKINISFYNLKE 893
Db      830 -----SNLKALTSINISDNKEATSPSEEMFKSLANLYKINISHFYNLKE 873
QY      894 LPTSLASINALKHLEHSCVALESLEPBGYKGLISTOUSTYCEMLQCLPBGLOHLYTL 933
Db      874 LPTSLASINALKSLKIQWCCALSIPEBGKGLSTLTLVFCNMLKCLPBGLOHLYTL 933
QY      954 TNLSEFCPTLAKRC 968
Db      934 TRVKGCCPOLIKRC 948

RESULT 4
Q6TAF8  PRELIMINARY;  PRT;  947 AA.
AC      Q6TAF8;
DT      05-JUL-2004 (TREMblrel. 27, Created)
DT      05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE      Blight resistance protein SH20 (Fragment).
OS      Solanum tuberosum (Potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      lamids; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxId=4113;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=14675451;
RA      Van Der Vossen E., Sikkema A., Hekkert B.T., Gros J., Stevens P.,
RA      Muskens M., Mouters D., Pereira A., Stiekema W., Allefs S.,
RT      "An ancient R gene from the wild potato species Solanum bulbocastanum

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RT confers broad-spectrum resistance to Phytophthora infestans in
RL cultivated potato and tomato."
RL Plant J. 36:867-882(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA van der Vossen E., Allefs S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426265; AAR29075.1; -
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 9.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
DR PROSITE; PS01186; BGF_2; UNKNOWN_1.
DR NON TER 947 947
SQ SEQUENCE 947 AA; 108156 MW; ED8B31B5044339EB CRC64;

Query Match 71.9%; Score 3687.5; DB 2; Length 947;
Best Local Similarity 75.4%; Pred. No. 6.3e-201;
Matches 734; Conservative 83; Mismatches 124; Indels 33; Gaps 7;

QY 1 MAEAFLOVLDNLCTFQEGELIGFDEBEKQSTFTTIOAVLEDAOKKQKDAIEN 60
DB 1 MAEAFIOVLENTITSFQEGELIGFDEBEKSTSRSTIOAVLEDAOKKQKDAIEN 60
QY 61 WLQQLNAAVEADILDCEKTEAPIROKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 120
DB 61 WLQQLNAAVYVVDLLDECKA---ARLEQSLGCHHPRAIYFRHKIGKRIEMMEKDAI 117
QY 121 AAEIRKTHLDEBTEROVATQGTGVLNEPOVYGKDEKDEIVKILNNVNAQTLPYLP 180
DB 118 AKERTDTHLHEKIIERQVAREPTEGTVLTPQVYGGDEKEDEIVKILNNVNAQELSTLP 177
QY 181 ILGNGGIGKTTLAQVFNVDORVIEHFHFKIWCSEDENEKRLKEIYESIEEKSLGMD 240
DB 178 ILGNGGIGKTTLAQVFNVDORVIEHFHFKIWCSDDEKRLLENIIGNERSLVDYD 237
QY 241 LAPQKTLRDLDLNGSKYLLVLDVWNEPDQKMAKLRQYLVKYGASGASVLTTRLEKYSI 300
DB 238 LASFOKTLQQLLNKRYLLVLDVWNEPDQKMDLRVVLKYGASGASVLTTRLEKYSV 297
QY 301 MGLQPYELNSQEDCWLFMQRAFGHQBENINLVAIGKIVKCGVPLAAKTLGSI 360
DB 298 MGLQPYQLSNLSQDDCWLFTIQRAFRHQEISPLVLAIGKIVKCGVPLAAKTLGSL 357
QY 361 LRFREBROWHVDSEIWKLPQEBSSILPRLSYHNLPLDLAQCFYCAVPKDTME 420
DB 358 LRFREBROWHVDSEIWKLPQEBSSILPRLSYHNLPLDLAQCFYCAVPKDTME 417
QY 421 KGNLISLMAHGFILSKGNLELVNNGVNMELYLSPFOEIEVSGQTFKMDLIHDL 480
DB 418 KKKVYISLMAHGFILSKGNLELVNNGVNMELYLSPFOEIEVSGQTFKMDLIHDL 477
QY 481 ATSLFSASTSSSNIIEIYENYIH-MMSIGFTKVVSYSLSHLOKFSVRLVNLSDIKL 539
DB 478 AXSLLSANTSSSNIIEIYENYIH-MMSIGFTKVVSYSLSHLOKFSVRLVNLSDIKL 537
QY 540 QLPBSIGDVLRLVNLASGNTSISLPVQLCKLQNLQTLDLHGHSGLCCLPKESKLSL 599
DB 538 ELPSISIGDVLRLVNLASGNTSISLPVQLCKLQNLQTLDLQYCTRCLCPKQTSKLSL 597
QY 600 RNLLDGCYGLCMPRIIGSLTCLKTSRPFVGIQKSCQGLBNLNLVYSIEITHLER 659
DB 598 RNLLDGHRLTRIPRIGSLTCLKTSRPFVGIQKSCQGLBNLNLVYSIEITHLER 656
QY 660 VQNDMAKEANLSAKENISLSMKWDDDERPRIYESKEVLEALKPHSNLTCLTINGFR 719
DB 657 VQNDMAKEANLSAKENISLSMKWDDDERPRIYESKEVLEALKPHSNLTCLTINGFR 716

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QY 720 GIRLPDMWNSVLRKNVSIIEISCKNSCLPPFGELPCLSLMLRGSAAE-VEX-----VD 774
DB 717 GIRLPDMWNSVLRKNVSIIEISCKNSCLPPFGELPCLSLMLRGSAAEVEEVIDVD 776
QY 775 SGFPTRRRPSLRKLTNIREGNLKGLLKGBEBCPVLIEIEICCMFVPTLSSVKL 834
DB 777 SGFPTRRRPSLRKLTNIREGNLKGLLKGBEBCPVLIEIEICCMFVPTLSSVKL 828
QY 835 VVSGDKSDAIGFSSISNLMALTSQIRYKEDASLPREMFKSLANLYKNISFYNLKEL 894
DB 829 -----PVLKALTSINSDNKENATSPPEMFKSLANLYKNISFYNLKEL 873
QY 895 PTLASINALKHLEIHSQYALLESIPBEGVXGLISLTQLSITYCEMLQCPBGLQHTALT 954
DB 874 PTLASINALKSLKIQWCCALLENIPKSGVGLTSLTELIVFSAVKLCPBGLHHTALT 933
QY 955 NLSVEPCPTLAKRC 968
DB 934 RLKIMGCPQLIKRC 947

RESULT 5
Q6TAF9 PRELIMINARY; PRT; 948 AA.
ID Q6TAF9
AC Q6TAF9;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Blight resistance protein SH10 (fragment).
OS Solanum tuberosum (potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
CX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14675451;
RA Van der Vossen E., Sikkema A., Heekert Bt B.L., Gros J., Stevens P.,
RA Muskens M., Moutere D., Pereira A., Stiekema W., Allefs S.;
RT "An ancient R gene from the wild potato species Solanum bulbocastanum
RT confers broad-spectrum resistance to Phytophthora infestans in
RL cultivated potato and tomato."
RL Plant J. 36:867-882(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA van der Vossen E., Sikkema S.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426264; AAR29074.1; -
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR006209; EGF_1like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 8.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
DR PROSITE; PS01186; BGF_2; UNKNOWN_1.
DR NON TER 948 948
SQ SEQUENCE 948 AA; 108223 MW; 593E29C0ECBCF06 CRC64;

Query Match 71.6%; Score 3669; DB 2; Length 948;
Best Local Similarity 70%; Pred. No. 7.1e-200;
Matches 734; Conservative 70; Mismatches 142; Indels 24; Gaps 5;

QY 1 MAEAFLOVLDNLCTFQEGELIGFDEBEKQSTFTTIOAVLEDAOKKQKDAIEN 60
DB 1 MAEAFIOVLENTITSFQEGELIGFDEBEKSTSRSTIOAVLEDAOKKQKDAIEN 60
QY 61 WLQQLNAAVEADILDCEKTEAPIROKKNYGCYHNPVITFRHKIGKRMKIMEKLDVI 120
DB 61 WLQQLNAAVYVVDLLDECKA---ARLEQSLGCHHPRAIYFRHKIGKRIEMMEKDAI 117

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Db      61 WLQKLNATAYEVDDILDDEYKTKA-TRFSQSAVGRVHPKVIIPFRHKVGRKMDQVKKLNAI 119
QY      121 AAEIRIKHLDERTIEROVAITQGTGVNLNEPQVYGRDKEDEIVKILINNNNAQTLPVLP 180
Db      120 AAEKRNPHLHKEKILIERQAVREBTSVLTEPQVYGRDKEDEIVKILINNNNAQTLPVLP 179
QY      181 ILGNGGIGKTTLAQMVFNDOVIEHFHFKIWCYSEDPENKRLIKELVESIEEKS-LOGM 239
Db      180 ILGNGGIGKTTLAQMVFNDOVIEHFHFKIWCYSEDPENKRLIKELVESIEEKS-LOGM 239
QY      240 DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVGSAGSVLTTLTEKGS 299
Db      240 DLALQKRLRLNGKTKTLVLDVNMEDQKMAKRLQVAKVGSAGSVLTTLTEKGS 299
QY      300 IMGTLOPEYLSNLSEODCWLTFMORAFGHOEINMLVAIGKEIVKCGGYPLAKTIGG 359
Db      300 IMGTLOPEYLSNLSEODCWLTFMORAFGHOEINMLVAIGKEIVKCGGYPLAKTIGG 359
QY      360 ILRFREREROMEHVARDSEIWLPOEBSILPALRLSYHHLPDLRQCFTYCAVFPKOTEM 419
Db      360 ILRFREREROMEHVARDSEIWLPOEBSILPALRLSYHHLPDLRQCFTYCAVFPKOTEM 419
QY      420 EKKMLISLMAHAGTILSKNLELVNGVWNEELYASFFOEIYKSGQTYFKMHLIHD 479
Db      420 EKKMLISLMAHAGTILSKNLELVNGVWNEELYASFFOEIYKSGQTYFKMHLIHD 479
QY      480 LATSLSFASTSSNIREIYENYIH-WMSIGFTKVVSYSLSHLOKFSYSLKVLNLSIDKL 538
Db      480 LATSLSFASTSSNIREIYENYIH-WMSIGFTKVVSYSLSHLOKFSYSLKVLNLSIDKL 538
QY      539 KOLPSSIGDLVHLRYNLNGNTSIRSLPNQJCKLQNLQTLDLHGCHSLCCLPKETSKGS 598
Db      540 EELSSSIGDLVHLRYNLNGNTSIRSLPNQJCKLQNLQTLDLHGCHSLCCLPKETSKGS 599
QY      599 LRNLILDCGYCLTQMPRIGSLTCLTKTSRPVNGIOKKSQCLGELRLNLYGSIETITHE 658
Db      600 LRNLILDCGYCLTQMPRIGSLTCLTKTSRPVNGIOKKSQCLGELRLNLYGSIETITHE 659
QY      659 RVKNDMDAKEANLSAKENLHLSMKMDDDERPRIYSESEKAVLALKPHSNLTCITRGF 718
Db      660 RVKNDMDAKEANLSAKENLHLSMKMDDDERPRIYSESEKAVLALKPHSNLTCITRGF 718
QY      719 RGIRLPMMNHSVLKNVSIIEIISCKNCSCLPRFGEIPLCKLSLELMWGSAAVEVYDSGFP 778
Db      719 RGIRLPMMNHSVLKNVSIIEIISCKNCSCLPRFGEIPLCKLSLELMWGSAAVEVYDSGFP 778
QY      779 TRRRFSLRLKLTREFGNLKGILKKGEGEOCPVLEIEIKCCPMFVPIITLSVAKLVSG 838
Db      779 TRRRFSLRLKLTREFGNLKGILKKGEGEOCPVLEIEIKCCPMFVPIITLSVAKLVSG 838
QY      839 DKSDAIGFSSISNLMALTSIQIRYKKEADSLPEEMFKSLANLKYINISFYNLKELPTSL 898
Db      839 DKSDAIGFSSISNLMALTSIQIRYKKEADSLPEEMFKSLANLKYINISFYNLKELPTSL 898
QY      899 ASLNALKHLBTHSCYALLESIPREGVKGILSTIOLISTYCEMLQCLPGLQHLNALINLSV 958
Db      899 ASLNALKHLBTHSCYALLESIPREGVKGILSTIOLISTYCEMLQCLPGLQHLNALINLSV 958
QY      959 EFCPTLAKRC 968
Db      959 EFCPTLAKRC 968
QY      939 RRCPOLIKRC 948
Db      939 RRCPOLIKRC 948

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OC      100 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      100 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      100 Lamids; Solanales; Solanaceae; Solanum.
OC      100 NCBI_TaxID=147425;
RN      [1]
RN      SEQUENCE FROM N.A., AND VARIANTS.
RN      PubMed=12872003; DOI=10.1073/pnas.1533501100;
RN      Song J., Bradeen J.M., Naess S.K., Raasch J.A., Wielgus S.M.,
RN      Haberlach G.T., Liu J., Kuang H., Austin-Phillips S., Buell C.R.,
RN      Heigeson J.P., Jiang J.;
RN      "Gene RB cloned from Solanum bulbocastanum confers broad spectrum
RN      resistance to potato late blight.";
RN      Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).
RN      [2]
RN      SEQUENCE FROM N.A.
RN      PubMed=14675451;
RN      Van Der Voosen E., Sikkema A., Hekkert Bt B.L., Gros J., Stevens P.,
RN      Muskens M., Wouters D., Pereira A., Sikkema M., Alfefs S.;
RN      "An ancient R gene from the wild potato species Solanum bulbocastanum
RN      confers broad-spectrum resistance to Phytophthora infestans in
RN      cultivated potato and tomato.";
RN      Plant J. 36:867-882 (2003).
CC      -1- FUNCTION: Disease resistance protein. Resistance proteins guard
CC      the plant against pathogens that contain an appropriate avirulence
CC      protein via a direct or indirect interaction with this avirulence
CC      protein. That triggers a defense system which restricts the
CC      pathogen growth.
CC      -1- INDUCTION: Constitutively expressed.
CC      -1- MISCELLANEOUS: Belongs to a four-gene family located at the same
CC      locus. Although the four genes are expressed in the resistant
CC      haplotype, only RGA2 confers the resistance to P.infestans. In the
CC      susceptible haplotype, RGA1 and RGA3 are likely to be pseudogenes
CC      created by deletions and mutations, while RGA2 contains also
CC      several modifications.
CC      -1- SIMILARITY: Belongs to the disease resistance NB-LRR family.
CC      -1- SIMILARITY: Contains 14 leucine-rich (LRR) repeats.
CC      -1- SIMILARITY: Contains 1 NB-ARC domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AY303170; AAP45166.1; -.
DR      EMBL; AY303171; AAP45174.1; -.
DR      EMBL; AY426262; AAR29072.1; -.
DR      InterPro: IPR001611; LRR.
DR      InterPro: IPR003591; LRR_Typ.
DR      InterPro: IPR002182; NB-ARC.
DR      Pfam; PF00560; LRR; 7.
DR      Pfam; PF00931; NB-ARC; 1.
DR      SMART; SM00369; LRR_Typ; 1.
DR      AWP-binding; Leucine-rich repeat; Plant defense; Repeat.
RN      KX
RN      AWP-binding; Leucine-rich repeat; NB-ARC.
RN      DOMAIN
RN      NP_BIND
RN      137 439
RN      184 191
RN      REPEAT
RN      526 548
RN      REPEAT
RN      549 572
RN      REPEAT
RN      574 595
RN      REPEAT
RN      596 620
RN      REPEAT
RN      638 662
RN      REPEAT
RN      674 696
RN      REPEAT
RN      751 776
RN      REPEAT
RN      784 808
RN      REPEAT
RN      829 851
RN      REPEAT
RN      852 876
RN      REPEAT
RN      878 900
RN      REPEAT
RN      901 925
RN      REPEAT
RN      927 950
RN      REPEAT
RN      966 988
RN      REPEAT
RN      VARIANT
RN      45 45
RN      L -> V (in susceptible haplotype).

```


[illegible]

Db 894 LPTSLTSLNMLKRLQIBSCSLSPFQEGELTSLQLFVKCKXMKLCPBGLQHTAL 953

QY 954 TNLVSFPCPLTARCEKIGEDWYKIAHTRVFIY 988

Db 954 TNLVSGSCPEVEKRCDEKIGEDWYKIAHINPLDIH 988

RESULT 7

RG3 SOLBU STANDARD; PRT; 947 AA.

ID RG3 SOLBU

AC Q7XA40; Q7XA25;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Putative disease resistance protein RG3 (RG1-b1b) (Blight resistance protein B149).

GN Name=RG3; Synonyms=I77013.36, CB3A14.6;

OS Solanum bulbocastanum (Wild potato).

OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride; Lamiales; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=147425;

11

SEQUENCE FROM N.A., AND VARIANTS.

RP PubMed=12872003; DOI=10.1073/pnas.1533501100;

RA Song J., Brieden J.M., Naess S.K., Raesch J.A., Wielgus S.M., Haberlach G.T., Liu J., Huang H., Austin-Phillips S., Buell C.R., Helgeson J.P., Jiang J.;

RT "Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:9128-9133 (2003).

12

SEQUENCE FROM N.A.

RP PubMed=14675451;

RA Van Der Vossen E., Sikkema A., Hekkert B.T., Gros J., Stevens P., Masmans M., Moutere D., Pereira A., Sikkema W., Allefs S.;

RT "An ancient R gene from the wild potato species Solanum bulbocastanum confers broad-spectrum resistance to Phytophthora infestans in cultivated potato and tomato.";

RL Plant J. 36:867-882 (2003).

CC -1- FUNCTION: Disease resistance protein. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via a direct or indirect interaction with this avirulence protein. That triggers a defense system which restricts the pathogen growth.

CC -1- INDUCTION: Constitutively expressed.

CC -1- MISCELLANEOUS: Belongs to a four-gene family located at the same locus. Although the four genes are expressed in the resistant haplotype, only RG2 confers the resistance to P.infestans. In the susceptible haplotype, RG1 and RG3 are likely to be pseudogenes created by deletions and mutations, while RG2 contains also several modifications.

CC -1- SIMILARITY: Belongs to the disease resistance NB-LRR family.

CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC -1- SIMILARITY: Contains 1 NB-ARC domain.

CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).

CC -----

DR EMBL; AY303170; AAP45165.1; -

DR EMBL; AY303171; AAP45181.1; -

DR EMBL; AY426260; AAR29070.1; -

DR EMBL; AY426263; AAR29073.1; -

DR InterPro; IPR001611; LRR.

DR InterPro; IPR003591; LRR typ.

DR InterPro; IPR002187; NB-ARC.

Pfam; PF00560; LRR; 7.

Db	480	ATSMFSASASRSRIROIYNKDEDMNFVITNYKDMMSIGPSEVSSYSPSLFRFVSLRV	539
Qy	531	LNLSIDTKLQLPSSSIDLVHLIRYLTNSGNTSIRSLPNOLCKLONLOTLDHGSHLCCLP	590
Db	540	LNINSNPFQLPBSVVDLVHLIRLIDLSGN-KICSLPKRLCKLONLOTLDLYNCOSLSCP	599
Qy	591	KETSKTGLSLRNLLDGCYGLTCMPPIGSLTCLKTLISRFVVGIOKKSQOLGELRNINLYG	650
Db	599	KQTSKLSKSLRNVLHHC-PLTSPAPPIGLTCLKTIGFVVG-ERKGQYGLGELRNINLRG	656
Qy	651	SIETITLKVNDMDKXANLSAKENLHSLSMKWDDDERPRITYESKVEYTLAKHSHNL	710
Db	657	ALSIITHLEVKNDMEKXENLSAKANLHSLNSWD---RPNRYSESEVKLELAKHPNL	713
Qy	711	TCLTTRGFRGIRLPPMNMNSVLKAVSIIIBISCKNCSCLPPGELPCLKSLBLMRGSAEV	770
Db	714	KYLEIIFDFCGFCLPPMNMNSVLKAVSIIISGNCNCSCLPPGELPCLSLBLDQSDVEV	773
Qy	771	EYV-DSGPFCRRRPFSLRKLNTREFGNLKGILKKGSEBECPLLEIEIICCPFFVYPTLS	829
Db	774	EYVDSGFLTRRRPFSRLKRLHIGFCNLKGLQRMKGAEOPVLEEKIKSDCMPFVPTLS	833
Qy	830	SVKCLVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPREMFKSLANLYKLNISFYF	889
Db	834	SVKCLEIWGE-ADAGGLSISNLSITLSIKTIPSNTLVYSLSEMPFNLENLYLSVSFLE	892
Qy	890	NKKEPLTSLASLNALKHEIHSCTALBESPEGVK 924	
Db	893	NKKEPLTSLASLNALKDIRYCALESIPBEGLE 927	
RESULT 8			
ID	Q94J89	PRELIMINARY; PRT; 1110 AA.	
AC	Q94J89		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Putative NBS-LRR type resistance protein.		
GN	Name=PF0702B09.8;		
OS	Oryza sativa (japanese cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehharatoidaeae; Oryzeae; Oryza.		
OX	NCBI_TaxID=39947;		
RP	SEQUENCE FROM N.A.		
RX	PubMed=12447438; DOI=10.1038/nature01184;		
RA	Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,		
RA	Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,		
RA	Hosokawa S., Masubukawa M., Arikawa K., Chiden Y., Hayashi M.,		
RA	Okamoto M., Ando T., Aoki H., Arita K., Hanada M., Harada C.,		
RA	Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,		
RA	Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,		
RA	Karasewa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,		
RA	Mechita K., Maehara T., Mizuno H., Mizukeyashi T., Mukai Y.,		
RA	Nagasaki H., Nakashima W., Nakama Y., Nakamichi Y., Nakamura M.,		
RA	Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,		
RA	Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,		
RA	Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,		
RA	Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,		
RA	Yano M., Jiang J., Gotohori T.,		
RT	"the genome sequence and structure of rice chromosome 1,"		
RL	Nature 420:312-316(2002).		
DR	EMBL; AP003073; BAB44079.1; -		
DR	Gramene; Q94J89; -		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0006915; P:apoptosis; IEA.		
DR	GO; GO:0042829; P:defense response to pathogen; IEA.		
DR	InterPro; IPR007067; Disease_resist.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR002182; NB-ARC.		
DR	InterPro; IPR009058; Wing_hlx_DNA_bnd.		

QY	DR	PFam: PF00560; IRR 1; 8.
QY	DR	PFam: PF00931; NB-ARC; 1.
QY	DR	PRINTS: PR00364; DISASERDIST.
QY	DR	SEQUENCE 1110 AA; 126126 MW; C43D1BDB40C3A3F CRC64;
QY	DR	Query Match 29.6%; Score 1517; DB 2; Length 1110;
QY	DR	Best Local Similarity 34.9%; Pred. No. 1.5e-77;
QY	DR	Matches 396; Conservative 189; Mismatches 345; Indels 206; Gaps 35
QY	Db	4 AFLQVLDNLTCFIOGELGLII--GPKDEPKLOSTFTTIOAVLEDAQKOLKDKAKIN 60
QY	Db	9 AFMQLTFOKLS---EATLDHFISMRGIIHGKLETSISTTSIQLOAFLLDAEKKOLTVASVGR 65
QY	Db	61 WLQKLNAAAYEADDLIDBECKTEAPLRQKKKKXGCVHNPIVF-----RHKIGKR 109
QY	Db	66 WLAKIKDAIYDDLDLIDLSYSAS-MKKMKQKQ--VIFPYASFLSSSFLSRNIYQHKIKK 122
QY	Db	110 MKKIMKEDLVIAERIKFHLDERTTERQVATR---QTGVLANPQVYGGKDEKDELVK-I 165
QY	Db	123 INILIERDKIAQEHDTIGLQWICEMRARDTERQSSLSVSAVFGERRERREHVRIV 182
QY	Db	166 LINNVSNAQTLPVLDPLDGMGSLGKTTLAQWVENDQVIEHPFKIWIQVSEDPNKKLIK 225
QY	Db	183 LSDNHNHSCNLCVIRYVVGWGLGKTTLMQWYHDDRREHFLRIWIVYSESFDEKRLQ 242
QY	Db	226 EIVSEIE-EKSLGSGNDLAPLOKKLADLNGKRYLLVDVNMEDQDKAKLQVLKVGAS 284
QY	Db	243 ETLLESDYDQASASTNMNMLQSTLSRVLGRKRYLLVLDVNMEDLDKMSYDALISGGF 302
QY	Db	285 GASVLTTRLEKVGSIIMGTLQPEYELSNLSQEDCWLTFMORAF-----GHQEIINILVA 338
QY	Db	303 GSKIVVTSRNNVGVIMGIEIEPYKLOKLSDDDSWGSFKAHARDGCSAHP-----LEA 357
QY	Db	339 IGKEIVKCCGVPLAKTLTGILRFKREERQWEHVRDSEIWKLPQBSSEILPALRLSYH 398
QY	Db	358 IGMEIVKTKLKGIPLASKALGSLFCKTDEEEKDILQNDIWEIPLADKNNIILPALRLSYH 417
QY	Db	399 LPDLRQCFYCAVPRKPTMEKGNLISLMMHGFILSGNLELVNGEVMNVELYLSF 458
QY	Db	418 LPPIHKQFAFCSTVPRKDYMFREKLVKIMLGFIRQSKRMEDTGNAYFNELLSRF 477
QY	Db	459 FOEIEVKSQGTQYFKKNDLIHDLATSL----- 484
QY	Db	478 FQPYE-----NNYVNHADMHDLAKSISWEDCOHLDYGRHNDAIKTRHLSFPCDAKCMH 532
QY	Db	485 FSASTSSNIREIYENTYTHMMSIGFTKVVSYSLSHLOKQFSLKVLNLSIDTLKOLPSS 544
QY	Db	533 FNPVYGFKKLTLLT-IH-----GYKSRMSQLPFGLFWKLEYLTLVDHMGOGELKELPES 585
QY	Db	545 IGDVHLNLYLVNIGSTSIISLPNOICQONLQTLIDHGHSICCLPKERSKIGSLRNL-- 602
QY	Db	586 IGNLQGLNPLDLS-STEIETDPAISLVKLYNLDILKLSDCNFIREFVQGITRLINLHLEA 644
QY	Db	603 ---LLDGCYGLTCMPRIIGSLTCLTLRSFVVGIOKRS-CQGLERNLNL-LYGSIEIYTHL 657
QY	Db	645 STRLLSRHGG-----IGSLVCLQELBEFVY--QKRSQHVNTALNMDELQOQSLIRGL 695
QY	Db	658 ERVKDKMDAKENLSAKENLSLSMKMDD--ERRRIYSEKVEYVLBAKPSNLTCLTI 715
QY	Db	696 NNVPNGQDAVCAKLNKKEHLRTLHIWEDCESNP-----SEQOEVLGEGPHIDIKELVI 751
QY	Db	716 RGRFRIRLRPDMWNHSLVKNVSEIIEISCGNCSCLPPFGELPCKLSLELRGSAEVEYDS 775
QY	Db	752 KGFPEVRRPPSWLASSFLPKLQTIYHLCNCRS-TRLRPLQGLPFLKYLIVT-AGTTEYVQLSS 809
QY	Db	776 ---GPTRRRPPSLKMLNIREFQNLKGLIKKEGEGCPVLEIEIKCPMF--VIFPTLSS 830
QY	Db	810 EPTFGGQKGFALDLDLLEDMPNLSWIFVADQQLPQLTELGLIKCPQLKKLDPPIPT 869
QY	Db	831 VKKVLVSGDKSAIAIPSSISNLM-----ALSTL 858
QY	Db	870 LRTLTWISSS-----GIESLPELONNSCBSSPSTSLYINDCPNLTSLRVLGLLAAYRPTLAKSL 924

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Oy QIRNKXSDA;PEEMFSPSLANKYKNTISFY;-----FNKE---LPTS----- 897
Db 925 TIACBEGVLSPECFRPLISLSLH--YECPLVWMTALBGLLPTSLIEDILNCTP 982
Oy 898 -----LASLNAKLKELIHSYVALBESLPEBGVGHISLTLSITYCEMLQCLPEGLQH 949
Db 983 LASVTLNGLSYLPRLRPFELIADCPDINNPAEGLPH--TLQFLIESCDPDQLCPGLHN 1040
Oy 950 LTA-----LTNLSVECFPLARCEGIGEDMWKIH 982
Db 1041 ISSLETIRISNCPGVESLPREGLPWGLNEDYIKGCPQIKQCCQCG-GEYHAKIAHI 1095

RESULT 9
O6LAD9 PRELIMINARY; PRT; 1222 AA.
O6LAD9
AC O6LAD9,
DT 05-JUL-2004 (TReMBLrel, 27, Created)
DT 05-JUL-2004 (TReMBLrel, 27, Last sequence update)
DT 25-OCT-2004 (TReMBLrel, 28, Last annotation update)
DE Putative NBS-LRR resistance protein (Putative NBS-LRR protein).
GN Name=OSUNBA008M05.1; Synonyms=O6L126_B11.12;
OS Oryza sativa (Japionica cultivar group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
CX NCBI_Taxid=35947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Haing Y.-I. C., Chen C.-S., Chen H.-H., Liu S.-W.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chao Y.-T., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Haing Y.-I. C., Chen C.-S., Chen H.-H., Liu S.-W.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chao Y.-T., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; ACJ36222; AAT38049.1; -.
DR EMBL; ACJ05767; AAU3949.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR00767; Disease_resist.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 7.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERIST.
DR SMART; SM00369; LRR_TYP; 4.
SQ SEQUENCE 1222 AA; 138744 MW; 74AE6599BA128B5B CRC64;

Query Match 29.6%; Score 1516; DB 2; Length 1222;
Best Local Similarity 32.9%; Pred. No. 2e-77;
Matches 408; Conservative 194; Mismatches 355; Indels 284; Gaps 35;

Oy 1 MAE--AFLOVLDNLTCTFQGBELGLILGFDFEKLQSTFTTTQAVLEDAQKQKLDKA 57
Db 1 MAELISALPALAKKAGESLGTERRSPFGIGERRSESLYTLILANOVINDAEDASKPA 60

58 IEMVLQCLNAAVEADILD-----ECKTEAPTRQKNGKVG-----CYHPVITPRKIG 107
Db 61 VKSIATKAKIACADADALDELAHYELRCEALRGKIKNTGVAAFPSSHNPPLFKRIG 120

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108 KMKKIMKLDVIAAEIRK-----HDERTIEROVAITQTPVNLNPOVYGRDKRD 160
121 KRLQOIVIRIDQVLSQMMRFGLNCSMPYDER-----MOTYSYVEOEYIGDKRD 172
161 EIVKILNNVNAQTLPVLPILGMGLKTTLAQVFNDOVIEHPKRIWICVSEEDNE 220
173 EIVHMLTSL--AETDELLILPIVIGLIGLKTTLAQVFNDOVIEHPKRIWICVSEEDNE 230
221 KRLKEIYESI--EKSISGMDLAPLOKRLDLNGKTYLVDVNMEDODKAKLRQV 278
231 PVIVGIIIDTVAIGNCGLKPNLELLQRLREEGQKRYLVLDVNMEDODKAKLRQV 290
279 LKVGASGASVLTTLTLEKVGSMGLQVLELNLNPOEDCMLFMORAGHOEINLVVA 338
291 LGSQMGSAVVVTRNVKVASIMESISPLCENLNPEISWIFSRACGTQVETPELVE 350
339 IGKELVKKCGVPLAAKTLGGILRPEREROMEHVDESIKLPQESSIIPALRLSYHH 398
351 VGRIVERCCGIPALIKMGALMSTQETRDMLSTLESNW---DEESQIIPALSLGYKN 407
399 LPDLROCFETCAVEPKDTEMEKNTLSLMMAHGFIISKNGLELVNENVEWNLVLSF 458
408 LPSHKOCFAVCAVFPKDYELDKDLHLNWSNGFIPEKMSDIENGNHVPWELWMSF 467
459 FOEIEV-----KSGQTYFKMHDILHDIATSLF--SASTSSNIREI--IVENY 502
468 FQVVKQIGSIFQKRVYRGSDVTFPKIHDLMHDLVAHISDECEALLENLAKIKKIPNV 527
503 IHM-----MSIGF-----TKVVS--YSLF-----HLOKVS-----LRVLNSDLKOLPS 543
528 HHMAFEGQOKIGFIMOHCRVIRSFALDKNDMHAODIKFENSPRLVGLHIFGIEKFPV 587
544 SIGDLVHLRYNLNGTSIRSLPQOLCKOYLQTLTDHGHSLCCLPETSCKLSLNL 603
588 EPAMKHLRIYDLBG--SYINTLPRASALNLYOVLINRCRLTYHDPGKMFSLHAY 646
604 LDGCGYLTCEMPRIIGSLTCLTSLRFPVVGIOKSCQJGELNMLNYSIEITHLERYND 663
647 LDDCARLTSPWAGGOLINLTTLTKFVPG--NESGRIINELNDLKGGLQIFNLIKVTNP 705
664 MDAREANLSAKENHLSMKKDD-----ERRPIYSEVAVLEALKPHSNLTCTIR 716
706 IEAEANLECKTNLQOLALCWGTSKSAELQAEIDLHLYRHE--EVLDAKPNGLTIVKLR 763
717 GFRGIRLPDMNNHSHV--LKNVVSIEISCJNCSCLPFGELPCLSKLEIMGSAVEVYDS 775
764 QYMTTPIIMENGTITRNIYKAKVTSINCMKLPVWKLPFLVLEKYL--KOMKJLKYCN 822
776 GFPTRRR-----PSLRKLNIREFNGNLKGLKKEGEE---OCPLYELEIKCCP--MF 823
823 GFCSDKCDHQLVAFPKKLSTLERMESLEWQEDVVEQVTPANFPVLDAMEIIDCPKLT 882
824 VIPTLSSVKLVSGDSDAIGF--SISINLM-----OCPLYELEIKCCP--MF 883
883 AMPAPAVLKSLSVGNKI--LIGLSSVSNSLYIVLASQGSLEBKRTLYHYKENLEGT 941
854 -----ALTSIQ-----PEMFKSLANLYKN-----IRYNKE 865
942 DSKOHVLAHHFSSWGSITLKLHLGFSALAPEDIONISGHVMSVQNDLISCDCTIQYDTL 1001
866 DASI-----PEMFKSLANLYKN-----IRYNKE 884
1002 QSPILMFWSFACLOHLLTEYCNLSLTFWPGSEFQSLTKRLDIRYCNFTGMPPAQVSVK 1061
885 -----ISFYNLXELPTSLASLAKHLHISCVALESLP-----920
1062 SFEDGEMNLERIEIEFCYMLVAFPTSL-----YLRISCVNLEDPGLGCLGALRS 1115
921 -----EGVKGILSLTQSLSTYCEMLQCL 943
1116 LSLIDVNPRLKSLPSTIORLSNLTRLVYIGTNDLSLTLPEGMHNTLALNDLAINNCPSLKAL 1175
944 PBGL-QHILTLNLSVEFCPTLAKRCEKIGEDWYKIAHP 983

1176 PBGLQRLHSLKLPFRCQPLVARKRG--GDWYSKYDLP 1215
RESULT 10
084XGO PRELIMINARY; PRT; 1035 AA.
ID 084XGO
AC 084XGO
DT 01-JUN-2003 (TREMBLERel. 24, Created)
DT 01-JUN-2003 (TREMBLERel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLERel. 26, Last annotation update)
DE NBS-LRR resistance protein RGL1.
OS Manihot esculenta (Cassava) (Manihot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids I; Malpighiales; Euphorbiaceae; Crotonoideae; Manihoteae;
OC Manihot.
OX NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2835941; PubMed=12827500; DOI=10.1007/s00438-003-0868-5;
RA Lopez C.E., Zuluaga A.P., Cooke R., Delseny M., Toinne V., Verdier V.,
RT "Isolation of Resistance Gene Candidates (RGCs) and Characterization
of an RGC cluster in cassava."
RL Mol. Genet. Genomics 269:658-671 (2003).
DR EMBL: AY188523; AAC37645.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0042829; P:defense response to pathogen; IEA.
DR InterPro: IPR000767; P:defense response to pathogen; IEA.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR 1; 5.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERel.
SQ SEQUENCE 1035 AA; 118190 MW; 60A081C6F6DD176 CRC64;
Query Match 28.9%; Score 1479.5; DB 2; Length 1035;
Best Local Similarity 35.8%; Pred. No. 1.9e-75;
Matches 363; Conservative 196; Mismatches 354; Indels 101; Gaps 25;
20 ELGLILGFQDEPEKQSTFTTQDAVLDAQKQKQKALLENMLQKLNAAAYEADDIIDEC 79
24 EIGLMVGKGLKTLKATVSSIRNVLLDAEQKLRQYGVLEVEVYDADDLVDPF 83
80 KTAAPIRQ-----KKNKYGCHPNVITFRKIKGRKKIMKLDVIAAEIRKTHDE 131
84 ATEALRRVWTGNRMTEKVSLEFSSSNKLVYGRFMGHKVKALIRELADIADR--KENLEV 142
132 RTTERQVATP--OTGFVLANEPQVYGRDKEDYKILINNVSNAQTLPVLPILGMGLGK 190
143 RTQRIERIVWRDQYTTSLP--VVGREGDKKAITQVLSS--NGECCSVLSIVIGLIGLT 200
191 TLAQVFNDOVIEHPKRIWICVSEDPNEKRLIKEIVIESIEKSLGMDLAPLOKRD 250
201 TLAQIILNDEMINGSPEPRITWCSEHFPVKMTVVGKILTSATGKNSKSEDLGELAKSLRK 260
251 LKNGKRYLVLDVNMEDODKAKLRQVLKVGASGASVLTTLRLEKVGSMGLQVYELS 310
261 IISGKRYLVLDVNMENKREKEMNLKRLLVGSSGSKILITTRSKKAVADISGTTAHVLE 320
311 NLQEDCMLFMORAGHOEINLVVAIGKEIVKCGVPLAAKTLGGILRPEREROM 370
321 GLSLDSWLSFLVHNLGEGEPKNAVRENKKEILKKCHVPLAKITIASLVAKNPETEM 380
371 EHVROSEIKLPOESSIIPALRLSYHHLPDLROCFETCAVFPKDYKTEMEKNTLSLMA 430
381 LPFLTELRSIQDQNDIMPLKLSYDHLPSHLKHCFAVCAVTPKDYVIDVTTLHLMLTA 440
431 HGFIISKNLLE--LENVGNVMEVLYRSFQIE-----VSGQTYFKMHDILHDIAT 483
441 QGFIESPSTSDCLDGLGLEYFMKLMWRSFQIEVERDRGCVNES---CMMHDLMDLATT 496

484 LFSASTSSNIREIIVENYIHMSIGF-----TKVSSYSLSHL----QKFV--- 526
497 VGGKRIQLVNSDTPNIDKETHVVALNVAPQEIINKAKRVASILLSEHVNDQLFIYKN 556
527 --SLRVNLSDIKKOLPSISGIDLVLRLYNLNGSTSRSLPNQCKQNIQTLDHCH 584
557 LKFLVFTWYSYRI--MNSIKMLRYRLVDVSDNEKALKALSNTTDLNLTQVLDVSYCV 614
585 SLCCLPKETSGLRLNLDDCYGLTCMPPRIGSLTCLTSLRPVVG---IQKSC-QI 640
615 QKELPKOIKLVLNRLHYCEGNSLTTHMPRGQLTSLQTLISLFAVAKHISSDVCKI 674
641 GELRNL-NLYGSEITLHERYKNDMAKANLSAKENLSLSMKWDDERPRIYSEKYE 699
675 NEINLNLNRLGELIRNLGCV--DDEIIVNVLKEKPLQSLRLRWES-----WEDSNVD 727
700 ----VLKALKHSNLTCLTIGFRGIRLPDMNHSVLKNVSIETISCKNSCLPFPBEL 755
728 RDEMAFQNLQPHPNKELLVFGYGRFPSPWF--SSLNLNLYLCTWCKRYOHLPPMDQI 785
756 PCLSLSLMRGSAEVEYVD--SGFPTRRRPSLRKLNIREFNLKGLLKEGEGQCPVLEE 814
786 PSLQTLER-LGLDDEIYMEIGOPT--SEFPISLKSGLVNCPLKGMQKK--EDDSTALEL 842
815 IEIKCCPMFV--IPTLSSVKKLVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPE 871
843 LQFPLSYFVCEDECNLSIPQF-----PSLDD 870
872 EMFSLNLAKLNTISFYNNKELPTSLASLNALKLEIHSCLALSPREGVKGLISLTQ 931
871 SLHLHASPOLVHOIFTPSSISSSSIIPLSLKXLMIRDIKELESPPDGLRNLTCLQR 930
932 LSITFCENLQCLPBGLOHLTALTNLSVEFCPTLAKCEKGIGBDWYKIAHAPRV 985
931 LTIECPAIKCLPQEMBSLTSLRELINDDCCPOLKERCGRKAGADWAFISHIPNI 984

RESULT 11

084XFP9 PRELIMINARY; PRT; 1024 AA.
AC 084XFP9; 01-JUN-2003 (TREMBLREL. 24, Created)
DT 01-JUN-2003 (TREMBLREL. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLREL. 26, Last annotation update)
DB NBS-LRR resistance protein RGH2.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Malpighiales; Euphorbiaceae; Crotonoideae; Manihoteae;
OC Manihot.
OC NCBI_TaxID=3983;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22835941; PubMed=12827500; DOI=10.1007/s00438-003-0868-5;
RA Lopez C.E., Zuluga A.P., Cooke R., Delseny M., Tohme J., Verdier V.;
RT "Isolation of Resistance Gene Candidates (RGSs) and characterization
of an RGC cluster in cassava";
RL Mol. Genet. Genomics 269:658-671(2003).
DR EMBL; AY188524; AAC37646.1; -
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resistc.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 4.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERSIST.
SQ SEQUENCE 1024 AA; 116977 MW; 99EAE9E39364A9C2 CRC64;

Query Match 28.8%; Score 1479; DB 2; Length 1024;
Best Local Similarity 35.0%; Pred. No. 2e-75;
Matches 355; Conservative 208; Mismatches 350; Indels 100; Gaps 24;

20 ELGILGKDFEKLQSTFTTITQAVLEDAQKQOLKDAIENMLQKNAAAAEADILDEC 79
24 EIGLMGVKSLKLELATVSSIRNVLLDAEEOQLNQGVMLERLERLEIVDADLDVDF 83
80 KTEAPIRO-----KKNKGYCHENVITFRHKGKMKIMKLDVIAERIKFHIDE 131
84 ATEALRRRVMTGNMTKEVSLFFSSNQLVYFGKGRKVRKIRRELRIDEADR-NFNLEV 142
132 RTIERQVATR-QTGFVLENPQVGRDKDEIVLILINNNSAQTLPVLPILMGGLGKT 190
143 RTDQESIVMRDQTSSLPE-VVIREGDKAITLVLS-NGEECVSLVIGIGLAKT 200
191 TLAQVFNDQVRVIFHPKIMIVCSDEDENKRLIKEIVSEIEESLGMDLAPLOKLRD 250
201 TLAQIIFNDELKNSFPERIMVCSSEFPDVMTYQKILLESATGSRSDIGLEALKSLREK 260
251 LUNGKTLVLVDVWNEODDKMAKQVLYKVASGASVLTTRLEKVGSLNGTLQPYELS 310
261 IISGKTLVLVDVWNEENREKEMIKRLLVGSSGSKILITTRSKVADISSTWAPVYLE 320
311 NLGQEDCMILPMQAPGHQENINLVAIGKEIVKKGQVPLAKTLGILRFRERROW 370
321 GLSPDESMSLFLHALRGQEPKANNVREMEKELIKKRGVPLAKITIASLYAKNPETEW 380
371 ENHVDSEIMKLPQESSILPALRLSYHPLPLDRQCFYCAVPFKOTEMEKNLISLMA 430
381 PPLITKLSRIQDGNIMPTLKSLDYHLSNKLKCHCAIYKDVIVDKRLIHLMTA 440
431 HGFILSKGNLE-LNNVGENVELLYRSFPOEIE-----VKSQGYFKMHLIDHATS 483
441 QGFIESPSTDCLEDIDIGLEYFMKLMWRSFQEVDRDRYGWES-----CKMHLMDHATT 496
484 LFSASTSSNIREIIVENYIHMSIGFTYVSSLSLHLOKQFVRLV----- 531
497 VGGKRIQLVNSDALNINEKIHVALNL-DVASKELIINNARKVRSLLFEKYDCQLFIYK 555
532 NLSDIKL-----KOLPSSIGDLVHLRYNLNGSTSRSLPNQCKQNIQTLDHCHS 585
556 NUKFLRVFKHASTRYTNNISKILKIYIYLDVSDNKGKALKASHSTDLNLTQVLDVSYCVQ 615
586 LCCLPKETSGLRLNLDDCYGLTCMPPRIGSLTCLTSLRPVVG---IQKSCQ-LG 641
616 LKELPKOIKLVLNRLHYCEGCVSLHMPGQLTSLQTLISLFAVAKHISSDVEKIN 675
642 ELRNL-NLYGSEITLHERYKNDMAKANLSAKENLSLSMKWDDERPRIYSEKYE- 699
676 ELNKLNNLQGRLEIINIGCVDNEL--VNVNLKEKPLQSLRLRWES-----WEDSNVDR 728
700 ----VLKALKHSNLTCLTIGFRGIRLPDMNHSVLKNVSIETISCKNSCLPFPBEL 756
729 DEMAFOQLQPHPNKELSVIGYGRFPSPWF--SSLNLNLYLCTWCKRYOHLPPMDQI 786
757 CLKSLSLMRGSAEVEYVD--SGFPTRRRPSLRKLNIREFNLKGLLKEGEGQCPVLEE 815
787 SLOVLTQW-GVDDLEIYMEIGOPT--SEFPISLKTLDHGCPLKGMQKK--RDDSTALEL 842
816 IEIKCCPMFV--IPTLSSVKKLVVSGDKSDAIGFSSISNLMALTSIQIRYNKEDASLPE 872
843 QFPLSYFLECECPNLTSIPQF-----PSLDDS 870
873 MFSNLNLAKLNTISFYNNKELPTSLASLNALKLEIHSCLALSPREGVKGLISLTOL 932
871 LHLHASPOLVHOIFTPSSISSSSIIPLSLKXLMIRDIKELESPPDGLRNLTCLQR 930
933 SITVCENLQCLPBGLOHLTALTNLSVEFCPTLAKCEKGIGBDWYKIAHAPRV 985
931 TIOICPAIKCLPQEMBSLTSLRELINDDCCPOLKERCGRKAGADWAFISHIPNI 983

RESULT 12

08LL82 PRELIMINARY; PRT; 1108 AA.
ID 08LL82

AC Q8L82; 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE NBS-LRR-like protein.
GN Name=YR48;
OS Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OK NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=leaf;
RA Yang Q.-Z., Yang P.W., Zeng L., Wang Q., Cheng Z.Q., Yang B., Li J.R.,
Huang X.Q., Yang P.W., Zeng L., Wang Q., Cheng Z.Q., Yang B., Li J.R.,
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF456247; AAN03742.1; -.
DR Gramene; Q8L82; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resistc.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002182; NB-ARC.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00560; LRR_1; 6.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.
SQ SEQUENCE 1108 AA; 125209 MW; DA015AAACBA4B471 CRC64;

Query Match 28.8%; Score 1477.5; DB 2; Length 1108;
Best Local Similarity 34.4%; Pred. No. 2.7e-75;
Matches 392; Conservative 181; Mismatches 345; Indels 221; Gaps 37;

QY 4 AFLQVLDNLTCFQGEGLILGFDEFEKLGSTFTTTQAVLEDAQKKOLKKAIEWMLQ 63
DB 10 AFQWALFEKAAVAASSELKFPONIAVELQNLSSSTILIAHVEDAEERQLDQARSWLS 69
QY 64 KLNAAAYEADDIIDCKTEARFIRKKNKYGCGYCHNNV-----TRHHIGKRMK 111
DB 70 RLKQVAIEMDLDLDBEHAENV-LRSLAGPSNYHUKVATCCICIMKNGELNRLDVLVQIM 128
QY 112 KIMERLDVIAER-----IKFHLDERTIERQVATR-QTGFLVNEPOYGGDEKKEDEIVK 164
DB 129 RIEBKIDRLIKDRHIVDPIMRNREE-----IERPRTSLIDSSVYGGEDKEVIYN 182
QY 165 ILI-NNVSNACTLVLPILMGGLGKTTLAQMVFNDOAVIEHFPKTIWCYSEDPNKRL 223
DB 183 MLITNNNSNHVNLSILPLVGGVGKTTLTQLVNDVAVKKGHQLARWMLCVSENFDEAKL 242
QY 224 IKELVESIE---EKSLGMDLAPLOKKLRDLNKGKYLVLVDVWNEEDODKWLRLQVLK 280
DB 243 TKETIESVAGSLSATTNMNI--LQEDLSNKLKGRFLVLDVWNEEDPDMDYRCALV 300
QY 281 VASGASAVLTTRLEKVGISINGTQPYELSNLSOEDCMLFMORAFGH-OEILNLTVAI 339
DB 301 AGAGSKIMVITTRNENVGKLVGLTPYLLQSLTNDCHLFRSVAFAFDGSSAHPNLEMI 360
QY 340 GKELVKKCGVPLAKLTGLLKRKREBEROWEHYRDEIMKLPOEBSIILPALRLSTHHL 399
DB 361 GKELVHKLKGLPLAARALGSLCKMDNEDWKNLISEIHELPEDKNNIIPALRLSTHHL 420
QY 400 PLDRQCFYCAVPPKOTEMEKGNLISLMAHGFILSKNMLELVNENWNLVYLSFF 459
DB 421 PLLIKRFACSVNHQYVEKDLVQIMAVGTIQGRRRRMEIGNNTFDELSRSPF 480
QY 460 QELIEVKSQGYFKMHLIHLATS-----LFSASTSSGNIREI-----I 498
DB 481 Q--KHKG---YVWHDAMHDLAQSISDECRDLNLPNNSTTERNAHLSFSQNKSGQT 535
QY 499 VENVYHMSIGFTKVVVSYSLSHLOK-----PVSILVNLSDI---KLQLPBSIG 546

DB 536 FEAF-----RGFNARSLILLNGYKSTSSIPSDLFLNRLHVLIDLNRQETELPESVG 590
QY 547 DLVHLRYLINSQNTSISLNPOLCKLQNLQTLDIHGC-HSICCLPKETSKLGSRLNILD 605
DB 591 KLNKRLRYLNLSG-TVVRKLPSSICKLYQLTKLRNCSHNLVNL-----LSLE 637
QY 606 GCYGLTCMPPIGSLTCLKTLSPRVGIIQKSCCOLGELRYNLN-LYGSIEITHLERVNDM 664
DB 638 ARTELITGIRIGTTLQKLEEVVH-KDKGYVSELKMNKKGICHTCKNLBSVSAE 696
QY 665 DAKENLSAKENLHSLSMKWDDEPRRIYSEK-----VEVLEALKPNSNTLCTIRPFG 720
DB 697 EADBALSEKXAHISILDLIWSS--RDFTESEANQDIETLTSLEPDELKELTVKAFAG 753
QY 721 IRLPDMNHVYLNKVSIEIISCNGCCLPPFGELPCLKSLIELMRGSAEYVDSGPP- 779
DB 754 FEFPW---LHSLQTLHSDCTNCSILPALQGLPLKTY-----IIGGPTI 798
QY 780 -----RRPFLKRLNREFGNLKGLLKKEGECQPVLEIEIKCCPMFY-IP 826
DB 799 IKIGDERSSSEYKGFPSLKEIVEDTPNLEPRTSTQDGFPLPRLQVLDGPKYTEL 858
QY 827 TL-SSVKLVSGDKSDAIGPSSISN-----LMAUTSLQIRYNKEDASL----- 869
DB 859 LIPSTLVELKIS-----EAGFSYLPVEVHAPRFLPSLTRLIHRCPNLTSIQQGLSQOLS 913
QY 870 -----PEEMFKSIANKYXNLISFYNNLKLPTS----- 897
DB 914 ALQQLTTNCPPELLHPTEBELRTLTALQSLHI---DQPLRLVAEHRGLLPRMIEDLRIT 970
QY 898 -----LASINALKHLIHSQYALDESLEP-----GVAGLIS----- 928
DB 971 SCGNIINPLDELNELPALKNVIAADVSLNTPPEKLPATLKLEIFNCSNLASLPACLO 1030
QY 929 ----LTLSTTYEMLQCLP-BGLQHLTALTNLSVEFCPTLARCCEKIGEDMYKIAHI 982
DB 1031 EASCLKMTIYNLCVSIKCLPAHGLP--LSLEELYIKRCPLARCOENSGEDWPKISHI 1087

RESULT 13
Q6L4D7 PRELIMINARY; PRT; 1259 AA.
AC Q6L4D7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Putative NBS-LRR resistance protein.
GN Name=OSUNBA0088W05.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OK NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=leaf;
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen S.-K., Chen T.-R.,
Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-F., Lin S.-U., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AC136222; AAT38051.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resistc.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003591; LRR_TYP.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00560; LRR_1; 8.
DR Pfam; PF00931; NB-ARC; 1.
DR PRINTS; PR00364; DISEASERISIT.

PRINTS: PR00019; LEURICRPT.
DR SMART; SMO0369; LRR_TYP; 3.
SEQUENCE 1259 AA; 142887 MW; 7893B44D90685941 CRC64;

Query Match 28.6%; Score 1464.5; DB 2; Length 1259;
Beet Local Similarity 31.8%; Pred. No. 1.7e-74;
Matches 398; Conservative 190; Mismatches 365; Indels 297; Gaps 32;

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QY 1 MAE---AFLOVLDNLTCFIOGELGLIGFDEBEKLOSTFTTIOAVLEDAOKQOLDKXA 57
DB 1 MAELISALLPALPKKAGSISTEFAFGIEKSELSTLAINOVLYGAEBOASKCPA 60
QY 58 IENMLOKLNAAYEADILDECKTEAPYROKKNKY-----CYHPNVITFRHXI 106
DB 61 VKSMIAKAKMAACEADALDELHYEA-LRSEALRGHKINSVAPAFSSHNPILFKRI 119
QY 107 GKRMKTKMEKLDVIAERIKF-----HLDERTEROVATROGFVINEPOVYGRDKK 159
DB 120 GKRLQOIVKIDKVLQWNRFGFLNCPMPVDER-----MQTVSYVDEOEVIGRQKER 171
QY 160 DEYKILINNVSNAQTLPVLPILMGSLGKTTLAQMVFNDQVIEHHPKIMICVSEDFN 219
DB 172 DEITHMLLS--AKSDOKLILPIVIGIGLKTTLAQVLVNDVKYAHFOKHMVVCSENF 229
QY 220 EKRLIKEIVESI--EEKSLGMDLAPLOKRLDLNGKYYLLVDVWNEODQKMAKLRO 277
DB 230 VPDVKGITDPAIGNDGLKSDNLELQORLRRELSQRYLLVDDVWNEBOKREALRT 289
QY 278 VLKVGASGASVLTTRLEKVSINGTLOPYELSNISOEDCMLFMQAFGHOBEINLNLV 337
DB 290 LLLCCKMGSAAVVVTRNSNVASVNGTVPPLLEQLSQDSWTLFCERAFRTGVAKSCFEV 349
QY 338 AIGSEIYKKGCGVPLAATLIGLILFRKREBQWHEVRSEIWKLPQSESSILPLRLSYH 397
DB 350 EIGRTIVQKCGVPLAINSMGSLSRKRSVRDMLAIIQNTNT---EENNTLLTVLSISK 405
QY 398 HLPLDLNQCTFYCAVFPKOTEMEKNLISLMAHGFILSKNLELENANGVNNELYLR 457
DB 406 HLPBFMOCFAFCVAFPKDYEDIDKODLHLMTISNCFISKETSDEEGNKVFFELMRS 465
QY 458 PFQIEIVKSGQ-----TYFKMDLILHDLATS-----LFSASTSSSNIR 495
DB 466 PFQNAKQRRSRKEIYGVKDTTCKIHDLMDLAIVSISGECVTLQVLVEINMKPKVH 525
QY 496 EIIYENYTHMSISGPT---KVSSYSLSHQKPSLVNLSDIKLKOLPSSI----- 545
DB 526 HLTV---PFPHPKIGFVWQRCPIRSLSFLAKRMDSMK---DVEFVVSCEVYGLAHC 577
QY 546 -----GDLVHLRYNLISGNTSIRSLPNOLCKLOVLTLDLHGCHSLCCLPKETSKL 596
DB 578 GNEIFSVEPAYMKILRYIDLSSDIKTLFPAVSAVLYNLQILMLAKRCGLTHLPDMKFM 636
QY 597 GSLNLLLDGCGYGLTCMPRIIGSLTCLKTLISRFVVGIOKSCOLGELNMLVYSIEITH 656
DB 637 ISLRHVYLDGSSLRQMPRGGLQGLSLARTLTVMYVG-NESDRRLHELKDELGLGLQHN 695
QY 657 LERKQMDAKBANLSAKENHLSLMKDD-----DERPRIYESKRYVLEALK 705
DB 696 LLLKTNPLQAEKANLENKKNLQOLALCWDSSNFTCSHSHSDEYLOLCPP--EYLDALK 753
QY 706 PHSNLTCLTIGFPGIRLPDMWNNHSLV-LKNVSTIEIISCKNCSCLPFGELPKLSIELM 764
DB 754 PPNGLKYLAKQYMGSDPFPMHMDGVTIQLNIVKLSIRASVNCVKLPYMWQJLPFLVLRK 813
QY 765 RGSAAVEVVDGFFTRRR-----PFLARKLNIREFGNLGLKKEGEE-----OCPLYE 813
DB 814 R-MERLAKYLGRYPTDEYGNQLVVFQKLKLSLEMMESLENMHEYDQQTSTVTPFLD 872
QY 814 EIEIKCCP-MVVIPLSSVKLVSGKSDAIGRSSINMLA-----TSLQIR----- 861
DB 873 AMEIIDCKLALPVPVPLIKSLSTGNKYLGLVSGISLNLVLYLGASGSSRRVRLYY 932
QY 862 -YNKE-----DASL- 869

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DB 933 IYNGEREGSTDTKDEHILPDHLISWGSILTKLHLOGFNTPAPENYKISIGHMMSYQDVLVS 992
QY 870 -----PEEMFKSL----- 877
DB 993 SCDFIOHEGLQSPLMFWISFGCLOQLEIYWCDLSTWPEEFPSRLSYLEKLFYVDCKNF 1052
QY 878 -----ANLKYNISFEYNL----- 891
DB 1053 TGVPEDLSARPSITDGGPCNLIEYQIDRCRLVVPFPIFCLRTLVTHSNVLEGLPGCF 1112
QY 892 -----KEPFSLASINAPLKHLEIHSCYALESIPERGCVGLISLTOLSI 934
DB 1113 GCQDTLTTLVLIGCPSPSSLPASIRCLSNLKSLELASNNLSLSP-BGMQVLTALKTLHF 1171
QY 935 TYCEMLQCPBGL-QHITALTNLSEVCPTLAKCEKIGEDWYKIAHP 983
DB 1172 IKCPGITALPBGLOQLRHGLQTFVEDCPALARRCRG-GDYWEKVXDIP 1220

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RESULT 14

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ID 065XG9 PRELIMINARY; PRT; 1259 AA.
AC 065XG9;
DT 25-OCT-2004 (TREMBlrel, 28, Created)
DT 25-OCT-2004 (TREMBlrel, 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel, 28, Last annotation update)
DE Putative NBS-LRR resistance protein.
GN Name=OJ1126_B11.11;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
CX NCBI_TaxID=38947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OJ1126 B11 genomic sequence."
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC105767; AAU33948.1; -
SQ SEQUENCE 1259 AA; 142923 MW; 635FD2CC81B24E7 CRC64;

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Query Match 28.5%; Score 1463.5; DB 2; Length 1259;
Beet Local Similarity 31.9%; Pred. No. 2e-74;
Matches 397; Conservative 190; Mismatches 371; Indels 287; Gaps 32;

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QY 1 MAE---AFLOVLDNLTCFIOGELGLIGFDEBEKLOSTFTTIOAVLEDAOKQOLDKXA 57
DB 1 MAELISALLPALPKKAGSISTEFSFGIEHRSELYTLILAINOVLYGAEBOASKCPA 60
QY 58 IENMLOKLNAAYEADILDECKTEAPYROKKNKY-----CYHPNVITFRHXI 106
DB 61 VKSMIAKAKMAACEADALDELHYEA-LRSEALRGHKINSVAPAFSSHNPILFKRI 119
QY 107 GKRMKTKMEKLDVIAERIKFHL-----DERTIEROVAATROGFVINEPOVYGRDKK 159
DB 120 GKRLQOIVKIDKVLQWNRFGFLNCPMPDER-----MQTVSYVDEOEVIGRQKER 171
QY 160 DEYKILINNVSNAQTLPVLPILMGSLGKTTLAQMVFNDQVIEHHPKIMICVSEDFN 219
DB 172 DEITHMLLS--AKSDOKLILPIVIGIGLKTTLAQVLVNDVKYAHFOKHMVVCSENF 229
QY 220 EKRLIKEIVESI--EEKSLGMDLAPLOKRLDLNGKYYLLVDVWNEODQKMAKLRO 277
DB 230 VPDVKGITDPAIGNDGLKSDNLELQORLRRELSQRYLLVDDVWNEBOKREALRT 289
QY 278 VLKVGASGASVLTTRLEKVSINGTLOPYELSNISOEDCMLFMQAFGHOBEINLNLV 337

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Db 290 LUCSCMGASAVVTVTRNSNVASVMGTVPDLALBQLSQEDSWTLFCERAFRTGVAKSCFV 349
QY AIGKEIVKCGVPLAATLGGIILFKREEROMEHVROSEIWKLPQESSIILPALRLSYH 397
Db 350 EIGTIVKCGVPLAATLGGIILFKREEROMEHVROSEIWKLPQESSIILPALRLSYH 405
QY 398 HLPDLROCFYCAVFPKOTEMEKGNLISLWMAHGFILSKGULEENYGENEVMNELYR 457
Db 406 HLPSPMKGCFACVFPKDEYDKNODLIHIMISNCFISKEISDLEEGNVFLEMLRS 465
QY 458 FPOEIEVKSQ-----TYRKMDLIHDLATS-----LFSASTSSNIR 495
Db 466 FFOAKQORRSKEEYIYGVKVTTCIKIDMLHDVAVISGDECYTLQMLVAINKPKVNH 525
QY 496 EIIYENYIHMMSIGFTK-----VVSYSLSL-----RVNLSDIKKOL 541
Db 526 HLV---FPHPKIGVVMORCPILRSFLHKNHMSKMDVFPWSPCALGHIHCDNERF 582
QY 542 PSSIGDLVHLRYLNLGNTSIRSLPNOCLQNLQTLDLHGCHSLCCLPKETSKLGSIRN 601
Db 583 SVEPAMGHLRYLDLS-SSDIKTLPEAVSALYNIQILMLNRCGLTHLPDGMKFMISLRH 641
QY 602 LLLDGCYGLTCMPPRIGSLTCLKTLSPFVVGIOKKSQGLGELRLNLVYGSIEITHLERVK 661
Db 642 VYLDGCSLLQMPMPGLQGLSLRLTYMVG-NSSDCLHBLKDLGKLIQIHNLLKVT 700
QY 662 NDMDAKEANLSAKENLHSLSMKMD-----DERPRIYSEKVEVLEALKPHSNL 710
Db 701 NPLQAKENLNLKKNLQOLALCWSRNFTCSHGSADBYLQCRPE-EVLDALKFPNGL 758
QY 711 TCLTRGFRGIRLDPMMNHSV-LKNVVSIEIISCKNSCLPPFELPKLSLEIMRGSAB 769
Db 759 KVLKLRQYMGSNFPMWMDGVTLQNIYKLSRGSVMCYKLPVPVQLEFLVRLKR-MER 817
QY 770 VEYVDSGPPRR-----PESLRKINIRFGLKGLKKEGSE-----QCPVLEELIK 818
Db 818 LKYLCTYRPIDEEYGNOLVVFQKTLKLSLEWESLENNHEVDTOQVTSVTFPKLDAMEII 877
QY 819 CCP-MFYPLTSSYKLVSGDSKDAIGFSSISNIML-----TSIQIR-----YNKE 865
Db 878 DCPRLTALPNVPIKLSLSTGNKYLGLVSGISNLSYIYLGASGSSRRVATLYIYNGE 937
QY 866 -----DAST----- 869
Db 938 REGSTDTEBHILPDHLLWSGLTKLHLQGFNTPAPENVKSISSGHMMSVQDLVLSCDF 997
QY 870 -----PEEMFKSL----- 877
Db 998 IQHGLQSPLMFWSFGCLQQLLEIWCDSLTFWPEEERSLTSLKFLPYDCKNFTGVP 1057
QY 878 -----ANLKYLNISFYENL----- 891
Db 1058 DRLSARSTDOGPNLEYLQIDRCPNLVVFPPTNFCIRILVITDSNVLEGLPGFGCGT 1117
QY 892 -----KELPTSLASLNAKLELHSCALLESPEBGYKGLISLTQUSTYCEM 939
Db 1118 LTTLVILGCPSSFLPASIRCLSNLKSLELTSNNLSLSP-EGQONTALTAKTLFIKCPG 1176
QY 940 LQCPBEGL-OHLTALTNLSVEFCPTLAKRCEKJGEMWYKIANHP 983
Db 1177 ITALPBGLOQRHGLQFTTVEDECPALAKRCRG-GDYWEKVDLP 1220

RESULT 15
06ZJF7
ID 06ZJF7 PRELIMINARY; PRT; 1048 AA.
AC 06ZJF7;
DT 05-JUL-2004 (Tremblere). 27, Created)
DT 05-JUL-2004 (Tremblere). 27, last sequence update)
DE Putative NBS-LRR resistance protein RGH1.
GN Name=OJ1521.G02.25;
OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoidae; Oryzae; Oryza.
OK NCBI_taxid=35947;
RN
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AP003914, BAD08985.1; -.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0042829; P:defense response to pathogen; IEA.
DR InterPro; IPR000767; Disease_resist.
DR InterPro; IPR01611; LRR.
DR Pfam; PF00560; LRR_1; 8.
DR PRINTS; PR00364; DISEASERIST.
SQ SEQUENCE 1048 AA; 119519 MW; 5D3FFCB4D055000 CRC64;
Query Match 28.0%; Score 1436; DB 2; Length 1048;
Best Local Similarity 34.4%; Pred. No. 5,7e-73;
Matches 372; Conservative 199; Mismatches 377; Indels 134; Gaps 32;
QY 1 MAEAFLOVLIDNLTCPIQGL-----GIIGFKDEFEKLGSTFTTQDAVLDAQKQIKDK 56
Db 1 MAESILLPVVRGVVGAAGALVQSVTFMCGVDDBRHKLQLALVQCKLSDAEAKSETSP 60
QY 57 ALENWLOKNAAYEADDLIDBEKTEAPTRQKK-----NKYGCYHP-VNIFPRHIGK 108
Db 61 AVKRMKMDLVAAYEADVDLDDHYEALRRDAQIGDSTDKVLGYTFPHSPILFRVAMSK 120
QY 109 RMKIMEKLDVIAERIKFHLDERTERQVATRGTFVLINEPO-----VYGRDKE 158
Db 121 KLSVLTAKINEIYVEMNKKFLVER-----ADQATVHVH-PTHSGLSLAMEI VGRDD 173
QY 159 KDEIVKILINNVNAQTLPLPLTGMGLKTTLAQVFNQDQVYIHFHFKYICVSEDF 218
Db 174 KEMVNVILLLEQRSK-RWVEVLSIVGSGLKTTLAKVNVNDTRVQRFELPMWLCVSDPE 232
QY 219 NEKRLKEIYESIEEKSIGMD-LAPLOKKRLDLNGKTYLALDVVNNEDDQKMKLRQ 277
Db 233 NVSVLRSTIELATRGNTLPDRIBELRSRLHEVVGKRYLVLDDVYMEBEKMBELR 292
QY 278 VL-KVAGSASVLTTRLEKVSIMGTLOPYELSNLSQEDCWLIFMORAFHQEETINL 336
Db 293 LHSAGAPGSVVLVTRRSORVASIMGTVPAAHTLSYLNHDSWELFKKAFSKEEQPER 352
QY 337 VAIGKEIVKCGVPLAATLGGIILFKREEROMEHVROSEIWKLPQESSIILPALRLSY 396
Db 353 AETGNRIYKCKGKPLALKTGMGLMSKRIQEWELIAGSKSWEDVGTNEIILSTIKLSY 412
QY 397 HLPDLROCFYCAVFPKOTEMEKGNLISLWMAHGFILSKGULEENYGENEVMNELYR 456
Db 413 RHLPLEMKQCFACVFPKDYMERKLVQVIMANNFIDEBGMDEEGQVFPVFNLYVR 472
QY 457 SFPQIEVKS-----QGYFK-----NHDLIHDLATSLFSASTSS--NIREIIVENYIM 505
Db 473 SFPQDVKVESFHVGIQGYKTSITCYWHDLMHDLAKSVTEECVDAQDLNOQKASKMDOVRL 532
QY 506 MSLG-----FTKVSSYSL-----SHLOKVSRLRYNLNSI-----KLQPLS 543
Db 533 MSSAKIQENSELFKHVGLPLTLLSPYWSKSSPLPR--NIKRNLVTSRLALHNDKLVNSPK 590
QY 544 SIGDLVHLRYLNLGNTSIRSLPNOCLQNLQTLDLHGCHSLCCLPKETSKLGSIRN 603
Db 591 ALASITHLRYLDLSHSHSKLHLRPSICMLYSIQALRLNCKLQIHLPEGRMRSKLRLHY 650
QY 604 LLDGCYGLTCMPPRIGSLTCLKTLSPFVVGIOKKSQGLGELRLNLVYGSIEITHLERVK 662
Db 651 LIGCHSLKQMPPRIGLQKULRTLTFFVVD-TKQGGLEBELKDLHHLGRLLEFNLKAIQS 709
QY 663 DMDAKEANLSAKENLHSLSMKMDDEDRPRIYE-----SEVYVLEALKPHSNLT 711
Db 710 GSNARBANLHIDENVTETLLHWCHD---IFEYSDDHFDLVDVNDKKEIVFSPSLPSRL 765

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